



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 119468

TO: Sean McGarry
Location: 2d19/3c18
Wednesday, April 21, 2004
Art Unit: 1635
Phone: 272-0761
Serial Number: 10 / 006430

2018

From: Jan Delaval
Location: Biotech-Chem Library
Rem 1A51
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Search Notes

6

107	15	1.0	15	1	CF313320	ACCESSION:CF313320	C 180	14	0.9	14	1	CF334281	ACCESSION:CF334281
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C 325	12	0.8	12	1	13	1	CF313356	ACCSSION:CF313356	C 398	11	0.7	11	1	CF327885	ACCSSION:CF327885

c 399 11 0.7 11 1 CF328618 ACCESSION:CF328618
 400 11 0.7 11 1 CF328619 ACCESSION:CF328619
 c 401 11 0.7 11 1 CF329242 ACCESSION:CF329242
 c 402 11 0.7 11 1 CF329344 ACCESSION:CF329344
 c 403 11 0.7 11 1 CF329345 ACCESSION:CF329345
 c 404 11 0.7 11 1 CF331049 ACCESSION:CF331049
 c 405 11 0.7 11 1 CF331066 ACCESSION:CF331066
 c 406 11 0.7 11 1 CF331814 ACCESSION:CF331814
 407 11 0.7 11 1 CF331815 ACCESSION:CF331815

ALIGNMENTS

RESULT 1
 CF302409/c
 LOCUS
 DEFINITION 7LEAF--07-N19-g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
 sativa cDNA clone 7LEAF--07-N19, mRNA sequence.

ACCESSION
 CF302409.1 GI:33674170
 VERSION
 EST.

SOURCE
 Oryza sativa
 ORGANISM
 Oryza sativa

REFERENCE
 AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

TITLE
 COMMENT 1 (bases 1 to 18)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)

CONTACT: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source

1. .18
 Location/Qualifiers
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="7LEAF--07-N19"
 /tissue_type="leaf"
 /dev_stage="7 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
 /note="Vector: PCR4-TOPO; Site:1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 1.2%; Score 18; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAATAAAAAAAAAAAAAA 1496
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 Db 18 CTAATAAAAAAAAAAAAAA 1

RESULT 2
 AZ450180
 LOCUS
 DEFINITION 1M0248K13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0248K13 R, genomic survey sequence.

ACCESSION
 AZ450180
 VERSION
 AZ450180.1 GI:10604710
 KEYWORDS
 GSS.

SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 19)

AUTHORS
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.

TITLE
 COMMENT Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL

COMMENT

Contact: Robert B. Weiss
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0248 row: K column: 13

Seq primer: CACACAGGAACACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

FEATURES

source

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 /mol_type="genomic DNA"
 /strain="C57BL/6J"
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 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 1.2%; Score 18; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAATAAAAAAAAAAAAAA 1496
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 Db 1 CTAATAAAAAAAAAAAAAA 18

RESULT 3

BQ590128/c

LOCUS

DEFINITION BQ590128 17 bp mRNA linear EST 06-DEC-2002
 E012843-024-019-E19-T7 MP12-ADIS-024-storage root Beta vulgaris
 cDNA clone 024-019-E19 3-PHIME, mRNA sequence.

ACCESSION BQ590128

VERSION BQ590128.1 GI:26119711

KEYWORDS EST.

SOURCE Beta vulgaris

ORGANISM Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;


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Db      17 TAAAAAAAAAAAAAAAAA 1
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CF336950      17 bp mRNA linear EST 18-AUG-2003
JMT--07-D04.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa cDNA clone JMT--07-D04, mRNA sequence.
CF336950
VERSION      CF336950.1 GI:33822280
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 17)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..17
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="JMT--07-D04"
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cDNA library (JMT)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match      1.1%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1480 TAAAAAAAAAAAAAAAAA 1496
|||||
Db      17 TAAAAAAAAAAAAAAAAA 1
|||||
CF301151/c
LOCUS      7LEAF--05-005.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--05-005, mRNA sequence.
CF301151
VERSION      CF301151.1 GI:33672912
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 18)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

Query Match      1.1%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1480 TAAAAAAAAAAAAAAAAA 1496
|||||
Db      17 TAAAAAAAAAAAAAAAAA 1
|||||
CF301151/c
LOCUS      7LEAF--05-005.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--05-005, mRNA sequence.
CF301151
VERSION      CF301151.1 GI:33672912
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 18)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..18
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--05-005"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/cdna_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      1.1%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1480 TAAAAAAAAAAAAAAAAA 1496
|||||
Db      18 TAAAAAAAAAAAAAAAAA 2
|||||
CF320046/c
LOCUS      HD--10-M11.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--10-M11, mRNA sequence.
CF320046
VERSION      CF320046.1 GI:33691807
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 18)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..18
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD--10-M11"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/cdna_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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/organism="Oryza sativa"
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/cultivar="Nackdong"
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/lab_host="E.coli DH10B"
/cdna_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

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Query Match 1.1%; Score 17; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAAAAAAA 1496
 |||||
 Db 17 TAAAAAAAAAAAAAAAAA 1

RESULT 9
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 DEFINITION IM0080H09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0080H09 R, genomic survey sequence.
 ACCESSION AZ345795
 VERSION AZ345795.1 GI:10425032
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 19)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0080 row: H column: 09
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers
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 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0080H09"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (GI|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

FEATURES

source
 1. .19
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0080H09"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (GI|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 1.1%; Score 17; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 44;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAAAAAAA 1496
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 Db 2 TAAAAAAAAAAAAAAAAA 18

RESULT 10
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 DEFINITION IM0520P13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0520P13 R, genomic survey sequence.
 ACCESSION AZ650575
 VERSION AZ650575.1 GI:11785200
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 19)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0520 row: P column: 13
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers
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 /mol_type="genomic DNA"
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 /db_xref="taxon:10090"
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 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
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 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (GI|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

FEATURES

source
 1. .19
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0520P13"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (GI|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 1.1%; Score 17; DB 1; Length 19;

Best Local Similarity 100.0%; Pred. No. 44;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAAAAAAA 1496
|||||
Db 2 TAAAAAATAAAAAAAAAA 18

RESULT 11
AL587759/c
LOCUS
DEFINITION AL587759 BP Chicken Brain Library EST 02-MAR-2001
ROS061G06, mRNA sequence.

ACCESSION AL587759.1 GI:13192793
VERSION
KEYWORDS
SOURCE
ORGANISM Gallus gallus (chicken)

REFERENCE
AUTHORS
TITLE BP Chicken Brain Library
JOURNAL
COMMENT Contact: Frazer Murray
Dept. Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
Email: frazer.murray@brc.ac.uk
CGCGCGCTTTT TTTT TTTT TTTT TTTT 3' Poly A RNA purchased from Clontech
(*6854-

Seq primer: M13F.
Location/Qualifiers
1..20

/organism="Gallus gallus"
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/dev stage="Unknown"
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/note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. 5' adaptor sequence: 5' TCACCTCGAG 3'; 3' adaptor sequence: 5' GCGCGCGCTTTT TTTT TTTT TTTT TTTT 3' Poly A RNA purchased from Clontech (*6854-1)"

Query Match 1.1%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAAAAAAA 1496
|||||
Db 20 TAAAAAATAAAAAAAAAA 4

RESULT 12
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DEFINITION 7LEAF--03-K09.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--03-K09, mRNA sequence.

ACCESSION CF299570.1 GI:33671331
VERSION
KEYWORDS
SOURCE
ORGANISM Oryza sativa

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0315 row: C column: 20
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1..20

/organism="Mus musculus"
/mol_type="genomic DNA"

REFERENCE 1 (bases 1 to 20)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..20
/organism="Oryza sativa"
/mol_type="mRNA"
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/db_xref="taxon:4530"
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/tissue type="leaf"
/dev stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
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Best Local Similarity 100.0%; Pred. No. 53;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAAAAAAA 1496
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Db 17 TAAAAAATAAAAAAAAAA 1

RESULT 13

AZ486784/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1..20

/organism="Mus musculus"

/mol_type="genomic DNA"

/clone="UUGC1M0315C20 F, genomic survey sequence."

/dev stage="7 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="Rice leaf plasmid cDNA library Mus musculus genomic survey sequence."

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

/tissue type="leaf"

/dev stage="7 days after germination"

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/clone_lib="Rice leaf plasmid cDNA library Mus musculus genomic survey sequence."

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

/tissue type="leaf"

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/lab_host="E.coli DH10B"

/clone_lib="Rice leaf plasmid cDNA library Mus musculus genomic survey sequence."

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

/tissue type="leaf"

/dev stage="7 days after germination"

/lab_host="E.coli DH10B"


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/db_xref="taxon:10090"
/clone="UUGC1M0315C20"
/sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (G1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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```

Query Match      1.1%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1480 TAAAAA...AAAAA 1496
Db 20 TAAAAA...AAAAA 4

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RESULT 14
AZ849506
LOCUS
DEFINITION
2M0150P21R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0150P21 R, genomic survey sequence.

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ACCESSION
AZ849506
VERSION
AZ849506.1 GI:13033596
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)

```

ORGANISM

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)

```

```

AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

```

```

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

```

JOURNAL

```

COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

```

```

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

```

```

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0150 row: P column: 21
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Class: plasmid ends
High quality sequence stop: 20.

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FEATURES

source

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/mol_type="genomic DNA"
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/sex="Male"

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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (G1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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Query Match      1.1%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1480 TAAAAA...AAAAA 1496
Db 2 TAAAAA...AAAAA 18

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RESULT 15

AZ858419

LOCUS

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DEFINITION
2M0163003R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0163003 R, genomic survey sequence.

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ACCESSION AZ858419

VERSION AZ858419.1 GI:13051545

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)

```

REFERENCE

AUTHORS

```

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

```

```

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

```

JOURNAL

COMMENT

```

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

```

```

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

```

```

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0163 row: O column: 03
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.

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FEATURES

source

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/mol_type="genomic DNA"
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/clone="UUGC2M0163003"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
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 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 53;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAA 1496
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 Db 1 TAAAAAATAAAAA 17

RESULT 16

CF291665/c
 LOCUS 19 bp mRNA linear EST 14-AUG-2003
 DEFINITION 14ROOT--02-D01.g1 Rice root plasmid cDNA library (14ROOT) Oryza sativa cDNA clone 14ROOT--02-D01, mRNA sequence.

CF291665
 VERSION GI:33660698
 KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 19)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

TITLE

CONTACT: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

Location/Qualifiers

1. .19

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

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/tissue_type="root"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="Rice root plasmid cDNA library (14ROOT)"

/note="Vector: PCR4-TOPO; Site:1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 1.1%; Score 16.4; DB 1; Length 19;
 Best Local Similarity 94.4%; Pred. No. 62;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1479 CTAAAAAATAAAAA 1496
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 Db 18 CAAAAAATAAAAA 1

RESULT 17

CF295672/c

LOCUS 19 bp mRNA linear EST 14-AUG-2003

DEFINITION 30DGS--05-L12.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza sativa cDNA clone 30DGS--05-L12, mRNA sequence.

ACCESSION CF295672

VERSION 1 GI:33664705

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 19)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

CONTACT: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

Location/Qualifiers

1. .19

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

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/dev_stage="30 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"

/note="Vector: PCR4-TOPO; Site:1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

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 Best Local Similarity 94.4%; Pred. No. 62;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1476 ATGCTAAAAAATAAAA 1493
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 Db 18 ATGTTAAAAAATAAAA 1

RESULT 18

CF298396/c

LOCUS 19 bp mRNA linear EST 15-AUG-2003

DEFINITION 7LEAF--01-M05.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--01-M05, mRNA sequence.

ACCESSION CF298396

VERSION CF298396.1 GI:33670157

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 19)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

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 /organism="Oryza sativa"
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 /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

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 Best Local Similarity 94.4%; Pred. No. 62;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1479 CTAAAAA...AAAAA 1496
 Db 19 CAAAAA...AAAAA 2

RESULT 19

CF302456/c
 LOCUS 19 bp mRNA linear EST 15-AUG-2003
 DEFINITION 7LEAF--07-P22.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
 sativa cDNA clone 7LEAF--07-P22, mRNA sequence.

ACCESSION CF302456
 VERSION CF302456.1 GI:33674217
 KEYWORDS EST.
 SOURCE Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 19)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

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 Location/Qualifiers
 /organism="Oryza sativa"
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 /clone="7LEAF--07-P22"
 /tissue_type="leaf"
 /dev_stage="7 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 1.1%; Score 16.4; DB 1; Length 19;
 Best Local Similarity 94.4%; Pred. No. 62;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match

1.1%; Score 16.4; DB 1; Length 19;
 Best Local Similarity 94.4%; Pred. No. 62;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1479 CTAAAAA...AAAAA 1496
 Db 19 CAAAAA...AAAAA 2

RESULT 20

CF327587/c
 LOCUS 19 bp mRNA linear EST 18-AUG-2003
 DEFINITION NACL--02-C04.b1 Rice callus plasmid cDNA library (NACL) Oryza
 sativa cDNA clone NACL--02-C04, mRNA sequence.

ACCESSION CF327587

VERSION CF327587.1 GI:33803426

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 19)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

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 /lab_host="E.coli DH10B"
 /clone_lib="Rice callus plasmid cDNA library (NACL)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match

1.1%; Score 16.4; DB 1; Length 19;
 Best Local Similarity 94.4%; Pred. No. 62;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1479 CTAAAAA...AAAAA 1496
 Db 18 CCAAAAAA...AAAAA 1

RESULT 21

BQ590166/c
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 DEFINITION E012844-024-019-K18-T7 MP1Z-ADIS-024-storage root Beta vulgaris
 cDNA clone 024-019-K18 3-PRIME, mRNA sequence.

ACCESSION BQ590166

VERSION BQ590166.1 GI:26119749

KEYWORDS EST.

SOURCE Beta vulgaris

ORGANISM Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Amaranthaceae; Beta.

1 (bases 1 to 16)

AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL Plant J. 32 (5), 845-857 (2002)

MEDLINE 22362189

PUBMED 12472698

COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@piz-koeln.mpg.de
Insert Length: 16 Std Error: 0.00
Plate: 19 row: K column: 18
Seq primer: T7; GTAATACGACTACTATAGGCG.
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/db_xref="taxon:161934"
/clone="024-019-K18"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

FEATURES
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Query Match 1.1%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
Db 16 AAAAAAAAAAAAAA 1

RESULT 22
BQ590507/c
LOCUS E012844-024-019-M04-T7 MPIZ-ADIS-024-storage root Beta vulgaris
DEFINITION cDNA clone 024-019-M04 3-PRIME, mRNA sequence.
ACCESSION BQ590507
VERSION BQ590507.1 GI:26120090
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 16)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)

JOURNAL MEDLINE 22362189

PUBMED 12472698

COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPZ

Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@piz-koeln.mpg.de
Insert Length: 16 Std Error: 0.00
Plate: 19 row: M column: 04
Seq primer: T7; GTAATACGACTACTATAGGCG.
Location/Qualifiers
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line)"
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/clone_lib="MPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 1.1%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAAA 1495
Db 16 TAAAAAAAAAAAAA 1

RESULT 23
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DEFINITION vulgaris cDNA clone 024-028-F08 5-PRIME, mRNA sequence.
ACCESSION BQ592600
VERSION BQ592600.1 GI:26122183
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 16)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)

JOURNAL MEDLINE 22362189

PUBMED 12472698

COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@piz-koeln.mpg.de
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Seq primer: SP6r; ATTAGGTGACACTATAGAAGA.
Location/Qualifiers
1. .16
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/notes="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      1.1%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1496
Db 1 AAAAAAAAAAAAAA 16

RESULT 24
BQ592965/c
LOCUS
DEFINITION
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cDNA clone 024-028-A01 3-PRIME, mRNA sequence.
ACCESSION
BQ592965
VERSION
BQ592965.1 GI:26122548
KEYWORDS
EST.
SOURCE
Beta vulgaris
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE
1 (bases 1 to 16)
Herrig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M.,
Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
and Radelof, U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
JOURNAL
MEDLINE
22362189
PUBMED
12472698
COMMENT
Contact: Weisshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 16 Std Error: 0.00
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Seq primer: T7; GTAATACGACTCTACTATAGGC.
Location/Qualifiers
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cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

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cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      1.1%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1496
Db 16 AAAAAAAAAAAAAA 1

RESULT 25
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DEFINITION
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cDNA clone 024-022-P02 3-PRIME, mRNA sequence.
ACCESSION
BQ595369
VERSION
BQ595369.1 GI:26124952
KEYWORDS
EST.
SOURCE
Beta vulgaris
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE
1 (bases 1 to 16)
Herrig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M.,
Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
and Radelof, U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
JOURNAL
MEDLINE
22362189
PUBMED
12472698
COMMENT
Contact: Weisshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 16 Std Error: 0.00
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Location/Qualifiers
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/clone_lib="MP1Z-ADIS-024-developing root"
/notes="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

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Query Match      1.1%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAAA 1495
Db 16 TAAAAAAAAAAAAA 1

RESULT 26
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LOCUS
DEFINITION      BQ595717 16 bp mRNA linear EST 06-DEC-2002
CDNA clone 024-022-H07-SP6 MP12-ADIS-024-developing root Beta vulgaris
ACCESSION      BQ595717
VERSION
KEYWORDS
SOURCE
ORGANISM      Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE
AUTHORS      Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE      Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL      Plant J. 32 (5), 845-857 (2002)
MEDLINE
PUBMED      12472698
COMMENT      Contact: Weisshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@piz-koeln.mpg.de
Insert length: 16 Std Error: 0.00
Plate: 22 Row: H column: 07
Seq primer: SP6; CATACGATTAGGTGACACTATAG.
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/clone="024-022-H07"
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/lab_host="EMDH10B"
/clone_lib="MP12-ADIS-024-developing root"
/notes="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      1.1%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
Db 1 AAAAAAAAAAAAAA 16

RESULT 27
BQ595717
LOCUS
DEFINITION      BQ595717 16 bp mRNA linear EST 14-AUG-2003
CDNA clone 024-022-H07 5-PRIME, mRNA sequence.
ACCESSION      BQ595717
VERSION
KEYWORDS
SOURCE
ORGANISM      Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
LOCATION/Qualifiers
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/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
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/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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Best Local Similarity 100.0%; Pred. No. 41;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
Db 16 AAAAAAAAAAAAAA 1

RESULT 28
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LOCUS
DEFINITION      CF296130 16 bp mRNA linear EST 14-AUG-2003
30DGS--06-F22.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
sativa cDNA clone 30DGS--06-F22, mRNA sequence.
ACCESSION      CF296130
VERSION
KEYWORDS
SOURCE
ORGANISM      Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
LOCATION/Qualifiers
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/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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Email: bhnaheggbio.com, bhnaheggbio.myongji.ac.kr.
Location/Qualifiers
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match
Best Local Similarity 100.0%; Pred. No. 41;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAAA 1495
Db 16 TAAAAAATAAAAAA 1

RESULT 29
CF311057/c
LOCUS
DEFINITION
ABF--06-C03.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--06-C03, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 16)
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnaheggbio.com, bhnaheggbio.myongji.ac.kr.

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derived from rice Histone Deacetylase overexpression
line."

Query Match
Best Local Similarity 100.0%; Pred. No. 41;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 16 TAAAAAATAAAAAA 1

RESULT 31
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DEFINITION
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library (HD) Oryza sativa cDNA clone HD--02-001, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 16)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnaheggbio.com, bhnaheggbio.myongji.ac.kr.

FEATURES
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/notes="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
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line."

Query Match
Best Local Similarity 100.0%; Pred. No. 41;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 TAAAAAATAAAAAA 1496
Db 16 TAAAAAATAAAAAA 1496

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JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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  derived from rice Histone Deacetylase overexpression
  line."

Query Match      1.1%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAAAAAA 1496
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Db

RESULT 33
CF315789/c
LOCUS
DEFINITION      HD--04-N10.g1 OshDAC1-overexpressing transgenic rice plasmid
CDNA library (HD)
ACCESSION      CF315789
VERSION
KEYWORDS
SOURCE
ORGANISM
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 16)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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  derived from rice Histone Deacetylase overexpression
  line."

Query Match      1.1%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAAAAAA 1496
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        16 AAAAAAAAAAAAAAAAAA 1

Db

RESULT 34
CF317718/c
LOCUS
DEFINITION      HD--07-I05.g1 OshDAC1-overexpressing transgenic rice plasmid
CDNA library (HD)
ACCESSION      CF317718
VERSION
  
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treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      1.1%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAAAAAA 1496
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Db

RESULT 33
CF316056/c
LOCUS
DEFINITION      HD--05-D07.b1 OshDAC1-overexpressing transgenic rice plasmid
CDNA library (HD)
ACCESSION      CF316056
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 16)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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  /db_xref="taxon:4530"
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  /tissue_type="callus"
  /dev_stage="proliferated callus on 2N6 media for 2 weeks"
  /lab_host="E.coli DH10B"
  /clone_lib="OshDAC1-overexpressing transgenic rice plasmid
  cDNA library (HD)"
  /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
  treated with ABA(20um) for 1hr. Oligo-capped mRNA was
  reverse transcribed and then used for PCR. mRNA was
  derived from rice Histone Deacetylase overexpression
  line."

Query Match      1.1%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAAAAAA 1496
        |||
        16 AAAAAAAAAAAAAAAAAA 1

Db

RESULT 34
CF317718/c
LOCUS
DEFINITION      HD--07-I05.g1 OshDAC1-overexpressing transgenic rice plasmid
CDNA library (HD)
ACCESSION      CF317718
VERSION
  
```



```

RESULT 37
CF329320/c
LOCUS       16 bp      mRNA      linear      EST 18-AUG-2003
DEFINITION   NACL--04-J17.bi Rice callus plasmid cDNA library (NACL) Oryza
              sativa cDNA clone NACL--04-J17, mRNA sequence.
ACCESSION   CF329320
VERSION     CF329320.1  GI:33806877
KEYWORDS    EST.
SOURCE      Oryza sativa
            Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 16)
AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL    Unpublished (2003)
COMMENT    Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
     source           1..16
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--04-J17"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

Query Match      1.1%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1480 TAAAAAATAAAAA 1495
Db      16 TAAAAAATAAAAA 1

RESULT 38
CF333386
LOCUS       16 bp      mRNA      linear      EST 18-AUG-2003
DEFINITION   JMT--02-E05.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
              library (JMT) Oryza sativa cDNA clone JMT--02-E05, mRNA sequence.
ACCESSION   CF333386
VERSION     CF333386.1  GI:33815044
KEYWORDS    EST.
SOURCE      Oryza sativa
            Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 16)
AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL    Unpublished (2003)
COMMENT    Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355

```

```

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
     source           1..16
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="JMT--02-E05"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     prepared from Arabidopsis Jasmonate Carboxyl
                     methyltransferase overexpression line."

Query Match      1.1%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAATAAAAA 1496
Db      1 AAAAAAATAAAAA 16

RESULT 39
BQ590687
LOCUS       17 bp      mRNA      linear      EST 06-DEC-2002
DEFINITION   S013717-024-018-B24-T7 MP12-ADIS-024-storage root Beta vulgaris
              cDNA clone 024-018-B24 3-PRIME, mRNA sequence.
ACCESSION   BQ590687
VERSION     BQ590687.1  GI:26120270
KEYWORDS    EST.
SOURCE      Beta vulgaris
            Beta vulgaris
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1 (bases 1 to 17)
AUTHORS    Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
TITLE      Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
            Plant J. 32 (5), 845-857 (2002)
JOURNAL    22362189
MEDLINE   12472698
PUBMED    12472698
COMMENT    Contact: Weisshaar B
            ADIS DNA core facility at MP1Z
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaar@mpiz-koeln.mpg.de
            Insert Length: 17 Std Error: 0.00
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            Seq primer: T7; GTAATACGACCTCATATAGGCG.

FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:189432"
                     /db_xref="taxon:161934"
                     /clone="024-018-B24"
                     /tissue_type="storage root"
                     /lab_host="EMDH10B"
                     /clone_lib="MP12-ADIS-024-storage root"
                     /note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:

```

b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:
 SP6-Sali-CCACGCGTCGCG-3prime-cDNA-polyA-CC-NotI-T7; Note:
 Sequencing granted in the context of the GABI-Beet
 project, local PI: Dr. Katharina Schneider, coordinator:
 Prof. Christian Jung; Sequence submission managed by
 RZPD/GABI-Primary database: <http://gabi.rzpd.de>

Query Match 1.1%; Score 16; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
 |||||
 Db 1 AAAAAAAAAAAAAA 16

RESULT 40

LOCUS BQ591177/c

DEFINITION E012715-024-017-B22-T7 MP1Z-ADIS-024-storage root Beta vulgaris
 cDNA clone 024-017-B22 3-PRIME, mRNA sequence.

ACCESSION BQ591177

VERSION BQ591177.1

KEYWORDS GI:26120760

SOURCE Beta vulgaris

ORGANISM Beta vulgaris

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

1 (bases 1 to 17)

Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M.,

Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.

and Radelof, U.

Construction of a 'unigene' cDNA clone set by oligonucleotide

fingerprinting allows access to 25 000 potential sugar beet genes

Plant J. 32 (5), 845-857 (2002)

22362189

12472698

COMMENT Contact: Weisshaar B

ADIS DNA core facility at MP1Z

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weisshaar@piz-koeln.mpg.de

Insert Length: 17 Std Error: 0.00

Plate: 17 row: B column: 22

Seq primer: T7; GTAATACGACTACTATAGGC.

Location/Qualifiers

1. .17

/organism="Beta vulgaris"

/mol_type="mRNA"

/cultivar="KWS2320 (double haploid, monogerm breeding

line)"

/db_xref="GABI:188948"

/db_xref="taxon:161934"

/clone="024-017-B22"

/tissue_type="storage root"

/lab_host="EMDH10B"

/clone_lib="MP1Z-ADIS-024-storage root"

/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;

cDNA library from sugar beet, library provided by KWS

Kleinwanzlebener Saatgut AG Einbeck, Germany, contact:

b.schulz@kws.de; cloning sites Sali-NotI, primer sites and

orientation:

SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:

Sequencing granted in the context of the GABI-Beet

project, local PI: Dr. Katharina Schneider, coordinator:

Prof. Christian Jung; Sequence submission managed by

RZPD/GABI-Primary database: <http://gabi.rzpd.de>

Query Match

1.1%; Score 16; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 52;

LOCUS

CF290854/c

17 bp mRNA linear EST 14-AUG-2003

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496

|||||

Db 17 AAAAAAAAAAAAAA 2

RESULT 41

LOCUS BQ591181/c

DEFINITION E012715-024-017-H16-T7 MP1Z-ADIS-024-storage root Beta vulgaris

cDNA clone 024-017-H16 3-PRIME, mRNA sequence.

ACCESSION BQ591181

VERSION BQ591181.1

KEYWORDS GI:26120764

SOURCE Beta vulgaris

ORGANISM Beta vulgaris

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

1 (bases 1 to 17)

Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M.,

Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.

and Radelof, U.

Construction of a 'unigene' cDNA clone set by oligonucleotide

fingerprinting allows access to 25 000 potential sugar beet genes

Plant J. 32 (5), 845-857 (2002)

22362189

12472698

COMMENT Contact: Weisshaar B

ADIS DNA core facility at MP1Z

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weisshaar@piz-koeln.mpg.de

Insert Length: 17 Std Error: 0.00

Plate: 17 row: H column: 16

Seq primer: T7; GTAATACGACTACTATAGGC.

Location/Qualifiers

1. .17

/organism="Beta vulgaris"

/mol_type="mRNA"

/cultivar="KWS2320 (double haploid, monogerm breeding

line)"

/db_xref="GABI:188932"

/db_xref="taxon:161934"

/clone="024-017-H16"

/tissue_type="storage root"

/lab_host="EMDH10B"

/clone_lib="MP1Z-ADIS-024-storage root"

/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;

cDNA library from sugar beet, library provided by KWS

Kleinwanzlebener Saatgut AG Einbeck, Germany, contact:

b.schulz@kws.de; cloning sites Sali-NotI, primer sites and

orientation:

SP6-Sali-CCACGCGTCGCG-3prime-cDNA-polyA-CC-NotI-T7; Note:

Sequencing granted in the context of the GABI-Beet

project, local PI: Dr. Katharina Schneider, coordinator:

Prof. Christian Jung; Sequence submission managed by

RZPD/GABI-Primary database: <http://gabi.rzpd.de>

Query Match

1.1%; Score 16; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 52;

LOCUS

CF290854/c

17 bp mRNA linear EST 14-AUG-2003

QY 1480 TAAAAAAAAAAAAA 1495

|||||

Db 16 TAAAAAAAAAAAAA 1

RESULT 42

LOCUS CF290854/c


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LOCUS       CF299639                17 bp    mRNA    linear    EST 15-AUG-2003
DEFINITION   7LEAF--03-L20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
VERSION      CF299639
SOURCE       CF299639.1 GI:33671400
ORGANISM     Oryza sativa
REFERENCE    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS      Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzaceae; Oryza.
              1 (bases 1 to 17)
              Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
              Large-scale Sequencing Analysis of Rice ESTs
              Unpublished (2003)
              Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES             source
     source
     1..17
     /organism="Oryza sativa"
     /mol_type="mRNA"
     /cultivar="Nackdong"
     /db_xref="taxon:4530"
     /clone="7LEAF--03-L20"
     /tissue_type="leaf"
     /dev_stage="7 days after germination"
     /lab_host="E.coli DH10B"
     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
     /notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
     with oligoribonucleotides and then used as templates for
     RT-PCR."

Query Match      1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAAA 1496
Db      16 AAAAAAAAAAAAAAA 1

RESULT 46
CF302447/c
LOCUS       CF302447                17 bp    mRNA    linear    EST 15-AUG-2003
DEFINITION   7LEAF--07-P11.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
VERSION      CF302447
SOURCE       CF302447.1 GI:33674208
ORGANISM     Oryza sativa
REFERENCE    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS      Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzaceae; Oryza.
              1 (bases 1 to 17)
              Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
              Large-scale Sequencing Analysis of Rice ESTs
              Unpublished (2003)
              Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES             source
     source
     1..17
     /organism="Oryza sativa"
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     /tissue_type="leaf"
     /dev_stage="14 days after germination"
     /lab_host="E.coli DH10B"
     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
     /notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
     with oligoribonucleotides and then used as templates for
     RT-PCR."

Query Match      1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAAA 1496
Db      16 AAAAAAAAAAAAAAA 1

RESULT 46
CF302447/c
LOCUS       CF302447                17 bp    mRNA    linear    EST 15-AUG-2003
DEFINITION   7LEAF--07-P11.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
VERSION      CF302447
SOURCE       CF302447.1 GI:33674208
ORGANISM     Oryza sativa
REFERENCE    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS      Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzaceae; Oryza.
              1 (bases 1 to 17)
              Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
              Large-scale Sequencing Analysis of Rice ESTs
              Unpublished (2003)
              Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES             source
     source
     1..17
     /organism="Oryza sativa"
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     /tissue_type="leaf"
     /dev_stage="14 days after germination"
     /lab_host="E.coli DH10B"
     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
     /notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
     with oligoribonucleotides and then used as templates for
     RT-PCR."

Query Match      1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAAA 1496
Db      17 AAAAAAAAAAAAAAA 2

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/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="7LEAF--07-P11"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAAA 1496
Db      16 AAAAAAAAAAAAAAA 1

RESULT 47
CF310219/c
LOCUS       CF310219                17 bp    mRNA    linear    EST 15-AUG-2003
DEFINITION   ABF--04-M02.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--04-M02, mRNA sequence.
VERSION      CF310219
SOURCE       CF310219.1 GI:33681980
ORGANISM     Oryza sativa
REFERENCE    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS      Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzaceae; Oryza.
              1 (bases 1 to 17)
              Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
              Large-scale Sequencing Analysis of Rice ESTs
              Unpublished (2003)
              Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES             source
     source
     1..17
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     /mol_type="mRNA"
     /cultivar="Nackdong"
     /db_xref="taxon:4530"
     /clone="ABF--04-M02"
     /tissue_type="leaf"
     /dev_stage="14 days after germination"
     /lab_host="E.coli DH10B"
     /clone_lib="ABF3-overexpressing transgenic rice plasmid
     cDNA library (ABF)"
     /notes="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
     for 2hrs. Oligo-capped mRNA was reverse transcribed and
     then used for PCR. mRNA was prepared from ABA-responsive
     element binding transcription factor 3 overexpression
     line."

Query Match      1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAAA 1496
Db      17 AAAAAAAAAAAAAAA 2

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RESULT 48
CF311499/c
LOCUS
DEFINITION
ABF--06-L20.b1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--06-L20, mRNA sequence.
ACCESSION
CF311499
VERSION
CF311499.1 GI:33683260
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 17)
/lab_host="E.coli DH10B"
/dev_stage="14 days after germination"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."
REFERENCE
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..17
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="ABF--06-L20"
/tissue_type="leaf"
/lab_host="E.coli DH10B"
/dev_stage="14 days after germination"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."
FEATURES
source
Query Match 1..18; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1480 TAAAAAAAAAAAAA 1495
Db 16 TAAAAAAAAAAAAA 1
RESULT 49
CF313013/c
LOCUS
DEFINITION
ABF--08-P19.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--08-P19, mRNA sequence.
ACCESSION
CF313013
VERSION
CF313013.1 GI:33684774
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 17)
/lab_host="E.coli DH10B"
/dev_stage="14 days after germination"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."
REFERENCE
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..17
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="ABF--06-L20"
/tissue_type="leaf"
/lab_host="E.coli DH10B"
/dev_stage="14 days after germination"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."
FEATURES
source
Query Match 1..18; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1480 TAAAAAAAAAAAAA 1495
Db 16 TAAAAAAAAAAAAA 1

```

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES source

1..17
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="ABF--08-P19"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 1..18; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
Db 16 AAAAAAAAAAAAAA 1

RESULT 50 CF319075/c

LOCUS
DEFINITION
HD--09-H06.g1 OshDACL-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--09-H06, mRNA sequence.

ACCESSION
CF319075
VERSION
CF319075.1 GI:33690836
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE AUTHORS

1 (bases 1 to 17)
Song,S.I., Kim,J.K., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Kim,J.S., Jun,K.M., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES source

1..17
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD--09-H06"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDACL-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was

derived from rice Histone Deacetylase overexpression line."

Query Match 1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1480 TAAAAAATAAAAAAAAAA 1495
DB 16 TAAAAAATAAAAAAAAAA 1

RESULT 51
CF334566/c
LOCUS
DEFINITION
JMT--03-013.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa cDNA clone JMT-03-013, mRNA sequence.
CF334566
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Erihartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .17
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="JMT-03-013"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."
Query Match 1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1481 AAAAAAATAAAAAAAAAA 1496
DB 17 AAAAAAATAAAAAAAAAA 2

RESULT 52
AL048754
LOCUS
DEFINITION
DKFZ566L173_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
AL048754
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Koehler, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
EST (Koehler, et al.)
Unpublished (1999)
Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES
source
1. .18
Location/Qualifiers

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZ566L173"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="Xl-2blue"
/clone_lib="566 (synonym: hfkd2)"
/notes="Vector: pAMPl; Site 1: NotI; Site 2: SalI"

Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1481 AAAAAAATAAAAAAAAAA 1496
DB 3 AAAAAAATAAAAAAAAAA 18

RESULT 53
BQ582676/c
LOCUS
DEFINITION
R01281-024-007-P18-SP6 MP1Z-ADIS-024-inflorescence Beta vulgaris
cDNA clone 024-007-P18 5-PRIME, mRNA sequence.
BQ582676
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Beta vulgaris
Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT
Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M.,
Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
and Radelof, U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
22362189
12472698
Contact: Weishaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mpiz-koeln.mpg.de
Insert Length: 18 Std Error: 0.00
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Seq primer: SP6; CATACGATTAGTGACACTATAG.

FEATURES
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1. .18
Location/Qualifiers
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/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:184018"
/db_xref="taxon:161934"
/clone="024-007-P18"
/tissue_type="inflorescence"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-inflorescence"

/notes=Vector: pCWSVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:
 SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 1.1%; Score 16; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 64;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
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 Db 18 AAAAAAAAAAAAAA 3

RESULT 54
 BQ590027/c
 LOCUS
 DEFINITION 18 bp mRNA linear EST 06-DEC-2002
 cDNA clone 024-019-E24 T7 MP1Z-ADIS-024-storage root Beta vulgaris
 cDNA clone 024-019-E24 3-PRIME, mRNA sequence.

ACCESSION BQ590027
 VERSION BQ590027
 KEYWORDS EST.

SOURCE Beta vulgaris
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

REFERENCE 1 (bases 1 to 18)
 AUTHORS Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M., Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H. and Radelof, U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL MEDLINE
 PUBMED 22362189
 COMMENT 12472698

CONTACT: Weisshaar B
 ADIS DNA core facility at MP1Z
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851
 Email: weisshaar@mpiz-koeln.mpg.de
 Insert Length: 18 Std Error: 0.00
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 Seq primer: T7; GTAATACGACTACTATAGGCG.

FEATURES
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 1..18
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 /db_xref="GABI:190095"
 /db_xref="taxon:161934"
 /clone="024-019-E24"
 /tissue_type="storage root"
 /lab_host="EMDH10B"
 /clone_lib="MP1Z-ADIS-024-storage root"

/notes=Vector: pCWSVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:
 SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 1.1%; Score 16; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 64;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
 |||||
 Db 18 AAAAAAAAAAAAAA 3

RESULT 55
 CF277873/c
 LOCUS
 DEFINITION 18 bp mRNA linear EST 14-AUG-2003
 14ETL--03-J04.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
 Oryza sativa cDNA clone 14ETL--03-J04, mRNA sequence.

ACCESSION CF277873
 VERSION CF277873.1
 KEYWORDS GI:33655259
 SOURCE EST.

ORGANISM Oryza sativa
 Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoidae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 18)
 AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)

TITLE Contact: Nahm B.H.
 JOURNAL Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 COMMENT Yongsin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@bio.myongji.ac.kr.

FEATURES
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 1..18
 Location/Qualifiers
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
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 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice etiolated leaf plasmid cDNA library (14ETL)"

/note=Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 1.1%; Score 16; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 64;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
 |||||
 Db 18 AAAAAAAAAAAAAA 3

RESULT 56
 CF297446/c
 LOCUS
 DEFINITION 18 bp mRNA linear EST 14-AUG-2003
 30DGS--08-F02.g1 Rice leaf plasmid cDNA library 1 (30DGS) Oryza
 sativa cDNA clone 30DGS--08-F02, mRNA sequence.

ACCESSION CF297446
 VERSION CF297446.1
 KEYWORDS GI:33666479
 SOURCE EST.

ORGANISM Oryza sativa
 Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoidae; Oryzaceae; Oryza.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 18)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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Location/Qualifiers
1..18
/organism="Oryza sativa"
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/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--03-M14"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
|||||
Db 18 AAAAAAAAAAAAAA 3

RESULT 60
CF300456/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CF300456 18 bp mRNA linear EST 15-AUG-2003
7LEAF--04-N23.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--04-N23, mRNA sequence.

CF300456
CF300456.1 GI:33672217
EST.
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 18)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..18
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--04-N23"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
|||||
Db 16 AAAAAAAAAAAAAA 1

RESULT 61
CF301057/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CF301057 18 bp mRNA linear EST 15-AUG-2003
7LEAF--05-M05.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--05-M05, mRNA sequence.

CF301057
CF301057.1 GI:33672818
EST.
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 18)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..18
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--05-M05"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
|||||
Db 17 AAAAAAAAAAAAAA 2

RESULT 62
CF301325/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CF301325 18 bp mRNA linear EST 15-AUG-2003
7LEAF--06-C12.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--06-C12, mRNA sequence.

CF301325
CF301325.1 GI:33673086
EST.
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzae; Oryza.
 1 (bases 1 to 18)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1. .18
 Location/Qualifiers
 /organism="Oryza sativa"
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 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="7LEAF--06-C12"
 /tissue_type="leaf"
 /dev_stage="7 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
 /notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."
 Query Match 1.1%; Score 16; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 64;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1481 AAAAAAAAAAAAAA 1496
 |||||
 Db 18 AAAAAAAAAAAAAA 3

RESULT 63

CF301760/c

LOCUS 18 bp mRNA linear EST 15-AUG-2003
 DEFINITION 7LEAF--06-L22.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
 sativa cDNA clone 7LEAF--06-L22, mRNA sequence.

ACCESSION CF301760

VERSION CF301760.1 GI:33673521

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzae; Oryza.

REFERENCE 1 (bases 1 to 18)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1. .18
 Location/Qualifiers
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="7LEAF--06-L22"
 /tissue_type="leaf"
 /dev_stage="7 days after germination"
 /lab_host="E.coli DH10B"

/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

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 Best Local Similarity 100.0%; Pred. No. 64;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496

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Db 18 AAAAAAAAAAAAAA 3

RESULT 64

CF309376/c

LOCUS 18 bp mRNA linear EST 15-AUG-2003
 DEFINITION ABF--03-I19.b1 ABF3-overexpressing transgenic rice plasmid cDNA
 library (ABF) Oryza sativa cDNA clone ABF--03-I19, mRNA sequence.

ACCESSION CF309376

VERSION CF309376.1 GI:33681137

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzae; Oryza.

REFERENCE 1 (bases 1 to 18)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1. .18
 Location/Qualifiers
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="ABF--03-I19"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="ABF3-overexpressing transgenic rice plasmid
 cDNA library (ABF)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
 for 2hrs. Oligo-capped mRNA was reverse transcribed and
 then used for PCR. mRNA was prepared from ABA-responsive
 element binding transcription factor 3 overexpression
 line."

Query Match 1.1%; Score 16; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 64;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAAA 1495

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Db 16 TAAAAAAAAAAAAA 1

RESULT 65

CF320418/c

LOCUS 18 bp mRNA linear EST 15-AUG-2003
 DEFINITION HD--11-E22.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
 library (HD) Oryza sativa cDNA clone HD--11-E22, mRNA sequence.

ACCESSION CF320418

VERSION CF320418.1 GI:33692179


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LOCUS      BE230585              15 bp      mRNA      linear      EST 07-JUL-2000
DEFINITION 99AS799 Rice Seedling Lambda ZAPII cDNA Library Oryza sativa
(indica cultivar-group) cDNA clone 99AS799, mRNA sequence.
ACCESSION  BE230585
VERSION     BE230585.1 GI:8956782
KEYWORDS
SOURCE      Oryza sativa (indica cultivar-group)
            Oryza sativa (indica cultivar-group)
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 15)
AUTHORS    Lee,M.C., Shin,Y.C., Lee,T.H., Jeong,S.H., Kim,J.K., Eun,M.Y. and
            Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of ESTs from Rice Seedling
JOURNAL     Unpublished (1999)
COMMENT     Contact: Eun M.Y.
            Department of Cytogenetics
            National Inst. of Agri. Sci. and Tech, RDA
            Suwon, Kyunggido, Korea
            Tel: 82 331 290 0301
            Fax: 82 331 290 0307
            Email: myeun@sun20.asti.re.kr.
            Location/Qualifiers
FEATURES             1..15
source              1..15
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                    /mol_type="mRNA"
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                    /clone="99AS799"
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                    /lab_host="E. coli SOLR"
                    /clone_lib="Rice Seedling Lambda ZAPII cDNA Library"
                    /notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
                    XhoI; Directional cDNA library inserted into lambda ZAPII
                    vector at 5' end with EcoRI and 3' end with Xho I site"

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Best Local Similarity 100.0%; Pred. No. 58;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAA 1495
Db      1 AAAAAAAAAAAAAA 15

RESULT 72
BQ582543/c
LOCUS      BQ582543              15 bp      mRNA      linear      EST 06-DEC-2002
DEFINITION 'S013300-024-007-B02-T7 MP1Z-ADIS-024-inflorescence Beta vulgaris
cDNA clone 024-007-B02 3-PRIME, mRNA sequence.
ACCESSION  BQ582543
VERSION     BQ582543.1 GI:26112120
KEYWORDS
SOURCE      Beta vulgaris
            Beta vulgaris
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1 (bases 1 to 15)
AUTHORS    Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
TITLE      Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL     Plant J. 32 (5), 845-857 (2002)
MEDLINE    22362189
PUBMED     12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MP1Z
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851

Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAA 1495
Db      1 AAAAAAAAAAAAAA 15

RESULT 73
BQ585820/c
LOCUS      BQ585820              15 bp      mRNA      linear      EST 06-DEC-2002
DEFINITION 'S012533-024-014-H17-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone
024-014-H17 5-PRIME, mRNA sequence.
ACCESSION  BQ585820
VERSION     BQ585820.1 GI:26115402
KEYWORDS
SOURCE      Beta vulgaris
            Beta vulgaris
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1 (bases 1 to 15)
AUTHORS    Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
TITLE      Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL     Plant J. 32 (5), 845-857 (2002)
MEDLINE    22362189
PUBMED     12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MP1Z
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851

```

```

Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 15 Std Error: 0.00
Plate: 7 Row: B Column: 02
Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             1..15
source              1..15
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                    line)"
                    /db_xref="GABI:184162"
                    /db_xref="taxon:161934"
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                    /lab_host="EMDH10B"
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                    /note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
                    cDNA library from sugar beet, library provided by KWS
                    Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
                    b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                    orientation:
                    SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
                    Sequencing granted in the context of the GABI-Best
                    Project, local PI: Dr. Katharina Schneider, coordinator:
                    Prof. Christian Jung; Sequence submission managed by
                    RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAA 1495
Db      15 AAAAAAAAAAAAAA 1

RESULT 73
BQ585820/c
LOCUS      BQ585820              15 bp      mRNA      linear      EST 06-DEC-2002
DEFINITION 'S012533-024-014-H17-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone
024-014-H17 5-PRIME, mRNA sequence.
ACCESSION  BQ585820
VERSION     BQ585820.1 GI:26115402
KEYWORDS
SOURCE      Beta vulgaris
            Beta vulgaris
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1 (bases 1 to 15)
AUTHORS    Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
TITLE      Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL     Plant J. 32 (5), 845-857 (2002)
MEDLINE    22362189
PUBMED     12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MP1Z
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaar@mpiz-koeln.mpg.de
            Insert Length: 15 Std Error: 0.00
            Plate: 14 Row: H Column: 17
            Seq primer: SP6; CATACGATTGATGTCGACACTATAG.
FEATURES             1..15
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/notes="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-SALI-CCACGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database:http://gabi.rzpd.de"

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 74
BO590410/c 15 bp mRNA linear EST 06-DEC-2002
LOCUS
DEFINITION E012844-024-019-M08-T7 MP1Z-ADIS-024-storage root Beta vulgaris
cDNA clone 024-019-M08 3-PRIME, mRNA sequence.
ACCESSION BO590410
VERSION
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 15)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE Construction of a 'unigenes' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@piz-koeln.mpg.de
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Seq primer: T7: GTAATACGACTCTACTATAGGC.

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line)"
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/clone="024-019-M08"
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/clone lib="MPIZ-ADIS-024-storage root"
/notes="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-SALI-CCACGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database:http://gabi.rzpd.de"

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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orientation:
SP6-SALI-CCACGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 75
BO590656/c 15 bp mRNA linear EST 06-DEC-2002
LOCUS
DEFINITION S015086-024-018-L13-SP6 MP1Z-ADIS-024-storage root Beta vulgaris
cDNA clone 024-018-L13 5-PRIME, mRNA sequence.
ACCESSION BO590656
VERSION
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Anaranthaceae; Beta.
REFERENCE 1 (bases 1 to 15)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE Construction of a 'unigenes' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@piz-koeln.mpg.de
Insert Length: 15 Std Error: 0.00
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Seq primer: SP6: CATACGATTAGTGCACACTATAG.

FEATURES
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/tissue type="storage root"
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/clone lib="MPIZ-ADIS-024-storage root"
/notes="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-SALI-CCACGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      15 AAAAAAAAAAAAAA 1

RESULT 76
BQ591170/c
LOCUS
DEFINITION
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CDNA clone 024-017-N18 3-PRIME, mRNA sequence.
ACCESSION
BQ591170
VERSION
BQ591170.1 GI:26120753
KEYWORDS
EST.
SOURCE
Beta vulgaris
ORGANISM
Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE
1 (bases 1 to 15)
AUTHORS
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL
MEDLINE
22362189
PUBMED
12472698
COMMENT
Contact: Weisshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 15 Std Error: 0.00
Plate: 17 row: N column: 18
Seq primer: T7; GTAATACGACTCATTATAGGCG.
FEATURES
Location/Qualifiers
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/cultivar="KWS2320 (double haploid, monogerm breeding
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/clone="024-017-N18"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-storage root"
/notes="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatgut AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Best
Project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"
Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAA 1495
Db      15 AAAAAAAAAAAAAA 1

RESULT 77
BQ591170/c
LOCUS
DEFINITION
E012715-024-017-F22-T7 MP1Z-ADIS-024-storage root Beta vulgaris
CDNA clone 024-017-F22 3-PRIME, mRNA sequence.
ACCESSION
BQ591170
VERSION
BQ591170.1 GI:26120761
KEYWORDS
EST.
SOURCE
Beta vulgaris
ORGANISM
Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE
1 (bases 1 to 15)
AUTHORS
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL
MEDLINE
22362189
PUBMED
12472698
COMMENT
Contact: Weisshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 15 Std Error: 0.00
Plate: 17 row: F column: 22
Seq primer: T7; GTAATACGACTCATTATAGGCG.
FEATURES
Location/Qualifiers
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/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
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/db_xref="GABI:188949"
/db_xref="taxon:161934"
/clone="024-017-F22"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-storage root"
/notes="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatgut AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Best
Project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"
Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAA 1495
Db      15 AAAAAAAAAAAAAA 1

RESULT 78
BQ591223/c
LOCUS
DEFINITION
E012715-024-017-H02-T7 MP1Z-ADIS-024-storage root Beta vulgaris
CDNA clone 024-017-H02 3-PRIME, mRNA sequence.
ACCESSION
BQ591223
VERSION
BQ591223.1 GI:26120806
KEYWORDS
EST.
SOURCE
Beta vulgaris
ORGANISM
Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE
1 (bases 1 to 15)

```


AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL Plant J. 32 (5), 845-857 (2002)

MEDLINE 22362189

PubMed 12472698

COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPZ
Max-planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
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FEATURES

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/note="Vector: pCMVSPORT6; Site.1: Sali; Site.2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatgut AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:
SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 15 AAAAAAAAAAAAAA 1

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ACCESSION BQ594689
VERSION BQ594689.1 GI:26124272
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 15)
Contact: Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
22362189
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Contact: Weisshaar B
ADIS DNA core facility at MPZ

FEATURES

source

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SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 1.0%; Score 15; DB 1; Length 15;
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Db 15 AAAAAAAAAAAAAA 1

RESULT 80
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LOCUS
DEFINITION CF277319 Oryza sativa cDNA clone 14ETL--02-M23, mRNA sequence.
ACCESSION CF277319
VERSION CF277319.1 GI:33654705
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 15)
Contact: Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.myongji.ac.kr.

FEATURES

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/tissue_type="leaf"
/dev_stage="14 days after germination"

AUTHORS Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 15 Std Error: 0.00
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SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 58;
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|||||
Db 15 AAAAAAAAAAAAAA 1

RESULT 80
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ACCESSION CF277319
VERSION CF277319.1 GI:33654705
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 15)
Contact: Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.myongji.ac.kr.

FEATURES

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RT-PCR."

Query Match      1.0%; Score 15; DB 1; Length 15;
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Db 15 AAAAAAAAAAAAAA 1

RESULT 81
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LOCUS
DEFINITION
14ETL--09-D04.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa cDNA clone 14ETL--09-D04, mRNA sequence.
ACCESSION
CF281923
VERSION
CF281923.1 GI:33659310
KEYWORDS
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
REFERENCE
1 (bases 1 to 15)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
JOURNAL
COMMENT
Contact: Nahm B.H.
of Bioscience and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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Db 15 AAAAAAAAAAAAAA 1

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CF290920/c
LOCUS
DEFINITION
14ROOT--01-C09.b1 Rice root plasmid cDNA library (14ROOT) Oryza
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ACCESSION
CF290920
VERSION
CF290920.1 GI:33659953

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KEYWORDS
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
REFERENCE
1 (bases 1 to 15)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
JOURNAL
COMMENT
Contact: Nahm B.H.
of Bioscience and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

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QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 83
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DEFINITION
14ROOT--01-E19.b1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa cDNA clone 14ROOT--01-E19, mRNA sequence.
ACCESSION
CF291029
VERSION
CF291029.1 GI:33660062
KEYWORDS
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
REFERENCE
1 (bases 1 to 15)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
JOURNAL
COMMENT
Contact: Nahm B.H.
of Bioscience and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

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DB 15 AAAAAAAAAAAAAA 1

RESULT 84
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VERSION     CF291103.1 GI:33660136
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SOURCE     Oryza sativa
ORGANISM   Oryza sativa
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 15)
AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL    Unpublished (2003)
COMMENT    Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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DEFINITION 14ROOT--02-E04.b1 Rice root plasmid cDNA library (14ROOT) Oryza
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ACCESSION  CF291717

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VERSION      CF291717.1 GI:33660750
KEYWORDS     EST.
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ORGANISM     Oryza sativa
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE    1 (bases 1 to 15)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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DB 15 AAAAAAAAAAAAAA 1

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DEFINITION 14ROOT--02-G02.b1 Rice root plasmid cDNA library (14ROOT) Oryza
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ACCESSION  CF291798
VERSION     CF291798.1 GI:33660831
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE    1 (bases 1 to 15)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 15 AAAAAAAAAAAAAA 1

RESULT 87
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LOCUS      15 bp mRNA linear EST 14-AUG-2003
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sativa cDNA clone 30DGS--01-E17, mRNA sequence.
ACCESSION  CF292458
VERSION     CF292458.1 GI:33661491
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 15)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
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with oligoribonucleotides and then used as templates for
RT-PCR."

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Best Local Similarity 100.0%; Pred. No. 58;
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Db 15 AAAAAAAAAAAAAA 1

RESULT 89
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sativa cDNA clone 30DGS--04-O02, mRNA sequence.
ACCESSION  CF295100
VERSION     CF295100.1 GI:33664133
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 15)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
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/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
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RT-PCR."

Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 58;
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Db 15 AAAAAAAAAAAAAA 1

RESULT 88
CF292461/c
LOCUS      15 bp mRNA linear EST 14-AUG-2003
DEFINITION 30DGS--01-E19.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
sativa cDNA clone 30DGS--01-E19, mRNA sequence.
ACCESSION  CF292461
VERSION     CF292461.1 GI:33661494
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 15)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
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Location/Qualifiers
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/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="30DGS--01-E19"
/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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LOCUS       CF300121                15 bp    mRNA    linear    EST 15-AUG-2003
DEFINITION   7LEAF--04-G12.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
ACCESSION   CF300121
VERSION     CF300121.1  GI:33671882
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Oryza sativa
REFERENCE   1 (bases 1 to 15)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
TITLE       Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
JOURNAL     Large-scale Sequencing Analysis of Rice ESTs
COMMENT     Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             source
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     /mol_type="mRNA"
     /cultivar="Nackdong"
     /db_xref="taxon:4530"
     /clone="7LEAF--03-L01"
     /tissue_type="leaf"
     /dev_stage="7 days after germination"
     /lab_host="E.coli DH10B"
     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
     /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
     with oligoribonucleotides and then used as templates for
     RT-PCR."

Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1481 AAAAAAAAAAAAAA 1495
Db   15 AAAAAAAAAAAAAA 1

RESULT 98
CF300361/c
LOCUS       CF300361                15 bp    mRNA    linear    EST 15-AUG-2003
DEFINITION   7LEAF--04-L16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
ACCESSION   CF300361
VERSION     CF300361.1  GI:33672122
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Oryza sativa
REFERENCE   1 (bases 1 to 15)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
TITLE       Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
JOURNAL     Large-scale Sequencing Analysis of Rice ESTs
COMMENT     Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             source
     1..15
     /organism="Oryza sativa"
     /mol_type="mRNA"
     /cultivar="Nackdong"
     /db_xref="taxon:4530"
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     /tissue_type="leaf"
     /dev_stage="7 days after germination"
     /lab_host="E.coli DH10B"
     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
     /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
     with oligoribonucleotides and then used as templates for
     RT-PCR."

Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1481 AAAAAAAAAAAAAA 1495
Db   15 AAAAAAAAAAAAAA 1

RESULT 97
CF300121/c
LOCUS       CF299608                15 bp    mRNA    linear    EST 15-AUG-2003
DEFINITION   7LEAF--03-L04.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
ACCESSION   CF299608
VERSION     CF299608.1  GI:33671369
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Oryza sativa
REFERENCE   1 (bases 1 to 15)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
TITLE       Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
JOURNAL     Large-scale Sequencing Analysis of Rice ESTs
COMMENT     Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             source
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     /cultivar="Nackdong"
     /db_xref="taxon:4530"
     /clone="7LEAF--03-L04"
     /tissue_type="leaf"
     /dev_stage="7 days after germination"
     /lab_host="E.coli DH10B"
     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
     /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
     with oligoribonucleotides and then used as templates for
     RT-PCR."

Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1481 AAAAAAAAAAAAAA 1495
Db   15 AAAAAAAAAAAAAA 1

RESULT 96
CF299608/c
LOCUS       CF299608                15 bp    mRNA    linear    EST 15-AUG-2003
DEFINITION   7LEAF--03-L04.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
ACCESSION   CF299608
VERSION     CF299608.1  GI:33671369
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Oryza sativa
REFERENCE   1 (bases 1 to 15)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
TITLE       Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
JOURNAL     Large-scale Sequencing Analysis of Rice ESTs
COMMENT     Unpublished (2003)
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             source
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     /cultivar="Nackdong"
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     /tissue_type="leaf"
     /dev_stage="7 days after germination"
     /lab_host="E.coli DH10B"
     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
     /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
     with oligoribonucleotides and then used as templates for
     RT-PCR."

Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1481 AAAAAAAAAAAAAA 1495
Db   15 AAAAAAAAAAAAAA 1

RESULT 96
CF299608/c
LOCUS       CF299608                15 bp    mRNA    linear    EST 15-AUG-2003
DEFINITION   7LEAF--03-L04.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
ACCESSION   CF299608
VERSION     CF299608.1  GI:33671369
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Oryza sativa
REFERENCE   1 (bases 1 to 15)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
TITLE       Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
JOURNAL     Large-scale Sequencing Analysis of Rice ESTs
COMMENT     Unpublished (2003)
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             source
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     /organism="Oryza sativa"
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     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
     /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
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     RT-PCR."

Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1481 AAAAAAAAAAAAAA 1495
Db   15 AAAAAAAAAAAAAA 1

RESULT 97
CF300121/c
LOCUS       CF300121                15 bp    mRNA    linear    EST 15-AUG-2003
DEFINITION   7LEAF--04-G12.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
ACCESSION   CF300121
VERSION     CF300121.1  GI:33671882
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Oryza sativa
REFERENCE   1 (bases 1 to 15)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
TITLE       Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
JOURNAL     Large-scale Sequencing Analysis of Rice ESTs
COMMENT     Unpublished (2003)
            Contact: Nahm B.H.
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            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             source
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     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
     /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
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/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 99
CF300992/c
LOCUS
DEFINITION
7LEAF--05-K19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--05-K19, mRNA sequence.
ACCESSION
CF300992
VERSION
CF300992.1 GI:33672753
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 15)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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/organism="Oryza sativa"
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/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 101
CF302124/c
LOCUS
DEFINITION
7LEAF--07-F16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--07-F16, mRNA sequence.
ACCESSION
CF302124
VERSION
CF302124.1 GI:33673885
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 15)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Contact: Nahm B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 101
CF302124/c
LOCUS
DEFINITION
7LEAF--07-F16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--07-F16, mRNA sequence.
ACCESSION
CF302124
VERSION
CF302124.1 GI:33673885
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 15)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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/tissue_type="leaf"
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/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 100

```


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Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

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1. .15
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/tissue_type="leaf"
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/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/notes="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

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Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495

Db 15 AAAAAAAAAAAAAA 1

RESULT 105

CF311907/c

LOCUS ABF--07-G04.b1 ABF3-overexpressing transgenic rice plasmid cDNA
DEFINITION library (ABF) Oryza sativa cDNA clone ABF--07-G04, mRNA sequence.

ACCESSION CF311907.1 GI:33683668

VERSION CF311907

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 15)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

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Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

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1. .15
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="ABF--07-G04"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/notes="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

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Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495

Db 15 AAAAAAAAAAAAAA 1

RESULT 106

CF313319/c

LOCUS HD--01-G13.b1 OshDACL1-overexpressing transgenic rice plasmid cDNA
DEFINITION library (HD) Oryza sativa cDNA clone HD--01-G13, mRNA sequence.

ACCESSION CF313319

VERSION CF313319.1 GI:33685080

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 15)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

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Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

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1. .15
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD--01-G13"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDACL1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
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reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

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Query Match 1.0%; Score 15; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 58;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495

Db 15 AAAAAAAAAAAAAA 1

RESULT 107

CF313320

LOCUS HD--01-G13.g1 OshDACL1-overexpressing transgenic rice plasmid cDNA
DEFINITION library (HD) Oryza sativa cDNA clone HD--01-G13, mRNA sequence.

ACCESSION CF313320

VERSION CF313320.1 GI:33685081

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

1 (bases 1 to 15)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE

Large-scale Sequencing Analysis of Rice ESTs

COMMENT

Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

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1. .15
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/mol_type="mRNA"
/cultivar="Nackdong"
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/lab_host="E.coli DH10B"
/clone_lib="OSHADAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495

Db 1 AAAAAAAAAAAAAA 15

RESULT 108

CF316251

LOCUS HD--05-H15.b1 OSHADAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--05-H15, mRNA sequence.

ACCESSION

CF316251

VERSION

CF316251.1

KEYWORDS

SOURCE

ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

1 (bases 1 to 15)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE

Large-scale Sequencing Analysis of Rice ESTs

JOURNAL

COMMENT

Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source

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/lab_host="E.coli DH10B"
/clone_lib="OSHADAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495

Db 1 AAAAAAAAAAAAAA 15

RESULT 109

CF318035/c

LOCUS

DEFINITION HD--07-P06.b1 OSHADAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--07-P06, mRNA sequence.

ACCESSION

CF318035

VERSION

CF318035.1

KEYWORDS

SOURCE

ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS

1 (bases 1 to 15)

TITLE

Large-scale Sequencing Analysis of Rice ESTs

JOURNAL

COMMENT

Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source

1. .15
/organism="Oryza sativa"
/mol_type="mRNA"
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/lab_host="E.coli DH10B"
/clone_lib="OSHADAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495

Db 15 AAAAAAAAAAAAAA 1

RESULT 110

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CF327434/c
LOCUS               15 bp mRNA linear EST 18-AUG-2003
DEFINITION          NACL--01-O18.b1 Rice callus plasmid cDNA library (NACL) Oryza
                     sativa cDNA clone NACL--01-O18, mRNA sequence.
ACCESSION            CF327434
VERSION              CF327434.1 GI:33803127
KEYWORDS             EST.
SOURCE               Oryza sativa
ORGANISM             Oryza sativa
                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                     Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                     Ehrhartoideae; Oryzeae; Oryza.
REFERENCE            1 (bases 1 to 15)
                     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
                     Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
                     Large-scale Sequencing Analysis of Rice ESTs
                     Unpublished (2003)
                     Contact: Nahm B.H.
                     Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
                     of Bioscience and Bioinformatics, Myongji University
                     Yongin, Kyeonggi, Korea
                     Tel: 82 31 330 6193
                     Fax: 82 31 321 6355
                     Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
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                     /notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

QUERY MATCH          1.0%; Score 15; DB 1; Length 15;
BEST LOCAL SIMILARITY 100.0%; Pred. No. 58;
MATCHES              15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAA 1495
DB      15 AAAAAAAAAAAAAA 1

RESULT 111
LOCUS    CF330195/c
DEFINITION          NACL--05-N03.b1 Rice callus plasmid cDNA library (NACL) Oryza
                     sativa cDNA clone NACL--05-N03, mRNA sequence.
ACCESSION            CF330195
VERSION              CF330195.1 GI:33808618
KEYWORDS             EST.
SOURCE               Oryza sativa
ORGANISM             Oryza sativa
                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                     Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                     Ehrhartoideae; Oryzeae; Oryza.
REFERENCE            1 (bases 1 to 15)
                     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
                     Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
                     Large-scale Sequencing Analysis of Rice ESTs
                     Unpublished (2003)
                     Contact: Nahm B.H.
                     Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
                     of Bioscience and Bioinformatics, Myongji University
                     Yongin, Kyeonggi, Korea
                     Tel: 82 31 330 6193
                     Fax: 82 31 321 6355
                     Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
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                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

QUERY MATCH          1.0%; Score 15; DB 1; Length 15;
BEST LOCAL SIMILARITY 100.0%; Pred. No. 58;
MATCHES              15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAA 1495
DB      15 AAAAAAAAAAAAAA 1

RESULT 111
LOCUS    CF330195/c
DEFINITION          NACL--05-N03.b1 Rice callus plasmid cDNA library (NACL) Oryza
                     sativa cDNA clone NACL--05-N03, mRNA sequence.
ACCESSION            CF330195
VERSION              CF330195.1 GI:33808618
KEYWORDS             EST.
SOURCE               Oryza sativa
ORGANISM             Oryza sativa
                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                     Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                     Ehrhartoideae; Oryzeae; Oryza.
REFERENCE            1 (bases 1 to 15)
                     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
                     Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
                     Large-scale Sequencing Analysis of Rice ESTs
                     Unpublished (2003)
                     Contact: Nahm B.H.
                     Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
                     of Bioscience and Bioinformatics, Myongji University
                     Yongin, Kyeonggi, Korea
                     Tel: 82 31 330 6193
                     Fax: 82 31 321 6355
                     Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

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FEATURES             Location/Qualifiers
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                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
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                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

QUERY MATCH          1.0%; Score 15; DB 1; Length 15;
BEST LOCAL SIMILARITY 100.0%; Pred. No. 58;
MATCHES              15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAA 1495
DB      15 AAAAAAAAAAAAAA 1

RESULT 112
LOCUS    CF330668/c
DEFINITION          NACL--06-H16.b1 Rice callus plasmid cDNA library (NACL) Oryza
                     sativa cDNA clone NACL--06-H16, mRNA sequence.
ACCESSION            CF330668
VERSION              CF330668.1 GI:33809572
KEYWORDS             EST.
SOURCE               Oryza sativa
ORGANISM             Oryza sativa
                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                     Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                     Ehrhartoideae; Oryzeae; Oryza.
REFERENCE            1 (bases 1 to 15)
                     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
                     Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
                     Large-scale Sequencing Analysis of Rice ESTs
                     Unpublished (2003)
                     Contact: Nahm B.H.
                     Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
                     of Bioscience and Bioinformatics, Myongji University
                     Yongin, Kyeonggi, Korea
                     Tel: 82 31 330 6193
                     Fax: 82 31 321 6355
                     Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa"
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                     /cultivar="Nackdong"
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                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

QUERY MATCH          1.0%; Score 15; DB 1; Length 15;
BEST LOCAL SIMILARITY 100.0%; Pred. No. 58;
MATCHES              15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAA 1495
DB      15 AAAAAAAAAAAAAA 1

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RESULT 113
CF332178/c
LOCUS      CF332178      15 bp      mRNA      linear      EST 18-AUG-2003
DEFINITION NACL--08-J10.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--08-J10, mRNA sequence.
ACCESSION  CF332178
VERSION     CF332178.1  GI:33812580
KEYWORDS    EST.
SOURCE      Oryza sativa
            Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 15)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.

FEATURES             source
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            /clone_lib="Rice callus plasmid cDNA library (NACL)"
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            with oligoribonucleotides and then used as templates for
            RT-PCR."

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Best Local Similarity 100.0%; Pred. No. 58;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 115
BQ590207/c
LOCUS      BQ590207      16 bp      mRNA      linear      EST 06-DEC-2002
DEFINITION E012843-024-019-015-T7 MP1Z-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-019-015 3-PRIME, mRNA sequence.
ACCESSION  BQ590207
VERSION     BQ590207.1  GI:26119790
KEYWORDS    EST.
SOURCE      Beta vulgaris
            Beta vulgaris
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1 (bases 1 to 16)
AUTHORS     Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
TITLE       Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL     Plant J. 32 (5), 845-857 (2002)
MEDLINE     22362189
PUBMED      12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaar@mpiz-koeln.mpg.de
            Insert length: 16 Std Error: 0.00
            Plate: 19 row: 0 column: 15
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FEATURES             source
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            /note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
            cDNA library from sugar beet, library provided by KWS
            Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:

RESULT 114
CF336202/c
LOCUS      CF336202      15 bp      mRNA      linear      EST 18-AUG-2003
DEFINITION JMT--06-C20.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--06-C20, mRNA sequence.
ACCESSION  CF336202
VERSION     CF336202.1  GI:33820794
KEYWORDS    EST.
SOURCE      Oryza sativa
            Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 15)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355

```

```

Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.

FEATURES             source
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            /organism="Oryza sativa"
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            cDNA library (JMT)"
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            prepared from Arabidopsis Jasminate Carboxyl
            methyltransferase overexpression line."

Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 115
BQ590207/c
LOCUS      BQ590207      16 bp      mRNA      linear      EST 06-DEC-2002
DEFINITION E012843-024-019-015-T7 MP1Z-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-019-015 3-PRIME, mRNA sequence.
ACCESSION  BQ590207
VERSION     BQ590207.1  GI:26119790
KEYWORDS    EST.
SOURCE      Beta vulgaris
            Beta vulgaris
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1 (bases 1 to 16)
AUTHORS     Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
TITLE       Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL     Plant J. 32 (5), 845-857 (2002)
MEDLINE     22362189
PUBMED      12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaar@mpiz-koeln.mpg.de
            Insert length: 16 Std Error: 0.00
            Plate: 19 row: 0 column: 15
            Seq primer: T7: GTAATACGACTCACTATAGGCG.

FEATURES             source
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            /mol_type="mRNA"
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            /lab_host="EMDH10B"
            /clone_lib="MP1Z-ADIS-024-storage root"
            /note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
            cDNA library from sugar beet, library provided by KWS
            Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:

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b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:

SP6-Sali-CCAGCGCTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Best Project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de>

Query Match 1.0%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
|||||
Db 15 AAAAAAAAAAAAAA 1

RESULT 116

CF318894/c

LOCUS

DEFINITION HD--09-D06.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--09-D06, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source

1. .16
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
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/lab_host="E.coli DH10B"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr_ Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Desacetylase overexpression line."

Query Match 1.0%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
|||||
Db 15 AAAAAAAAAAAAAA 1

RESULT 117

CF327923/c

LOCUS

DEFINITION NACL--02-J18.g1 Rice callus plasmid cDNA library (NACL) Oryza

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source

1. .16
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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Db 15 AAAAAAAAAAAAAA 1

RESULT 118

CF328223/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

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Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source

1. .16
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
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/tissue_type="callus"
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Query Match 1.0%; Score 15; DB 1; Length 16;

Best Local Similarity 100.0%; Pred. No. 74;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495

Db 15 AAAAAAAAAAAAAA 1

RESULT 119

CF328223/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

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COMMENT

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

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Fax: 82 31 321 6355

Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source

1. .16
/organism="Oryza sativa"
/mol_type="mRNA"
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Query Match 1.0%; Score 15; DB 1; Length 16;

Best Local Similarity 100.0%; Pred. No. 74;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495

Db 15 AAAAAAAAAAAAAA 1

RESULT 120

CF327923/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

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Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source

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/organism="Oryza sativa"
/mol_type="mRNA"
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Query Match 1.0%; Score 15; DB 1; Length 16;

Best Local Similarity 100.0%; Pred. No. 74;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495

Db 15 AAAAAAAAAAAAAA 1

RESULT 121

CF327923/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

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Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

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Query Match 1.0%; Score 15; DB 1; Length 16;

Best Local Similarity 100.0%; Pred. No. 74;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495

Db 15 AAAAAAAAAAAAAA 1

RESULT 122

CF327923/c

LOCUS

DEFINITION

ACCESSION

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REFERENCE

AUTHORS

TITLE

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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

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Yongin, Kyeonggi, Korea

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Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

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/organism="Oryza sativa"
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Query Match 1.0%; Score 15; DB 1; Length 16;

Best Local Similarity 100.0%; Pred. No. 74;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495

Db 15 AAAAAAAAAAAAAA 1

RESULT 123

CF327923/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

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Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source

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/organism="Oryza sativa"
/mol_type="mRNA"
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/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
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Best Local Similarity 100

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 /lab_host="E.coli DH10B"
 /clone_lib="Rice callus plasmid cDNA library (NACL)"
 /notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 1.0%; Score 15; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 74; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 0;

QY 1481 AAAAAAAAAAAAAA 1495
 |||||
 Db 15 AAAAAAAAAAAAAA 1

RESULT 119
 CF291802/c
 LOCUS 17 bp mRNA linear EST 14-AUG-2003
 DEFINITION 14ROOT--02-G05.b1 Rice root plasmid cDNA library (14ROOT) Oryza
 sativa cDNA clone 14ROOT--02-G05, mRNA sequence.

ACCESSION CF291802
 VERSION CF291802.1 GI:33660835
 KEYWORDS EST.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 17)
 AUTHORS Kim J.S., Jun K.M., Cheong P.J., Kim M.J., Lee T.H., Shin Y.C.,
 Song S.I., Kim J.K., Kim Y.-K. and Nahm B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Gyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 Location/Qualifiers
 1..17
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="14ROOT--02-G05"
 /tissue_type="root"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice root plasmid cDNA library (14ROOT)"
 /notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 1.0%; Score 15; DB 1; Length 17;
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 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
 |||||
 Db 17 AAAAAAAAAAAAAA 3

RESULT 120
 CF299997/c
 LOCUS 17 bp mRNA linear EST 15-AUG-2003

DEFINITION 7LEAF--04-D19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
 sativa cDNA clone 7LEAF--04-D19, mRNA sequence.

ACCESSION CF299997
 VERSION CF299997.1 GI:33671758
 KEYWORDS EST.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 17)

AUTHORS Kim J.S., Jun K.M., Cheong P.J., Kim M.J., Lee T.H., Shin Y.C.,
 Song S.I., Kim J.K., Kim Y.-K. and Nahm B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Gyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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 /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 1.0%; Score 15; DB 1; Length 17;
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 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
 |||||
 Db 15 AAAAAAAAAAAAAA 1

RESULT 121
 AW248457/c
 LOCUS 16 bp mRNA linear EST 07-JAN-2000
 DEFINITION 2820576.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820576 3',
 mRNA sequence.

ACCESSION AW248457
 VERSION AW248457.1 GI:6591450
 KEYWORDS EST.
 SOURCE Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 16)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Other ESTs: 2820576.5prime
 Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-r@mail.nih.gov

Tissue Procurement: DCTD/DP cDNA Library Preparation: Ling
 Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
 Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
 project Clone distribution: MGC clone distribution information can
 be found through the I.M.A.G.E. Consortium/LLNL at:
 www.bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
 Scores: PHRED from University of Washington Genome Center. Vector
 Trimming: cross_match from University of Washington Genome Center

PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: <http://www.genome.washington.edu/LowQuality> Sequence: 16 contiguous PHRD high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 16 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.

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High quality sequence stop: 16.

FEATURES

source

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  /lab_host="DH10B (phage-resistant)"
  /clone_lib="NIH_MGC_7"

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/notes="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 1.0%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1475 CATGCTAAAAAAA 1490

Db 16 CATCCTAAAAAAA 1

RESULT 122

CF317778/c

LOCUS 16 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--07-J13.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--07-J13, mRNA sequence.

ACCESSION CF317778

VERSION CF317778.1 GI:33689539

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 16)

AUTHORS Kim J.S., Jun K.M., Cheong P.J., Kim M.J., Lee T.H., Shin Y.C.,

Song S.I., Kim J.K., Kim Y.-K. and Nahm B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Gyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

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1. .16
Location/Qualifiers
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  /mol_type="mRNA"
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  /db_xref="taxon:4530"
  /clone="HD--07-J13"
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/lab_host="E.coli DH10B"
/clone_lib="OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 1.0%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496

Db 16 AAAAAAAAAAAAAA 1

RESULT 123

BQ586422/c

LOCUS 14 bp mRNA linear EST 06-DEC-2002
DEFINITION S013307-024-013-002-T7 MP12-ADIS-024-leaf Beta vulgaris cDNA clone 024-013-002 3-PRIME, mRNA sequence.

ACCESSION BQ586422

VERSION BQ586422.1 GI:26116004

KEYWORDS EST.

SOURCE Beta vulgaris

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

REFERENCE 1 (bases 1 to 14)

AUTHORS Herwig R., Schulz B., Weishaar B., Hennig S., Steinfath M., Drungowski M., Stahl D., Wruick W., Menze A., O'Brien J., Lehrach H. and Radelof U.

Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes

Plant J. 32 (5), 845-857 (2002)

JOURNAL MEDLINE

PUBMED 22362189

COMMENT 12472698

Contact: Weishaar B

ADIS DNA core facility at MP12

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weishaar@mpiz-koeln.mpg.de

Insert Length: 14 Std Error: 0.00

Plate: 13 row: O column: 02

Seq primer: T7; GTAATACGACTCACTATAGGCG.

FEATURES

source

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/db_xref="taxon:161934"

/clone="024-013-002"

/tissue_type="leaf"

/lab_host="EMDH10B"

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/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;

cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:

SP6-Sali-CCACGGGTCCG-Sprime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator:

Prof. Christian Jung; Sequence submission managed by

RZPD/GABI-Primary database: <http://gabi.rzpd.de>

Query Match

0.9%; Score 14; DB 1; Length 14;

Best Local Similarity 100.0%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 1

RESULT 124
BQ587890/c

LOCUS
DEFINITION BQ587890 14 bp mRNA linear EST 06-DEC-2002
CDNA clone 024-009-B02-T7 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone
024-009-B02 3-PRIME, mRNA sequence.

ACCESSION BQ587890
VERSION BQ587890.1 GI:26117472
KEYWORDS EST.
SOURCE Beta vulgaris

ORGANISM Beta vulgaris

REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Anaranthaceae; Beta.

1 (bases 1 to 14)
Herwig.R., Schulz.B., Weisshaar.B., Hennig.S., Steinfath.M.,
Drungowski.M., Stahl.D., Wruck.W., Menze.A., O'Brien.J., Lehrach.H.
and Radelof,U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698

COMMENT
Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@piz-koeln.mpg.de
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Plate: 9 row: B column: 02
Seq primer: T7; GTAATACGACTCACTATAGGCG.

FEATURES
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/notes="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database:http://gabi.rzpd.de"

Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 1

RESULT 125
BQ589191/c

LOCUS
DEFINITION BQ589191 14 bp mRNA linear EST 06-DEC-2002
CDNA clone 024-015-I20-T7 MP1Z-ADIS-024-storage root Beta vulgaris
024-015-I20 3-PRIME, mRNA sequence.

ACCESSION BQ589191
VERSION BQ589191.1 GI:26118774
KEYWORDS EST.
SOURCE Beta vulgaris

ORGANISM Beta vulgaris

REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Anaranthaceae; Beta.

1 (bases 1 to 14)
Herwig.R., Schulz.B., Weisshaar.B., Hennig.S., Steinfath.M.,
Drungowski.M., Stahl.D., Wruck.W., Menze.A., O'Brien.J., Lehrach.H.
and Radelof,U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698

COMMENT
Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@piz-koeln.mpg.de
Insert Length: 14 Std Error: 0.00
Plate: 15 row: I column: 20
Seq primer: T7; GTAATACGACTCACTATAGGCG.

FEATURES
source

1. .14
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/cultivar="KWS2320 (double haploid, monogerm breeding
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/db_xref="GABI:187878"
/db_xref="taxon:161934"
/clone="024-015-I20"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-storage root"
/notes="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 1

RESULT 126
BQ590242/c

LOCUS
DEFINITION BQ590242 14 bp mRNA linear EST 06-DEC-2002
CDNA clone 024-019-E16-SP6 MP1Z-ADIS-024-storage root Beta vulgaris
024-019-E16 5-PRIME, mRNA sequence.

ACCESSION BQ590242
VERSION BQ590242.1 GI:26119825
KEYWORDS EST.
SOURCE Beta vulgaris

ORGANISM Beta vulgaris

REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

REFERENCE AUTHORS	Caryophyllales; Amaranthaceae; Beta. 1 (bases 1 to 14) Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
TITLE	Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL MEDLINE PUBMED	Plant J. 32 (5), 845-857 (2002) 22362189 12472698
COMMENT	Contact: Weishaar B ADIS DNA core facility at MPIZ Max-Planck-Institute for Plant Breeding Research Carl-von-Linne Weg 10, 50829 Koeln, Germany Fax: 00492215062851 Email: weishaar@piz-koeln.mpg.de Insert Length: 14 Std Error: 0.00 Plate: 19 row: E column: 16 Seq primer: SP6; CATACGATTAGTGCACACTATAG.
FEATURES source	Location/Qualifiers 1. .14 /organism="Beta vulgaris" /mol_type="mRNA" /cultivar="KWS2320 (double haploid, monogerm breeding line)" /db_xref="GABI:189878" /db_xref="taxon:161934" /clone="024-019-E16" /tissue_type="storage root" /lab_host="EMDH10B" /clone_lib="MPIZ-ADIS-024-storage root" /note="Vector: PCMVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation: SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Best Project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"
Query Match	0.9%; Score 14; DB 1; Length 14;
Best Local Similarity	100.0%; Pred. No. 81;
Matches	14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1481 AAAAAAAAAAAAAA 1494
Db	14 AAAAAAAAAAAAAA 1
RESULT 127	
BQ590261/c	
LOCUS	14 bp mRNA linear EST 06-DEC-2002
DEFINITION	E012844-024-019-K14-T7 MPIZ-ADIS-024-storage root Beta vulgaris
ACCESSION	BQ590261
VERSION	BQ590261.1 GI:26119844
KEYWORDS	EST.
SOURCE	Beta vulgaris
ORGANISM	Beta vulgaris
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
AUTHORS	1 (bases 1 to 14) Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
TITLE	Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL MEDLINE PUBMED	Plant J. 32 (5), 845-857 (2002) 22362189 12472698
COMMENT	Contact: Weishaar B ADIS DNA core facility at MPIZ Max-Planck-Institute for Plant Breeding Research Carl-von-Linne Weg 10, 50829 Koeln, Germany Fax: 00492215062851 Email: weishaar@piz-koeln.mpg.de Insert Length: 14 Std Error: 0.00 Plate: 17 row: H column: 18 Seq primer: T7; GTAATACGACTCACTATAGGC.
FEATURES	Location/Qualifiers
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Query Match	0.9%; Score 14; DB 1; Length 14;
Best Local Similarity	100.0%; Pred. No. 81;
Matches	14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1481 AAAAAAAAAAAAAA 1494
Db	14 AAAAAAAAAAAAAA 1
RESULT 128	
BQ591168/c	
LOCUS	14 bp mRNA linear EST 06-DEC-2002
DEFINITION	E012713-024-017-H18-T7 MPIZ-ADIS-024-storage root Beta vulgaris
ACCESSION	BQ591168
VERSION	BQ591168.1 GI:26120751
KEYWORDS	EST.
SOURCE	Beta vulgaris
ORGANISM	Beta vulgaris
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
AUTHORS	1 (bases 1 to 14) Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
TITLE	Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL MEDLINE PUBMED	Plant J. 32 (5), 845-857 (2002) 22362189 12472698
COMMENT	Contact: Weishaar B ADIS DNA core facility at MPIZ Max-Planck-Institute for Plant Breeding Research Carl-von-Linne Weg 10, 50829 Koeln, Germany Fax: 00492215062851 Email: weishaar@piz-koeln.mpg.de Insert Length: 14 Std Error: 0.00 Plate: 17 row: H column: 18 Seq primer: T7; GTAATACGACTCACTATAGGC.
FEATURES	Location/Qualifiers
source	1. .14 /organism="Beta vulgaris" /mol_type="mRNA" /cultivar="KWS2320 (double haploid, monogerm breeding line)" /db_xref="GABI:189878" /db_xref="taxon:161934" /clone="024-019-K14" /tissue_type="storage root" /lab_host="EMDH10B" /clone_lib="MPIZ-ADIS-024-storage root" /note="Vector: PCMVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation: SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Best Project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"
Query Match	0.9%; Score 14; DB 1; Length 14;
Best Local Similarity	100.0%; Pred. No. 81;
Matches	14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1481 AAAAAAAAAAAAAA 1494
Db	14 AAAAAAAAAAAAAA 1
RESULT 128	
BQ591168/c	
LOCUS	14 bp mRNA linear EST 06-DEC-2002
DEFINITION	E012713-024-017-H18-T7 MPIZ-ADIS-024-storage root Beta vulgaris
ACCESSION	BQ591168
VERSION	BQ591168.1 GI:26120751
KEYWORDS	EST.
SOURCE	Beta vulgaris
ORGANISM	Beta vulgaris
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
AUTHORS	1 (bases 1 to 14) Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
TITLE	Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL MEDLINE PUBMED	Plant J. 32 (5), 845-857 (2002) 22362189 12472698
COMMENT	Contact: Weishaar B ADIS DNA core facility at MPIZ Max-Planck-Institute for Plant Breeding Research Carl-von-Linne Weg 10, 50829 Koeln, Germany Fax: 00492215062851 Email: weishaar@piz-koeln.mpg.de Insert Length: 14 Std Error: 0.00 Plate: 17 row: H column: 18 Seq primer: T7; GTAATACGACTCACTATAGGC.
FEATURES	Location/Qualifiers
source	1. .14 /organism="Beta vulgaris" /mol_type="mRNA" /cultivar="KWS2320 (double haploid, monogerm breeding line)" /db_xref="GABI:189878" /db_xref="taxon:161934" /clone="024-019-K14" /tissue_type="storage root" /lab_host="EMDH10B" /clone_lib="MPIZ-ADIS-024-storage root" /note="Vector: PCMVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation: SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Best Project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

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1. 14
/organism="Beta vulgaris"
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line)"
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/clone="024-017-H18"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MP12-ADIS-024-storage root"
/notes="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. NO. 81;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
    |||||
DB 14 AAAAAAAAAAAAAA 1

RESULT 129
BQ591176/c
LOCUS
DEFINITION
BQ591176 14 bp mRNA linear EST 06-DEC-2002
cDNA clone 024-017-N20-T7 MP12-ADIS-024-storage root Beta vulgaris
BQ591176
BQ591176.1 GI:26120759
EST.
SOURCE
Beta vulgaris
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 14)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
22362189
PUBMED
12472698
COMMENT
Contact: Weisshaar B
ADIS DNA core facility at MP1Z
Max-planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert length: 14 Std Error: 0.00
Plate: 17 row: N column: 20
Seq primer: T7; GTAATACGACTCATATAGGC.
Location/Qualifiers
1. 14
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line)"
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FEATURES
source

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RZPD/GABI-Primary database: <http://gabi.rzpd.de>

Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
|||||
Db 14 AAAAAAAAAAAAAA 1

RESULT 131
BQ591380/c
LOCUS
DEFINITION
E012714-024-017-B15-T7 MP1Z-ADIS-024-storage root Beta vulgaris
CDNA clone 024-017-B15 3-PRIME, mRNA sequence.

ACCESSION BQ591380
VERSION
KEYWORDS
SOURCE
ORGANISM

Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.

REFERENCE
AUTHORS
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.

TITLE
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL
MEDLINE
PUBMED
COMMENT

Contact: Weisshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 14 Std Error: 0.00
Plate: 17 row: B column: 15
Seq primer: T7; GTAATACGACTCACTATAGGCG.

FEATURES
source
Location/Qualifiers
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/cultivar="KWS2320 (double haploid, monogerm breeding
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/db_xref="taxon:161934"
/clone="024-017-B15"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-storage root"
/notes="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: <http://gabi.rzpd.de>"

Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
|||||
Db 14 AAAAAAAAAAAAAA 1

RESULT 132
BQ591482/c
LOCUS

DEFINITION
E012713-024-017-M04-T7 MP1Z-ADIS-024-storage root Beta vulgaris
CDNA clone 024-017-M04 3-PRIME, mRNA sequence.

ACCESSION BQ591482
VERSION
KEYWORDS
SOURCE
ORGANISM

Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.

REFERENCE
AUTHORS
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.

TITLE
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL
MEDLINE
PUBMED
COMMENT

Contact: Weisshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 14 Std Error: 0.00
Plate: 17 row: M column: 04
Seq primer: T7; GTAATACGACTCACTATAGGCG.

FEATURES
source
Location/Qualifiers
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line)"
/db_xref="GABI:188633"
/db_xref="taxon:161934"
/clone="024-017-M04"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-storage root"
/notes="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: <http://gabi.rzpd.de>"

Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
|||||
Db 14 AAAAAAAAAAAAAA 1

RESULT 133
BQ593052/c
LOCUS

DEFINITION
E012375-024-028-C03-SP6 MP1Z-ADIS-024-developing root Beta vulgaris
CDNA clone 024-028-C03 5-PRIME, mRNA sequence.

ACCESSION BQ593052
VERSION
KEYWORDS
SOURCE
ORGANISM

Beta vulgaris

```

ORGANISM  Beta vulgaris
REFERENCE  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
            1 (bases 1 to 14)
            Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M.,
            Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Leinrach, H.
            and Radelof, U.
TITLE      Construction of a 'unigene' cDNA clone set by oligonucleotide
JOURNAL    fingerprinting allows access to 25 000 potential sugar beet genes
MEDLINE    Plant J. 32 (5), 845-857 (2002)
PUBMED     22362189
COMMENT     12472698
            ADIS DNA core facility at MPiZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaar@mpiz-koeln.mpg.de
            Insert length: 14 Std Error: 0.00
            Plate: 28 row: C column: 03
            Seq primer: SP6; CATACGATTAGGTGACACTATAG.
FEATURES   Location/Qualifiers
            1..14
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            /mol_type="mRNA"
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            line)"
            /db_xref="GABI:193808"
            /db_xref="taxon:161934"
            /clone="024-028-C03"
            /tissue_type="developing root"
            /lab_host="EMD10B"
            /clone_lib="MPIZ-ADIS-024-developing root"
            /notes="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
            cDNA library from sugar beet, library provided by KWS
            Kleinwanzlebener Saatgut AG Einbeck, Germany, contact:
            b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
            orientation:
            SP6-Sali-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
            Sequencing granted in the context of the GABI-Reet
            project, local PI: Dr. Katharina Schneider, coordinator:
            Prof. Christian Jung; Sequence submission managed by
            RZPD/GABI-Primary database: http://gabi.rzpd.de"
            0.9%; Score 14; DB 1; Length 14;
            Best Local Similarity 100.0%; Pred. No. 81;
            Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 1

RESULT 134
CF277935/c
LOCUS
DEFINITION 14ETL--03-K11-g1 Rice etiolated leaf plasmid cDNA library (14ETL)
ORYZA SATIVA cDNA clone 14ETL--03-K11, mRNA sequence.
ACCESSION  CF277935
VERSION     CF277935.1 GI:33655321
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 14)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnamh@bio.myongji.ac.kr.
FEATURES   Location/Qualifiers
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            /mol_type="mRNA"
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            /clone_lib="Rice etiolated leaf plasmid cDNA library
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            /notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
            with oligoribonucleotides and then used as templates for
            RT-PCR."
            0.9%; Score 14; DB 1; Length 14;
            Best Local Similarity 100.0%; Pred. No. 81;
            Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 1

RESULT 134
CF277935/c
LOCUS
DEFINITION 14ETL--03-L21-g1 Rice etiolated leaf plasmid cDNA library (14ETL)
ORYZA SATIVA cDNA clone 14ETL--03-L21, mRNA sequence.
ACCESSION  CF278001
VERSION     CF278001.1 GI:33655387
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 14)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
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Fax: 82 31 321 6355
Email: bhnamh@bio.myongji.ac.kr.
FEATURES   Location/Qualifiers
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            /lab_host="E.coli DH10B"
            /clone_lib="Rice etiolated leaf plasmid cDNA library
            (14ETL)"
            /notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
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            RT-PCR."
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            Best Local Similarity 100.0%; Pred. No. 81;
            Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 1

RESULT 134
CF277935/c
LOCUS
DEFINITION 14ETL--03-K11-g1 Rice etiolated leaf plasmid cDNA library (14ETL)
ORYZA SATIVA cDNA clone 14ETL--03-K11, mRNA sequence.
ACCESSION  CF277935
VERSION     CF277935.1 GI:33655321
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 14)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

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of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnamh@bio.myongji.ac.kr.
FEATURES   Location/Qualifiers
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QY 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 1

RESULT 135
CF278001/c
LOCUS
DEFINITION 14ETL--03-L21-g1 Rice etiolated leaf plasmid cDNA library (14ETL)
ORYZA SATIVA cDNA clone 14ETL--03-L21, mRNA sequence.
ACCESSION  CF278001
VERSION     CF278001.1 GI:33655387
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 14)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnamh@bio.myongji.ac.kr.
FEATURES   Location/Qualifiers
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            /mol_type="mRNA"
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            Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 1

RESULT 135
CF278001/c
LOCUS
DEFINITION 14ETL--03-L21-g1 Rice etiolated leaf plasmid cDNA library (14ETL)
ORYZA SATIVA cDNA clone 14ETL--03-L21, mRNA sequence.
ACCESSION  CF278001
VERSION     CF278001.1 GI:33655387
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 14)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnamh@bio.myongji.ac.kr.
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            /tissue_type="leaf"
            /dev_stage="14 days after germination"
            /lab_host="E.coli DH10B"
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QY 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 1

RESULT 135
CF278001/c
LOCUS
DEFINITION 14ETL--03-L21-g1 Rice etiolated leaf plasmid cDNA library (14ETL)
ORYZA SATIVA cDNA clone 14ETL--03-L21, mRNA sequence.
ACCESSION  CF278001
VERSION     CF278001.1 GI:33655387
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 14)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnamh@bio.myongji.ac.kr.
FEATURES   Location/Qualifiers
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QY 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 1

RESULT 135
CF278001/c
LOCUS
DEFINITION 14ETL--03-L21-g1 Rice etiolated leaf plasmid cDNA library (14ETL)
ORYZA SATIVA cDNA clone 14ETL--03-L21, mRNA sequence.
ACCESSION  CF278001
VERSION     CF278001.1 GI:33655387
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 14)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

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Best Local Similarity 100.0%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 1

RESULT 136
CF278452/c
LOCUS
DEFINITION 14ETL--04-F22.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
ACCESSION CF278452
VERSION CF278452.1 GI:33655838
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
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RESULT 137
CF279473/c
LOCUS
DEFINITION 14ETL--05-M14.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
ACCESSION CF279473
VERSION CF279473.1 GI:33656859
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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TITLE
JOURNAL
COMMENT

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

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Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 1

RESULT 138
CF279992/c
LOCUS
DEFINITION 14ETL--06-I01.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
ACCESSION CF279992
VERSION CF279992.1 GI:33657378
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Unpublished (2003)
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

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with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 14 AAAAAAAAAAAAAA 1

RESULT 139
CF281958/c
LOCUS 14 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ETL--09-D24.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
ORyza sativa cDNA clone 14ETL--09-D24, mRNA sequence.

ACCESSION CF281958
VERSION CF281958.1 GI:33659345
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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/organism="Oryza sativa"
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Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
DB 14 AAAAAAAAAAAAAA 1

RESULT 140
CF282350/c
LOCUS 14 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ETL--09-N05.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa cDNA clone 14ETL--09-N05, mRNA sequence.

ACCESSION CF282350
VERSION CF282350.1 GI:33659737
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source

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/organism="Oryza sativa"
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Best Local Similarity 100.0%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
DB 14 AAAAAAAAAAAAAA 1

RESULT 141
CF294449/c

LOCUS 14 bp mRNA linear EST 14-AUG-2003
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sativa cDNA clone 30DGS--03-P15, mRNA sequence.

ACCESSION CF294449
VERSION CF294449.1 GI:33663482
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source

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/dev_stage="30 days after germination"

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/lab_host="E.coli DH10B"
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QY 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 1

RESULT 142
CF295570/c
LOCUS      14 bp      mRNA      linear      EST 14-AUG-2003
DEFINITION      30DGS--05-J06.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
ACCESSION      CF295570
VERSION      CF295570.1 GI:33664603
KEYWORDS      EST.
SOURCE      Oryza sativa
ORGANISM      Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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QY 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 1

RESULT 143
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DEFINITION      30DGS--06-F17.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
ACCESSION      CF296120
VERSION      CF296120.1 GI:33665153
KEYWORDS      EST.
SOURCE      Oryza sativa

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Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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with oligoribonucleotides and then used as templates for
RT-PCR."

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Db 14 AAAAAAAAAAAAAA 1

RESULT 144
CF297969/c
LOCUS      14 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION      7LEAF--01-Cl6.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
ACCESSION      CF297969
VERSION      CF297969.1 GI:33669730
KEYWORDS      EST.
SOURCE      Oryza sativa
ORGANISM      Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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QY 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 1

RESULT 145
CF298109/c
LOCUS              14 bp mRNA linear EST 15-AUG-2003
DEFINITION         7LEAF--01-F19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
ACCESSION          CF298109
VERSION            CF298109.1 GI:33669870
KEYWORDS           EST.
SOURCE             Oryza sativa
ORGANISM           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE           1 (bases 1 to 14)
AUTHORS            Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE             Large-scale Sequencing Analysis of Rice ESTs
JOURNAL            Unpublished (2003)
COMMENT           Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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Db 14 AAAAAAAAAAAAAA 1

RESULT 146
CF299368/c
LOCUS              14 bp mRNA linear EST 15-AUG-2003
DEFINITION         7LEAF--03-F21.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
ACCESSION          CF299368
VERSION            CF299368.1 GI:33671129
KEYWORDS           EST.

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SOURCE             Oryza sativa
ORGANISM           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE           1 (bases 1 to 14)
AUTHORS            Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE             Large-scale Sequencing Analysis of Rice ESTs
JOURNAL            Unpublished (2003)
COMMENT           Contact: Nahm B.H.
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Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 1

RESULT 147
CF300542/c
LOCUS              14 bp mRNA linear EST 15-AUG-2003
DEFINITION         7LEAF--05-B01.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
ACCESSION          CF300542
VERSION            CF300542.1 GI:33672303
KEYWORDS           EST.
SOURCE             Oryza sativa
ORGANISM           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE           1 (bases 1 to 14)
AUTHORS            Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE             Large-scale Sequencing Analysis of Rice ESTs
JOURNAL            Unpublished (2003)
COMMENT           Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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Db 14 AAAAAAAAAAAAAA 1

RESULT 149
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LOCUS
DEFINITION      14 bp mRNA linear EST 15-AUG-2003
sativa cDNA clone 7LEAF--05-M19, mRNA sequence.
ACCESSION      CF301083
VERSION
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
REFERENCE      1 (bases 1 to 14)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
COMMENT      Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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Best Local Similarity 100.0%; Pred. No. 81;
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Db 14 AAAAAAAAAAAAAA 1

RESULT 149
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LOCUS
DEFINITION      14 bp mRNA linear EST 15-AUG-2003
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ACCESSION      CF301083
VERSION
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
REFERENCE      1 (bases 1 to 14)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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COMMENT      Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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Best Local Similarity 100.0%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 14 AAAAAAAAAAAAAA 1

RESULT 149
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LOCUS
DEFINITION      14 bp mRNA linear EST 15-AUG-2003
sativa cDNA clone 7LEAF--05-M19, mRNA sequence.
ACCESSION      CF301083
VERSION
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
REFERENCE      1 (bases 1 to 14)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
COMMENT      Contact: Nahm B.H.
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Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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KEYWORDS
SOURCE      Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
REFERENCE      1 (bases 1 to 14)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
COMMENT      Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 14 AAAAAAAAAAAAAA 1

RESULT 150
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DEFINITION      14 bp mRNA linear EST 15-AUG-2003
sativa cDNA clone 7LEAF--06-D16, mRNA sequence.
ACCESSION      CF301380
VERSION
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
REFERENCE      1 (bases 1 to 14)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
COMMENT      Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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/organism="Oryza sativa"
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RT-PCR."

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Best Local Similarity 100.0%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 14 AAAAAAAAAAAAAA 1

RESULT 151
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LOCUS      14 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--08-G18.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--08-G18, mRNA sequence.
ACCESSION  CF302675
VERSION     CF302675.1 GI:33674436
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

REFERENCE
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 1

RESULT 152
CF302846/c
LOCUS      14 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--08-M05.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--08-M05, mRNA sequence.
ACCESSION  CF302846

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VERSION     CF302846.1 GI:33674607
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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1 (bases 1 to 14)
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/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

REFERENCE
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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/organism="Oryza sativa"
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RT-PCR."

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Best Local Similarity 100.0%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 1

RESULT 153
CF308006/c
LOCUS      14 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--01-K10.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--01-K10, mRNA sequence.
ACCESSION  CF308006
VERSION     CF308006.1 GI:33679767
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 14)
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

REFERENCE
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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1..14
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"

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/db_xref="taxon:4530"
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/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."
Query Match      0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 1

RESULT 154
CF308220/c
LOCUS
DEFINITION
ABF--01-P06.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--01-P06, mRNA sequence.
ACCESSION
CF308220
VERSION
CF308220.1 GI:33679981
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 14)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
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of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
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1..14
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/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="ABF--02-E10"
/tissue_type="leaf"
/dev_stage="14 days after germination"
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/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."
Query Match      0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 1

RESULT 156
CF308918/c
LOCUS
DEFINITION
ABF--02-O16.b1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--02-O16, mRNA sequence.
ACCESSION
CF308918
VERSION
CF308918.1 GI:33680679
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 14)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
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of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
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/cultivar="Nackdong"
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/tissue_type="leaf"
/dev_stage="14 days after germination"
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/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

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RESULT 155
CF308445/c
LOCUS
DEFINITION
ABF--02-E10.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--02-E10, mRNA sequence.
ACCESSION
CF308445
VERSION
CF308445.1 GI:33680206
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 14)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source
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/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="ABF--02-E10"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."
Query Match      0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 1

RESULT 156
CF308918/c
LOCUS
DEFINITION
ABF--02-O16.b1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--02-O16, mRNA sequence.
ACCESSION
CF308918
VERSION
CF308918.1 GI:33680679
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 14)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
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/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."
Query Match      0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 1

RESULT 156
CF308918/c
LOCUS
DEFINITION
ABF--02-O16.b1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--02-O16, mRNA sequence.
ACCESSION
CF308918
VERSION
CF308918.1 GI:33680679
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 14)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
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/cultivar="Nackdong"
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/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

```

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FEATURES

Location/Qualifiers

1..14

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="ABF--02-016"

/tissue_type="leaf"

/dev_stage="14 days after germination"

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/clone_lib="ABF3-overexpressing transgenic rice plasmid

cDNA library (ABF)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.9%; Score 14; DB 1; Length 14;

Best Local Similarity 100.0%; Pred. No. 81;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494

Db 14 AAAAAAAAAAAAAA 1

RESULT 157

CF310714/c

LOCUS

DEFINITION ABF--05-111.b1 ABF3-overexpressing transgenic rice plasmid cDNA

library (ABF) Oryza sativa cDNA clone ABF--05-111, mRNA sequence.

CF310714

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 14)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source

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/organism="Oryza sativa"

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/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="ABF--05-111"

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/lab_host="E.coli DH10B"

/clone_lib="ABF3-overexpressing transgenic rice plasmid

cDNA library (ABF)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression

line."

Query Match 0.9%; Score 14; DB 1; Length 14;

Best Local Similarity 100.0%; Pred. No. 81;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494

Db 14 AAAAAAAAAAAAAA 1

RESULT 158

CF311201/c

LOCUS

DEFINITION ABF--06-F09.g1 ABF3-overexpressing transgenic rice plasmid cDNA

library (ABF) Oryza sativa cDNA clone ABF--06-F09, mRNA sequence.

CF311201

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 14)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source

1..14

/organism="Oryza sativa"

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/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="ABF--06-F09"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="ABF3-overexpressing transgenic rice plasmid

cDNA library (ABF)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried

for 2hrs. Oligo-capped mRNA was reverse transcribed and

then used for PCR. mRNA was prepared from ABA-responsive

element binding transcription factor 3 overexpression

line."

Query Match 0.9%; Score 14; DB 1; Length 14;

Best Local Similarity 100.0%; Pred. No. 81;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494

Db 14 AAAAAAAAAAAAAA 1

RESULT 159

CF311813/c

LOCUS

DEFINITION ABF--07-D22.g1 ABF3-overexpressing transgenic rice plasmid cDNA

library (ABF) Oryza sativa cDNA clone ABF--07-D22, mRNA sequence.

CF311813

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 14)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

Contact: Nahm B.H.

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Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

Location/Qualifiers

source

1..14

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="ABF--07-D22"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="ABF3-overexpressing transgenic rice plasmid"

/note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match

Best Local Similarity 0.9%; Score 14; DB 1; Length 14;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1481 AAAAAAAAAAAAAA 1494

Db

14 AAAAAAAAAAAAAA 1

RESULT 160

CF318323/c

HD--08-G13.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--08-G13, mRNA sequence.

CF318323

CF318323.1 GI:33690084

EST.

Oryza sativa

Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 14)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

Location/Qualifiers

source

1..14

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="HD--08-G13"

/tissue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 2 weeks"

/lab_host="E.coli DH10B"

/clone_lib="OshDAC1-overexpressing transgenic rice plasmid"

/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match

Best Local Similarity 0.9%; Score 14; DB 1; Length 14;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1481 AAAAAAAAAAAAAA 1494

Db

14 AAAAAAAAAAAAAA 1

RESULT 161

CF318450/c

LOCUS

DEFINITION

CF318450

CF318450.1 GI:33690211

EST.

Oryza sativa

Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 14)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

Contact: Nahm B.H.

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Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

source

1..14

/organism="Oryza sativa"

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/cultivar="Nackdong"

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/tissue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 2 weeks"

/lab_host="E.coli DH10B"

/clone_lib="OshDAC1-overexpressing transgenic rice plasmid"

/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match

Best Local Similarity 0.9%; Score 14; DB 1; Length 14;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1481 AAAAAAAAAAAAAA 1494

Db

14 AAAAAAAAAAAAAA 1

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RESULT 162
CF319826/c
LOCUS
DEFINITION
  HD--10-H16.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA
  library (HD) Oryza sativa cDNA clone HD--10-H16, mRNA sequence.
ACCESSION
CF319826
VERSION
CF319826.1 GI:33691587
KEYWORDS
EST.
SOURCE
  Oryza sativa
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
    Ehrhartoideae; Oryzaceae; Oryza.
  1 (bases 1 to 14)
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  /lab_host="E.coli DH10B"
  /clone_lib="OshDAC1-overexpressing transgenic rice plasmid
  cDNA library (HD)"
  /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
  treated with ABA(20um) for 1hr. Oligo-capped mRNA was
  reverse transcribed and then used for PCR. mRNA was
  derived from rice Histone Deacetylase overexpression
  line."
REFERENCE
  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  Large-scale Sequencing Analysis of Rice ESTs
  Unpublished (2003)
  Contact: Nahm B.H.
  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
  of Bioscience and Bioinformatics, Myongji University
  Yongin, Kyeonggi, Korea
  Tel: 82 31 320 6193
  Fax: 82 31 321 6355
  Email: bhnam@bio.myongji.ac.kr.
  Location/Qualifiers
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    /cultivar="Nackdong"
    /db_xref="taxon:4530"
    /clone="HD--10-H16"
    /tissue_type="callus"
    /dev_stage="proliferated callus on 2N6 media for 2 weeks"
    /lab_host="E.coli DH10B"
    /clone_lib="OshDAC1-overexpressing transgenic rice plasmid
    cDNA library (HD)"
    /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
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    reverse transcribed and then used for PCR. mRNA was
    derived from rice Histone Deacetylase overexpression
    line."
FEATURES
  source
  QY 1481 AAAAAAAAAAAAAA 1494
  Db 14 AAAAAAAAAAAAAA 1
  Query Match 0.9%; Score 14; DB 1; Length 14;
  Best Local Similarity 100.0%; Pred. No. 81;
  Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 163
CF321246/c
LOCUS
DEFINITION
  HD--12-G24.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
  library (HD) Oryza sativa cDNA clone HD--12-G24, mRNA sequence.
ACCESSION
CF321246
VERSION
CF321246.1 GI:33693007
KEYWORDS
EST.
SOURCE
  Oryza sativa
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
    Ehrhartoideae; Oryzaceae; Oryza.
  1 (bases 1 to 14)
  /dev_stage="proliferated callus on 2N6 media for 30 days"
  /lab_host="E.coli DH10B"
  /clone_lib="Rice callus plasmid cDNA library (NACL)"
  /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
  with oligoribonucleotides and then used as templates for
  RT-PCR."
FEATURES
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  QY 1481 AAAAAAAAAAAAAA 1494
  Db 14 AAAAAAAAAAAAAA 1
  Query Match 0.9%; Score 14; DB 1; Length 14;
  Best Local Similarity 100.0%; Pred. No. 81;
  Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 164
CF327097/c
LOCUS
DEFINITION
  NACL--01-H01.bi Rice callus plasmid cDNA library (NACL) Oryza
  sativa cDNA clone NACL--01-H01, mRNA sequence.
ACCESSION
CF327097
VERSION
CF327097.1 GI:33802449
KEYWORDS
EST.
SOURCE
  Oryza sativa
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
    Ehrhartoideae; Oryzaceae; Oryza.
  1 (bases 1 to 14)
  /dev_stage="proliferated callus on 2N6 media for 2 weeks"
  /lab_host="E.coli DH10B"
  /clone_lib="OshDAC1-overexpressing transgenic rice plasmid
  cDNA library (HD)"
  /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
  treated with ABA(20um) for 1hr. Oligo-capped mRNA was
  reverse transcribed and then used for PCR. mRNA was
  derived from rice Histone Deacetylase overexpression
  line."
REFERENCE
  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  Large-scale Sequencing Analysis of Rice ESTs
  Unpublished (2003)
  Contact: Nahm B.H.
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  of Bioscience and Bioinformatics, Myongji University
  Yongin, Kyeonggi, Korea
  Tel: 82 31 320 6193
  Fax: 82 31 321 6355
  Email: bhnam@bio.myongji.ac.kr.
  Location/Qualifiers
    1..14
    /organism="Oryza sativa"
    /mol_type="mRNA"
    /cultivar="Nackdong"
    /db_xref="taxon:4530"
    /clone="HD--10-H16"
    /tissue_type="callus"
    /dev_stage="proliferated callus on 2N6 media for 2 weeks"
    /lab_host="E.coli DH10B"
    /clone_lib="OshDAC1-overexpressing transgenic rice plasmid
    cDNA library (HD)"
    /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
    treated with ABA(20um) for 1hr. Oligo-capped mRNA was
    reverse transcribed and then used for PCR. mRNA was
    derived from rice Histone Deacetylase overexpression
    line."
FEATURES
  source
  QY 1481 AAAAAAAAAAAAAA 1494
  Db 14 AAAAAAAAAAAAAA 1
  Query Match 0.9%; Score 14; DB 1; Length 14;
  Best Local Similarity 100.0%; Pred. No. 81;
  Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 165
CF327097/c
LOCUS
DEFINITION
  NACL--01-H01.bi Rice callus plasmid cDNA library (NACL) Oryza
  sativa cDNA clone NACL--01-H01, mRNA sequence.
ACCESSION
CF327097
VERSION
CF327097.1 GI:33802449
KEYWORDS
EST.
SOURCE
  Oryza sativa
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
    Ehrhartoideae; Oryzaceae; Oryza.
  1 (bases 1 to 14)
  /dev_stage="proliferated callus on 2N6 media for 2 weeks"
  /lab_host="E.coli DH10B"
  /clone_lib="OshDAC1-overexpressing transgenic rice plasmid
  cDNA library (HD)"
  /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
  treated with ABA(20um) for 1hr. Oligo-capped mRNA was
  reverse transcribed and then used for PCR. mRNA was
  derived from rice Histone Deacetylase overexpression
  line."
REFERENCE
  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  Large-scale Sequencing Analysis of Rice ESTs
  Unpublished (2003)
  Contact: Nahm B.H.
  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
  of Bioscience and Bioinformatics, Myongji University
  Yongin, Kyeonggi, Korea
  Tel: 82 31 320 6193
  Fax: 82 31 321 6355
  Email: bhnam@bio.myongji.ac.kr.
  Location/Qualifiers
    1..14
    /organism="Oryza sativa"
    /mol_type="mRNA"
    /cultivar="Nackdong"
    /db_xref="taxon:4530"
    /clone="HD--10-H16"
    /tissue_type="callus"
    /dev_stage="proliferated callus on 2N6 media for 2 weeks"
    /lab_host="E.coli DH10B"
    /clone_lib="OshDAC1-overexpressing transgenic rice plasmid
    cDNA library (HD)"
    /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
    treated with ABA(20um) for 1hr. Oligo-capped mRNA was
    reverse transcribed and then used for PCR. mRNA was
    derived from rice Histone Deacetylase overexpression
    line."
FEATURES
  source
  QY 1481 AAAAAAAAAAAAAA 1494
  Db 14 AAAAAAAAAAAAAA 1
  Query Match 0.9%; Score 14; DB 1; Length 14;
  Best Local Similarity 100.0%; Pred. No. 81;
  Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1494
    |||||
Db 14 AAAAAAAAAAAAAA 1

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RESULT 165	
CF327119/c	
LOCUS	14 bp mRNA linear EST 18-AUG-2003
DEFINITION	NACL--01-H14.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--01-H14, mRNA sequence.
ACCESSION	CF327119
VERSION	CF327119.1 GI:33802493
KEYWORDS	EST.
SOURCE	Oryza sativa
ORGANISM	Oryza sativa
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
AUTHORS	1 (bases 1 to 14) Kim, J. S., Jun, K. M., Cheong, P. J., Kim, M. J., Lee, T. H., Shin, Y. C., Song, S. I., Kim, J. K., Kim, Y. K. and Nahm, B. H.
TITLE	Large-scale Sequencing Analysis of Rice ESTs
JOURNAL	Unpublished (2003)
COMMENT	Contact: Nahm B. H. Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University Yongin, Gyeonggi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355 Email: bhnahm@qbio.com, bhnahm@bio.mvongji.ac.kr.

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FEATURES
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1. 14
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--01-H14"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E coli DH108"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

[illegible]

**JOURNAL
COMMENT**

Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Email: bhnahm@bio.com. bhnahm@bio.myongji.ac.kr.

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FEATURES
source
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Location/Qualifiers
/organism="Oryza sativa"
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/db_xref="taxon:4530"
/clone="NACL-01-024"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E. coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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Query Match      0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred.No. 81;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
      |||||
Db 14 AAAAAAAAAAAAAA 1

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RESULT	167
LOCUS	CF328490/c
DEFINITION	NACL--03-G21.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--03-G21, mRNA sequence.
ACCESSION	CF328490
VERSION	CF328490.1
KEYWORDS	GI:33805226
SOURCE	EST.
ORGANISM	Oryza sativa
	Oryza sativa
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoidae; Oryzaceae; Oryza.
REFERENCE	1 (bases 1 to 14)
AUTHORS	Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE	Large-scale Sequencing Analysis of Rice ESTs
JOURNAL	Unpublished (2003)

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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@cbio.com, bhnahm@bio.myongji.ac.kr.

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FEATURES
source
Location/Qualifiers
1. .14
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL-03-G21"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
Query Match 0.9%; Score 14; DB 1; Length 14;

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Query Match      0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 1

RESULT 171
CF329217/c
LOCUS      14 bp mRNA linear EST 18-AUG-2003
DEFINITION sativa cDNA clone NACL--04-H10, mRNA sequence.
ACCESSION  CF329217.1 GI:33806672
VERSION     EST.
SOURCE      Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 14)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES             source
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     /organism="Oryza sativa"
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     /cultivar="Nackdong"
     /db_xref="taxon:4530"
     /clone="NACL--05-111"
     /tissue_type="callus"
     /dev_stage="proliferated callus on 2N6 media for 30 days"
     /lab_host="E.coli DH10B"
     /clone_lib="Rice callus plasmid cDNA library (NACL)"
     /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 14

RESULT 173
CF330784/c
LOCUS      14 bp mRNA linear EST 18-AUG-2003
DEFINITION sativa cDNA clone NACL--06-K10, mRNA sequence.
ACCESSION  CF330784
VERSION     EST.
SOURCE      Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 14)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES             source
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     1..14
     /organism="Oryza sativa"
     /mol_type="mRNA"
     /cultivar="Nackdong"
     /db_xref="taxon:4530"
     /clone="NACL--04-H10"
     /tissue_type="callus"
     /dev_stage="proliferated callus on 2N6 media for 30 days"
     /lab_host="E.coli DH10B"
     /clone_lib="Rice callus plasmid cDNA library (NACL)"
     /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 1

RESULT 172
CF329990
LOCUS      14 bp mRNA linear EST 18-AUG-2003
DEFINITION sativa cDNA clone NACL--05-111, mRNA sequence.
ACCESSION  CF329990
VERSION     EST.
SOURCE      Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 14)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES             source
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     1..14
     /organism="Oryza sativa"
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     /db_xref="taxon:4530"
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     /tissue_type="callus"
     /dev_stage="proliferated callus on 2N6 media for 30 days"
     /lab_host="E.coli DH10B"
     /clone_lib="Rice callus plasmid cDNA library (NACL)"
     /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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Query Match 0.9%; Score 14; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 81;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
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 Db 14 AAAAAAAAAAAAAA 1

RESULT 174
 CF3311272/c
 LOCUS 14 bp mRNA linear EST 18-AUG-2003
 DEFINITION NACL--07-F09.b1 Rice callus plasmid cDNA library (NACL) Oryza
 sativa cDNA clone NACL--07-F09, mRNA sequence.
 CF331272
 ACCESSION CF331272.1 GI:33810755
 VERSION
 KEYWORDS
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 REFERENCE 1 (bases 1 to 14)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 321 6193
 Fax: 82 31 321 6355
 Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
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 1. .14
 /organism="Oryza sativa"
 /mol_type="mRNA"
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 /db_xref="taxon:4530"
 /clone="NACL--07-F09"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 30 days"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice callus plasmid cDNA library (NACL)"
 /notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.9%; Score 14; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 81;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
 |||||
 Db 14 AAAAAAAAAAAAAA 1

RESULT 175
 CF331861/c
 LOCUS 14 bp mRNA linear EST 18-AUG-2003
 DEFINITION NACL--08-C10.b1 Rice callus plasmid cDNA library (NACL) Oryza
 sativa cDNA clone NACL--08-C10, mRNA sequence.
 CF331861
 ACCESSION CF331861.1 GI:33811945
 VERSION
 KEYWORDS
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 REFERENCE 1 (bases 1 to 14)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 321 6193
 Fax: 82 31 321 6355
 Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
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 1. .14
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 /clone="NACL--08-C10"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 30 days"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice callus plasmid cDNA library (NACL)"
 /notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.9%; Score 14; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 81;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
 |||||
 Db 14 AAAAAAAAAAAAAA 1

RESULT 176
 CF333214/c
 LOCUS 14 bp mRNA linear EST 18-AUG-2003
 DEFINITION JMT--02-A10.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
 library (JMT) Oryza sativa cDNA clone JMT--02-A10, mRNA sequence.
 CF333214
 ACCESSION CF333214.1 GI:33814707
 VERSION
 KEYWORDS
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 REFERENCE 1 (bases 1 to 14)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 321 6193
 Fax: 82 31 321 6355
 Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
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 1. .14
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="JMT--02-A10"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="AtJMT-overexpressing transgenic rice plasmid
 cDNA library (JMT)"
 /notes="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA"

was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."

Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 1

RESULT 177
CF333215
LOCUS JMT--02-A10.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
DEFINITION library (JMT) Oryza sativa cDNA clone JMT--02-A10, mRNA sequence.
ACCESSION CF333215
VERSION CF333215.1 GI:33814709
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa

REFERENCE 1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
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1. .14
/organism="Oryza sativa"
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/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."

Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 1 AAAAAAAAAAAAAA 14

RESULT 178
CF333399/c
LOCUS JMT--02-E12.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
DEFINITION library (JMT) Oryza sativa cDNA clone JMT--02-E12, mRNA sequence.
ACCESSION CF333399
VERSION CF333399.1 GI:33815074
KEYWORDS EST.
SOURCE Oryza sativa

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
1. .14
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="JMT--02-E12"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."

Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 1

RESULT 179
CF334202/c
LOCUS JMT--03-Gil.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
DEFINITION library (JMT) Oryza sativa cDNA clone JMT--03-Gil, mRNA sequence.
ACCESSION CF334202
VERSION CF334202.1 GI:33816736
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa

REFERENCE 1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
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Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
1. .14
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"

/clone="JMT--03-G11"
 /tissue_type="leaf"
 /dev stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="AtJMT-overexpressing transgenic rice plasmid
 cDNA library (JMT)"
 /note="vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
 was reverse transcribed and then used for PCR. mRNA was
 prepared from Arabidopsis Jasmonate Carboxyl
 methyltransferase overexpression line."

Query Match 0.9%; Score 14; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 81;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1494

Db 14 AAAAAAAAAAAAAA 1

RESULT 180

CF334281/c
 LOCUS
 DEFINITION JMT--03-105.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
 library (JMT) Oryza sativa cDNA clone JMT--03-I05, mRNA sequence.
 CF334281
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

CF334281 14 bp mRNA linear EST 18-AUG-2003
 JMT--03-105.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
 library (JMT) Oryza sativa cDNA clone JMT--03-I05, mRNA sequence.
 CF334281
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Oryza sativa
 Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 14)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

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FEATURES

Location/Qualifiers

1..14

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="JMT--03-I05"

/tissue_type="leaf"

/dev stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="AtJMT-overexpressing transgenic rice plasmid
 cDNA library (JMT)"

/note="vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
 was reverse transcribed and then used for PCR. mRNA was
 prepared from Arabidopsis Jasmonate Carboxyl
 methyltransferase overexpression line."

Query Match 0.9%; Score 14; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 81;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1494

Db 14 AAAAAAAAAAAAAA 1

RESULT 181

CF334290/c

LOCUS
 DEFINITION JMT--03-I11.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
 library (JMT) Oryza sativa cDNA clone JMT--03-I11, mRNA sequence.
 CF334290
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Oryza sativa

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 14)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

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FEATURES

Location/Qualifiers

1..14

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="JMT--03-I11"

/tissue_type="leaf"

/dev stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="AtJMT-overexpressing transgenic rice plasmid
 cDNA library (JMT)"

/note="vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
 was reverse transcribed and then used for PCR. mRNA was
 prepared from Arabidopsis Jasmonate Carboxyl
 methyltransferase overexpression line."

Query Match 0.9%; Score 14; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 81;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1494

Db 14 AAAAAAAAAAAAAA 1

RESULT 182

CF335781/c

LOCUS

DEFINITION JMT--05-J13.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
 library (JMT) Oryza sativa cDNA clone JMT--05-J13, mRNA sequence.

CF335781

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 14)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

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FEATURES

Source
Location/Qualifiers
1..14
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="JMT--05-J13"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."

Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 1

RESULT 183
CF336094/c
LOCUS
DEFINITION
CF336094 14 bp mRNA linear EST 18-AUG-2003
library (JMT) Oryza sativa cDNA clone JMT--06-A10, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

Source
Location/Qualifiers
1..14
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="JMT--06-A10"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."

Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 1

RESULT 184

CF336106/c
LOCUS
DEFINITION
CF336106 14 bp mRNA linear EST 18-AUG-2003
library (JMT) Oryza sativa cDNA clone JMT--06-A17, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Fax: 82 31 321 6355
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FEATURES

Source
Location/Qualifiers
1..14
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="JMT--06-A17"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."

Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 1

RESULT 185

CF336287/c
LOCUS
DEFINITION
CF336287 14 bp mRNA linear EST 18-AUG-2003
library (JMT) Oryza sativa cDNA clone JMT--06-E15, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
AUTHORS
TITLE

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs

JOURNAL
COMMENT

Unpublished (2003)
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of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source

1. .14
Location/Qualifiers
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="JMT--06-E15"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
|||||
Db 14 AAAAAAAAAAAAAA 1

RESULT 186
CF336906/c
LOCUS
DEFINITION
JMT--07-C05.b1 AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT) Oryza sativa cDNA clone JMT--07-C05, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 14)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source

1. .14
Location/Qualifiers
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="JMT--07-C05"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was

prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
|||||
Db 14 AAAAAAAAAAAAAA 1

RESULT 187
CF296652/c
LOCUS
DEFINITION
30DGS--07-C02.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
sativa cDNA clone 30DGS--07-C02, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 15)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source

1. .15
Location/Qualifiers
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="30DGS--07-C02"
/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.9%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 18+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
|||||
Db 14 AAAAAAAAAAAAAA 1

RESULT 188
CF329379/c
LOCUS
DEFINITION
NACL--04-K23.g1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--04-K23, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

```

REFERENCE
1 (bases 1 to 15)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..15
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--04-K23"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.9%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 15 AAAAAAAAAAAAAA 2

RESULT 189
LOCUS
CF291803 16 bp mRNA linear EST 14-AUG-2003
DEFINITION
14ROOT--02-G05.g1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa cDNA clone 14ROOT--02-G05, mRNA sequence.
ACCESSION
CF291803
VERSION
CF291803.1 GI:33660836
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 16)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
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Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..16
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="ABF--08-G13"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 0.9%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAAA 1493
Db 14 TAAAAAAAAAAAAA 1

RESULT 191
LOCUS
CF290849 15 bp mRNA linear EST 14-AUG-2003
DEFINITION
14ROOT--01-A17.g1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa cDNA clone 14ROOT--01-A17, mRNA sequence.
ACCESSION
CF290849
VERSION
CF290849.1 GI:33659882
KEYWORDS
EST.

```

```

/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.9%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 3 AAAAAAAAAAAAAA 16

RESULT 190
LOCUS
CF312586/c 16 bp mRNA linear EST 15-AUG-2003
DEFINITION
ABF--08-G13.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--08-G13, mRNA sequence.
ACCESSION
CF312586
VERSION
CF312586.1 GI:33684347
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 16)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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Location/Qualifiers
1..16
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/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
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cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
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element binding transcription factor 3 overexpression
line."

Query Match 0.9%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAAA 1493
Db 14 TAAAAAAAAAAAAA 1

RESULT 191
LOCUS
CF290849 15 bp mRNA linear EST 14-AUG-2003
DEFINITION
14ROOT--01-A17.g1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa cDNA clone 14ROOT--01-A17, mRNA sequence.
ACCESSION
CF290849
VERSION
CF290849.1 GI:33659882
KEYWORDS
EST.

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SOURCE
ORGANISM
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 15)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
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/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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Best Local Similarity 93.3%; Pred. No. 1.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 1 AAAAAAAAAAAAAA 15

RESULT 193
CF291030 15 bp mRNA linear EST 15-AUG-2003
LOCUS
DEFINITION
14ROOT--01-E19.g1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa cDNA clone 14ROOT--01-E19, mRNA sequence.
ACCESSION
CF291030.1 GI:33660063
VERSION
EST.
KEYWORDS
Oryza sativa
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 15)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
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of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
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Location/Qualifiers
1..15
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/clone="14ROOT--01-E19"
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/clone_lib="Rice root plasmid cDNA library (14ROOT)"
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.9%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 1 AAAAAAAAAAAAAA 15

RESULT 192
CF291030 15 bp mRNA linear EST 14-AUG-2003
LOCUS
DEFINITION
14ROOT--01-E19.g1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa cDNA clone 14ROOT--01-E19, mRNA sequence.
ACCESSION
CF291030.1 GI:33660063
VERSION
EST.
KEYWORDS
Oryza sativa
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 15)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
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Location/Qualifiers
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/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ROOT--01-E19"
/tissue_type="root"
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/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.9%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 1 AAAAAAAAAAAAAA 15

RESULT 194
BQ583549 13 bp mRNA linear EST 06-DEC-2002
LOCUS
DEFINITION
E011978-024-005-C14-SP6 MP12-ADIS-024-inflorescence Beta vulgaris
cDNA clone 024-005-C14 5-PRIME, mRNA sequence.
ACCESSION
BQ583549
VERSION
BQ583549.1 GI:26113126

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/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.9%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 1 AAAAAAAAAAAAAA 15

RESULT 193
CF301470 15 bp mRNA linear EST 15-AUG-2003
LOCUS
DEFINITION
7LEAF--06-F15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--06-F15, mRNA sequence.
ACCESSION
CF301470
VERSION
EST.
KEYWORDS
Oryza sativa
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 15)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..15
/organism="Oryza sativa"
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/db_xref="taxon:4530"
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/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.9%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 194
BQ583549 13 bp mRNA linear EST 06-DEC-2002
LOCUS
DEFINITION
E011978-024-005-C14-SP6 MP12-ADIS-024-inflorescence Beta vulgaris
cDNA clone 024-005-C14 5-PRIME, mRNA sequence.
ACCESSION
BQ583549
VERSION
BQ583549.1 GI:26113126

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Email: weishaa@piz-koeln.mpg.de
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 Seq primer: SP6; CATACGATTAGTGACACTATAG.

FEATURES

source
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 /db_xref="taxon:161934"
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 /lab_host="EMDH10B"
 /clone_lib="MPI2-ADIS-024-storage root"
 /notes="Vector: PCWSP06; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:
 SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Best Project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary Database: http://gabi.rzpd.de"

Query Match 0.9%; Score 13; DB 1; Length 13;
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 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493

Db 1 AAAAAAAAAAAAAA 13
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RESULT 197

CF278426/c
 LOCUS
 DEFINITION 14ETL--04-F09.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
 Oryza sativa cDNA clone 14ETL--04-F09, mRNA sequence.

ACCESSION CF278426
 VERSION CF278426.1 GI:33655812

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 13)

AUTHORS Kim J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE

JOURNAL

COMMENT

Large-scale Sequencing Analysis of Rice ESTs
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source
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/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

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 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493

Db 13 AAAAAAAAAAAAAA 1
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RESULT 198

CF280420/c

LOCUS

DEFINITION

14ETL--07-B11.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
 Oryza sativa cDNA clone 14ETL--07-B11, mRNA sequence.

ACCESSION CF280420

VERSION CF280420.1 GI:33657806

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 13)

AUTHORS Kim J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE

JOURNAL

COMMENT

Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1. .13 Location/Qualifiers
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 /notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

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 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493

Db 13 AAAAAAAAAAAAAA 1
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RESULT 199

CF280707/c

LOCUS

DEFINITION

14ETL--07-H19.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
 Oryza sativa cDNA clone 14ETL--07-H19, mRNA sequence.

ACCESSION CF280707

VERSION CF280707.1 GI:33658093

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 13)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1. .13
Location/Qualifiers
/organism="Oryza sativa"
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Query Match

Best Local Similarity 0.9%; Score 13; DB 1; Length 13;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAA 1493

Db 13 AAAAAAAAAAAAA 1

RESULT 200

CF280757/c

LOCUS

DEFINITION 14ETL--07-121.b1 Rice etiolated leaf plasmid cDNA library (14ETL)

Oryza sativa cDNA clone 14ETL--07-121, mRNA sequence.

CF280757

CF280757.1 GI:33658143

KEYWORDS

SOURCE

ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 13)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1. .13
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/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAA 1493

Db 13 AAAAAAAAAAAAA 1

RESULT 201

CF282369/c

LOCUS

DEFINITION 14ETL--09-N16.b1 Rice etiolated leaf plasmid cDNA library (14ETL)

Oryza sativa cDNA clone 14ETL--09-N16, mRNA sequence.

CF282369

CF282369.1 GI:33659756

KEYWORDS

SOURCE

ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 13)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1. .13
Location/Qualifiers
/organism="Oryza sativa"
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/tissue_type="leaf"
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/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

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Best Local Similarity 0.9%; Score 13; DB 1; Length 13;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAA 1493

Db 13 AAAAAAAAAAAAA 1

RESULT 202

CF290970/c

LOCUS

DEFINITION 14ROOT--01-D13.b1 Rice root plasmid cDNA library (14ROOT) Oryza

sativa cDNA clone 14ROOT--01-D13, mRNA sequence.

CF290970

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VERSION      CF290970.1  GI:33660003
KEYWORDS     EST.
SOURCE       Oryza sativa
ORGANISM     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
             Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE    1 (bases 1 to 13)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
             Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
             Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
             of Bioscience and Bioinformatics, Myongji University
             Yongin, Kyeonggi, Korea
             Tel: 82 31 330 6193
             Fax: 82 31 321 6355
             Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

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             /notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
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             RT-PCR."

Query Match      0.9%; Score 13; DB 1; Length 13;
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAA 1493
Db      1 AAAAAAAAAAAAAA 13
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RESULT 204
CF291011/c
LOCUS
DEFINITION  14ROOT--01-E10.b1 Rice root plasmid cDNA library (14ROOT) Oryza
ACCESSION   CF291011
VERSION     CF291011.1  GI:33660044
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
             Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE    1 (bases 1 to 13)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
             Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
             Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
             of Bioscience and Bioinformatics, Myongji University
             Yongin, Kyeonggi, Korea
             Tel: 82 31 330 6193
             Fax: 82 31 321 6355
             Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

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Db      1 AAAAAAAAAAAAAA 13
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RESULT 205
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ACCESSION   CF291060
VERSION     CF291060.1  GI:33660044
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
             Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE    1 (bases 1 to 13)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
             Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
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             of Bioscience and Bioinformatics, Myongji University
             Yongin, Kyeonggi, Korea
             Tel: 82 31 330 6193
             Fax: 82 31 321 6355
             Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

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ACCESSION      CF291060
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ORGANISM       Oryza sativa
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               Ehrhartoideae; Oryzeae; Oryza.
REFERENCE      1 (bases 1 to 13)
AUTHORS        Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
               Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE          Large-scale Sequencing Analysis of Rice ESTs
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               Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
               of Bioscience and Bioinformatics, Myongji University
               Yongin, Kyeonggi, Korea
               Tel: 82 31 330 6193
               Fax: 82 31 321 6355
               Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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Ory 1481 AAAAAAAAAAAAAA 1493
Db 13 AAAAAAAAAAAAAA 1

RESULT 206
CF291061
LOCUS          14ROOT--01-F11.g1 Rice root plasmid cDNA library (14ROOT) Oryza
DEFINITION    sativa cDNA clone 14ROOT--01-F11, mRNA sequence.
ACCESSION     CF291061
VERSION       CF291061.1  GI:33660094
KEYWORDS
SOURCE        Oryza sativa
ORGANISM      Oryza sativa
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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               Ehrhartoideae; Oryzeae; Oryza.
REFERENCE      1 (bases 1 to 13)
AUTHORS        Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
               Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE          Large-scale Sequencing Analysis of Rice ESTs
JOURNAL        Unpublished (2003)
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               Yongin, Kyeonggi, Korea
               Tel: 82 31 330 6193
               Fax: 82 31 321 6355
               Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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Ory 1481 AAAAAAAAAAAAAA 1493
Db 13 AAAAAAAAAAAAAA 1

RESULT 206
CF291061
LOCUS          14ROOT--01-F11.g1 Rice root plasmid cDNA library (14ROOT) Oryza
DEFINITION    sativa cDNA clone 14ROOT--01-F11, mRNA sequence.
ACCESSION     CF291061
VERSION       CF291061.1  GI:33660094
KEYWORDS
SOURCE        Oryza sativa
ORGANISM      Oryza sativa
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REFERENCE      1 (bases 1 to 13)
AUTHORS        Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
               Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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               Tel: 82 31 330 6193
               Fax: 82 31 321 6355
               Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
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RT-PCR."

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Ory 1481 AAAAAAAAAAAAAA 1493
Db 1 AAAAAAAAAAAAAA 13

RESULT 207
CF291167/c
LOCUS          14ROOT--01-H20.b1 Rice root plasmid cDNA library (14ROOT) Oryza
DEFINITION    sativa cDNA clone 14ROOT--01-H20, mRNA sequence.
ACCESSION     CF291167
VERSION       CF291167.1  GI:33660200
KEYWORDS
SOURCE        Oryza sativa
ORGANISM      Oryza sativa
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
               Ehrhartoideae; Oryzeae; Oryza.
REFERENCE      1 (bases 1 to 13)
AUTHORS        Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
               Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE          Large-scale Sequencing Analysis of Rice ESTs
JOURNAL        Unpublished (2003)
COMMENT        Contact: Nahm B.H.
               Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
               of Bioscience and Bioinformatics, Myongji University
               Yongin, Kyeonggi, Korea
               Tel: 82 31 330 6193
               Fax: 82 31 321 6355
               Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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Ory 1481 AAAAAAAAAAAAAA 1493
Db 13 AAAAAAAAAAAAAA 1

RESULT 208
CF291214/c
LOCUS          14ROOT--01-I22.b1 Rice root plasmid cDNA library (14ROOT) Oryza
DEFINITION

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DEFINITION 14ROOT--01-017.b1 Rice root plasmid cDNA library (14ROOT) Oryza
ACCESSION sativa cDNA clone 14ROOT--01-017, mRNA sequence.
VERSION CF291479
KEYWORDS CF291479.1 GI:33660512
SOURCE EST.
ORGANISM Oryza sativa
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          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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Db 13 AAAAAAAAAAAAAA 1

RESULT 212
CF291514/c
LOCUS 13 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ROOT--01-P13.b1 Rice root plasmid cDNA library (14ROOT) Oryza
ACCESSION sativa cDNA clone 14ROOT--01-P13, mRNA sequence.
VERSION CF291514
KEYWORDS CF291514.1 GI:33660547
SOURCE EST.
ORGANISM Oryza sativa
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REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
Db 13 AAAAAAAAAAAAAA 1

RESULT 212
CF291514/c
LOCUS 13 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ROOT--01-P13.b1 Rice root plasmid cDNA library (14ROOT) Oryza
ACCESSION sativa cDNA clone 14ROOT--01-P13, mRNA sequence.
VERSION CF291514
KEYWORDS CF291514.1 GI:33660547
SOURCE EST.
ORGANISM Oryza sativa
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          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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          Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
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          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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Db 13 AAAAAAAAAAAAAA 13

RESULT 214
CF291596/c

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Db 13 AAAAAAAAAAAAAA 1

RESULT 213
CF291515
LOCUS 13 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ROOT--01-P13.g1 Rice root plasmid cDNA library (14ROOT) Oryza
ACCESSION sativa cDNA clone 14ROOT--01-P13, mRNA sequence.
VERSION CF291515
KEYWORDS CF291515.1 GI:33660548
SOURCE EST.
ORGANISM Oryza sativa
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          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
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          of Bioscience and Bioinformatics, Myongji University
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          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
Db 13 AAAAAAAAAAAAAA 13

RESULT 214
CF291596/c

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LOCUS       CF291596               13 bp    mRNA    linear    EST 14-AUG-2003
DEFINITION   14ROOT--02-B12.b1 Rice root plasmid cDNA library (14ROOT) Oryza
ACCESSION    CF291596
VERSION      CF291596.1 GI:33660629
KEYWORDS     Oryza sativa
SOURCE       Oryza sativa
ORGANISM     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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              Ehrhartoideae; Oryzeae; Oryza.
REFERENCE    1 (bases 1 to 13)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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RESULT 215
CF291597
LOCUS       CF291597               13 bp    mRNA    linear    EST 14-AUG-2003
DEFINITION   14ROOT--02-B12.g1 Rice root plasmid cDNA library (14ROOT) Oryza
ACCESSION    CF291597
VERSION      CF291597.1 GI:33660630
KEYWORDS     Oryza sativa
SOURCE       Oryza sativa
ORGANISM     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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REFERENCE    1 (bases 1 to 13)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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RESULT 215
CF291597
LOCUS       CF291597               13 bp    mRNA    linear    EST 14-AUG-2003
DEFINITION   14ROOT--02-B12.g1 Rice root plasmid cDNA library (14ROOT) Oryza
ACCESSION    CF291597
VERSION      CF291597.1 GI:33660630
KEYWORDS     Oryza sativa
SOURCE       Oryza sativa
ORGANISM     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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REFERENCE    1 (bases 1 to 13)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
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              Fax: 82 31 321 6355
              Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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     /mol_type="mRNA"
     /cultivar="Nackdong"
     /db_xref="taxon:4530"
     /clone="14ROOT--02-B12"
     /tissue_type="root"
     /dev_stage="14 days after germination"
     /lab_host="E.coli DH10B"
     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
     /notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
     with oligoribonucleotides and then used as templates for
     RT-PCR."

Query Match      0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAA 1493
Db      13 AAAAAAAAAAAAAA 1

RESULT 215
CF291597
LOCUS       CF291597               13 bp    mRNA    linear    EST 14-AUG-2003
DEFINITION   14ROOT--02-B12.g1 Rice root plasmid cDNA library (14ROOT) Oryza
ACCESSION    CF291597
VERSION      CF291597.1 GI:33660630
KEYWORDS     Oryza sativa
SOURCE       Oryza sativa
ORGANISM     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzeae; Oryza.
REFERENCE    1 (bases 1 to 13)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             source
     1..13
     /organism="Oryza sativa"
     /mol_type="mRNA"
     /cultivar="Nackdong"
     /db_xref="taxon:4530"
     /clone="14ROOT--02-B12"
     /tissue_type="root"
     /dev_stage="14 days after germination"
     /lab_host="E.coli DH10B"
     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
     /notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
     with oligoribonucleotides and then used as templates for
     RT-PCR."

Query Match      0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAA 1493
Db      13 AAAAAAAAAAAAAA 1

RESULT 217

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source      1..13
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/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ROOT--02-B12"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAA 1493
Db      13 AAAAAAAAAAAAAA 13

RESULT 216
CF291726/c
LOCUS       CF291726               13 bp    mRNA    linear    EST 14-AUG-2003
DEFINITION   14ROOT--02-E10.b1 Rice root plasmid cDNA library (14ROOT) Oryza
ACCESSION    CF291726
VERSION      CF291726.1 GI:33660759
KEYWORDS     Oryza sativa
SOURCE       Oryza sativa
ORGANISM     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzeae; Oryza.
REFERENCE    1 (bases 1 to 13)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             source
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     /organism="Oryza sativa"
     /mol_type="mRNA"
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     /db_xref="taxon:4530"
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     /tissue_type="root"
     /dev_stage="14 days after germination"
     /lab_host="E.coli DH10B"
     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
     /notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
     with oligoribonucleotides and then used as templates for
     RT-PCR."

Query Match      0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAA 1493
Db      13 AAAAAAAAAAAAAA 1

RESULT 217

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CF291903
LOCUS               13 bp      mRNA      linear      EST 14-AUG-2003
DEFINITION          14ROOT--02-I10.g1 Rice root plasmid cDNA library (14ROOT) Oryza
                    sativa cDNA clone 14ROOT--02-I10, mRNA sequence.
ACCESSION            CF291903
VERSION              CF291903.1  GI:33660936
KEYWORDS             EST.
SOURCE               Oryza sativa
ORGANISM             Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE            1 (bases 1 to 13)
AUTHORS              Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
                    Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE               Large-scale Sequencing Analysis of Rice ESTs
JOURNAL             Unpublished (2003)
COMMENT             Contact: Nahm B.H.
                    Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
                    of Bioscience and Bioinformatics, Myongji University
                    Yongin, Kyeonggi, Korea
                    Tel: 82 31 321 6355
                    Fax: 82 31 321 6355
                    Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--02-A19"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

Query Match          0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAA 1493
DB      13 AAAAAAAAAAAAAA 1

RESULT 219
CF298590/c
LOCUS               13 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION          7LEAF--02-A21.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
                    sativa cDNA clone 7LEAF--02-A21, mRNA sequence.
ACCESSION            CF298590
VERSION              CF298592.1  GI:33670353
KEYWORDS             EST.
SOURCE               Oryza sativa
ORGANISM             Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE            1 (bases 1 to 13)
AUTHORS              Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
                    Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE               Large-scale Sequencing Analysis of Rice ESTs
JOURNAL             Unpublished (2003)
COMMENT             Contact: Nahm B.H.
                    Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
                    of Bioscience and Bioinformatics, Myongji University
                    Yongin, Kyeonggi, Korea
                    Tel: 82 31 321 6355
                    Fax: 82 31 321 6355
                    Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
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                     /cultivar="Nackdong"
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                     /tissue_type="leaf"
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

Query Match          0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAA 1493
DB      1 AAAAAAAAAAAAAA 13

RESULT 218
CF298590/c
LOCUS               13 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION          7LEAF--02-A19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
                    sativa cDNA clone 7LEAF--02-A19, mRNA sequence.
ACCESSION            CF298590
VERSION              CF298590.1  GI:33670351
KEYWORDS             EST.
SOURCE               Oryza sativa
ORGANISM             Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE            1 (bases 1 to 13)
AUTHORS              Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
                    Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE               Large-scale Sequencing Analysis of Rice ESTs
JOURNAL             Unpublished (2003)
COMMENT             Contact: Nahm B.H.
                    Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
                    of Bioscience and Bioinformatics, Myongji University
                    Yongin, Kyeonggi, Korea
                    Tel: 82 31 321 6355
                    Fax: 82 31 321 6355
                    Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
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                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
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                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

Query Match          0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAA 1493
DB      13 AAAAAAAAAAAAAA 1

RESULT 219
CF298592/c
LOCUS               13 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION          7LEAF--02-A21.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
                    sativa cDNA clone 7LEAF--02-A21, mRNA sequence.
ACCESSION            CF298592
VERSION              CF298592.1  GI:33670353
KEYWORDS             EST.
SOURCE               Oryza sativa
ORGANISM             Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE            1 (bases 1 to 13)
AUTHORS              Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
                    Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE               Large-scale Sequencing Analysis of Rice ESTs
JOURNAL             Unpublished (2003)
COMMENT             Contact: Nahm B.H.
                    Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
                    of Bioscience and Bioinformatics, Myongji University
                    Yongin, Kyeonggi, Korea
                    Tel: 82 31 321 6355
                    Fax: 82 31 321 6355
                    Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
                     1..13
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                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--02-A21"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

Query Match          0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAA 1493
DB      13 AAAAAAAAAAAAAA 1

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RESULT 223
CF298908/c
LOCUS
DEFINITION
13 bp mRNA linear EST 15-AUG-2003
7LEAF--02-K03.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--02-K03, mRNA sequence.
ACCESSION
CF298908
VERSION
CF298908.1 GI:33670669
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source
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/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--02-K03"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
Db 13 AAAAAAAAAAAAAA 1

RESULT 224
CF299133/c
LOCUS
DEFINITION
13 bp mRNA linear EST 15-AUG-2003
7LEAF--03-A06.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--03-A06, mRNA sequence.
ACCESSION
CF299133
VERSION
CF299133.1 GI:33670894
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193

FEATURES

source
1. .13
/organism="Oryza sativa"
/mol_type="mRNA"
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/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
Db 13 AAAAAAAAAAAAAA 1

FEATURES

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/clone="7LEAF--03-A06"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
Db 13 AAAAAAAAAAAAAA 1

FEATURES

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1. .13
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--03-F15"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
Db 13 AAAAAAAAAAAAAA 1

RESULT 225
CF299359/c
LOCUS
DEFINITION
13 bp mRNA linear EST 15-AUG-2003
7LEAF--03-F15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--03-F15, mRNA sequence.
ACCESSION
CF299359
VERSION
CF299359.1 GI:33671120
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

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1. .13
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--03-F15"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
Db 13 AAAAAAAAAAAAAA 1

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RESULT 226
LOCUS CF299937/c 13 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--04-C12.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--04-C12, mRNA sequence.
ACCESSION CF299937
VERSION CF299937.1 GI:33671698
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source
1..13
/organism="Oryza sativa"
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/cultivar="Nackdong"
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/clone="7LEAF--04-C12"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAA 1493
Db 13 AAAAAAAAAAAAA 1

RESULT 227
LOCUS CF300118/c 13 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--04-G10.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--04-G10, mRNA sequence.
ACCESSION CF300118
VERSION CF300118.1 GI:33671879
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea

```

```

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Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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1..13
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--04-G10"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAA 1493
Db 13 AAAAAAAAAAAAA 1

RESULT 228
LOCUS CF300587/c 13 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--05-C01.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--05-C01, mRNA sequence.
ACCESSION CF300587
VERSION CF300587.1 GI:33672348
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source
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/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
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/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAA 1493
Db 13 AAAAAAAAAAAAA 1

```

Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnamh@gbio.com, bhnamh@bio.myongji.ac.kr.

FEATURES
source
1. .13
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/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF-05-J11"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
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Db 13 AAAAAAAAAAAAAA 1

RESULT 231
CF301247/c
LOCUS
DEFINITION
7LEAF--06-A15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa CDNA clone 7LEAF--06-A15, mRNA sequence.
ACCESSION
CF301247
VERSION
CF301247.1 GI:33673008
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 13)
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
|||||
Db 13 AAAAAAAAAAAAAA 1

RESULT 230
CF301247/c
LOCUS
DEFINITION
7LEAF--05-J11.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa CDNA clone 7LEAF--05-J11, mRNA sequence.
ACCESSION
CF300929
VERSION
CF300929.1 GI:33672690
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 13)
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/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

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Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
|||||
Db 13 AAAAAAAAAAAAAA 1

RESULT 230
CF300929/c
LOCUS
DEFINITION
7LEAF--05-J11.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa CDNA clone 7LEAF--05-J11, mRNA sequence.
ACCESSION
CF300929
VERSION
CF300929.1 GI:33672690
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 13)
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/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
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Db 13 AAAAAAAAAAAAAA 1

RESULT 230
CF300929/c
LOCUS
DEFINITION
7LEAF--05-J11.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa CDNA clone 7LEAF--05-J11, mRNA sequence.
ACCESSION
CF300929
VERSION
CF300929.1 GI:33672690
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 13)
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/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
|||||
Db 13 AAAAAAAAAAAAAA 1

RESULT 230
CF300929/c
LOCUS
DEFINITION
7LEAF--05-J11.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa CDNA clone 7LEAF--05-J11, mRNA sequence.
ACCESSION
CF300929
VERSION
CF300929.1 GI:33672690
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 13)
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
|||||
Db 13 AAAAAAAAAAAAAA 1

RESULT 230
CF300929/c
LOCUS
DEFINITION
7LEAF--05-J11.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa CDNA clone 7LEAF--05-J11, mRNA sequence.
ACCESSION
CF300929
VERSION
CF300929.1 GI:33672690
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
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/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
|||||
Db 13 AAAAAAAAAAAAAA 1

RESULT 230
CF300929/c
LOCUS
DEFINITION
7LEAF--05-J11.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa CDNA clone 7LEAF--05-J11, mRNA sequence.
ACCESSION
CF300929
VERSION
CF300929.1 GI:33672690
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 13)
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/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
|||||
Db 13 AAAAAAAAAAAAAA 1

RESULT 230
CF300929/c
LOCUS
DEFINITION
7LEAF--05-J11.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa CDNA clone 7LEAF--05-J11, mRNA sequence.
ACCESSION
CF300929
VERSION
CF300929.1 GI:33672690
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
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/dev_stage="7 days after germination"
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/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
|||||
Db 13 AAAAAAAAAAAAAA 1

RESULT 230
CF300929/c
LOCUS
DEFINITION
7LEAF--05-J11.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa CDNA clone 7LEAF--05-J11, mRNA sequence.
ACCESSION
CF300929
VERSION
CF300929.1 GI:33672690
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 13)
/dev_stage="7 days after germination"
/lab_host="E.coli DH


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QY      1481 AAAAAAAAAAAAAA 1493
      13 bp mRNA linear EST 15-AUG-2003
Db      13 AAAAAAAAAAAAAA 1

RESULT 235
CF302898/c
LOCUS   7LEAF--08-N08.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION   sativa cDNA clone 7LEAF--08-N08, mRNA sequence.
ACCESSION   CF302898
VERSION     CF302898.1 GI:33674659
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 13)
AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL    Unpublished (2003)
COMMENT    Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
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                        /mol_type="mRNA"
                        /cultivar="Nackdong"
                        /db_xref="taxon:4530"
                        /clone="7LEAF--08-N08"
                        /tissue_type="leaf"
                        /dev_stage="7 days after germination"
                        /lab_host="E.coli DH10B"
                        /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                        /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
                        with oligoribonucleotides and then used as templates for
                        RT-PCR."

Query Match      0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred.No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAA 1493
      13 bp mRNA linear EST 15-AUG-2003
Db      13 AAAAAAAAAAAAAA 1

RESULT 236
CF310516/c
LOCUS   ABF--05-D09.b1 ABF3-overexpressing transgenic rice plasmid cDNA
DEFINITION   library (ABF) Oryza sativa cDNA clone ABF--05-D09, mRNA sequence.
ACCESSION   CF310516
VERSION     CF310516.1 GI:33682277
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 13)
AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL    Unpublished (2003)
COMMENT    Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
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                        /organism="Oryza sativa"
                        /mol_type="mRNA"
                        /cultivar="Nackdong"
                        /db_xref="taxon:4530"
                        /clone="7LEAF--08-N08"
                        /tissue_type="leaf"
                        /dev_stage="7 days after germination"
                        /lab_host="E.coli DH10B"
                        /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                        /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
                        with oligoribonucleotides and then used as templates for
                        RT-PCR."

Query Match      0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred.No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAA 1493
      13 bp mRNA linear EST 15-AUG-2003
Db      13 AAAAAAAAAAAAAA 1

RESULT 237
CF310517/c
LOCUS   ABF--05-D09.g1 ABF3-overexpressing transgenic rice plasmid cDNA
DEFINITION   library (ABF) Oryza sativa cDNA clone ABF--05-D09, mRNA sequence.
ACCESSION   CF310517
VERSION     CF310517.1 GI:33682278
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 13)
AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL    Unpublished (2003)
COMMENT    Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
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                        /mol_type="mRNA"
                        /cultivar="Nackdong"
                        /db_xref="taxon:4530"
                        /clone="ABF--05-D09"
                        /tissue_type="leaf"
                        /dev_stage="14 days after germination"
                        /lab_host="E.coli DH10B"
                        /clone_lib="ABF3-overexpressing transgenic rice plasmid
                        cDNA library (ABF)"
                        /note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
                        for 2hrs. Oligo-capped mRNA was reverse transcribed and
                        then used for PCR. mRNA was prepared from ABA-responsive
                        element binding transcription factor 3 overexpression
                        line."

```

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES Location/Qualifiers
 source 1..13
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
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 /clone="ABF--05-D09"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
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 /clone_lib="ABF3-overexpressing transgenic rice plasmid
 cDNA library (ABF)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
 for 2hrs. Oligo-capped mRNA was reverse transcribed and
 then used for PCR. mRNA was prepared from ABA-responsive
 element binding transcription factor 3 overexpression
 line."

Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred.No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
 13 bp mRNA linear EST 15-AUG-2003
Db 13 AAAAAAAAAAAAAA 1

RESULT 237
CF310517/c
LOCUS ABF--05-D09.g1 ABF3-overexpressing transgenic rice plasmid cDNA
DEFINITION library (ABF) Oryza sativa cDNA clone ABF--05-D09, mRNA sequence.
ACCESSION CF310517
VERSION CF310517.1 GI:33682278
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred.No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
 13 bp mRNA linear EST 15-AUG-2003
Db 13 AAAAAAAAAAAAAA 1

RESULT 236
CF310516/c
LOCUS ABF--05-D09.b1 ABF3-overexpressing transgenic rice plasmid cDNA
DEFINITION library (ABF) Oryza sativa cDNA clone ABF--05-D09, mRNA sequence.
ACCESSION CF310516
VERSION CF310516.1 GI:33682277
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES Location/Qualifiers
 source 1..13
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="ABF--05-D09"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="ABF3-overexpressing transgenic rice plasmid
 cDNA library (ABF)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
 for 2hrs. Oligo-capped mRNA was reverse transcribed and
 then used for PCR. mRNA was prepared from ABA-responsive
 element binding transcription factor 3 overexpression
 line."

element binding transcription factor 3 overexpression
line."

Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1493
|||||
Db 1 AAAAAAAAAAAAAA 13

RESULT 238
CF312721/c
LOCUS 13 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--08-J13.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--08-J13, mRNA sequence.

ACCESSION CF312721
VERSION CF312721.1 GI:33684482
KEYWORDS EST.
SOURCE Oryza sativa

ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 13)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES Location/Qualifiers

1..13

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="ABF--08-J13"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="ABF3-overexpressing transgenic rice plasmid

cDNA library (ABF)"

/note="vector: PCR4-TOPO; Site_1: EcoRI; Leaf was dried

for 2hrs. Oligo-capped mRNA was reverse transcribed and

then used for PCR. mRNA was prepared from ABA-responsive

element binding transcription factor 3 overexpression

line."

Query Match 0.9%; Score 13; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1493
|||||
Db 13 AAAAAAAAAAAAAA 1

RESULT 239
CF313171/c
LOCUS 13 bp mRNA linear EST 15-AUG-2003

DEFINITION HD--01-D10.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA

library (HD) Oryza sativa cDNA clone HD--01-D10, mRNA sequence.

ACCESSION CF313171

VERSION CF313171.1 GI:33684932

KEYWORDS EST.

SOURCE Oryza sativa

1..13

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="ABF--08-J13"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="ABF3-overexpressing transgenic rice plasmid

cDNA library (ABF)"

/note="vector: PCR4-TOPO; Site_1: EcoRI; Leaf was dried

for 2hrs. Oligo-capped mRNA was reverse transcribed and

then used for PCR. mRNA was prepared from ABA-responsive

element binding transcription factor 3 overexpression

line."

Query Match 0.9%; Score 13; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1493

|||||

Db 13 AAAAAAAAAAAAAA 1

RESULT 239

CF313171/c

LOCUS 13 bp mRNA linear EST 15-AUG-2003

DEFINITION HD--01-D10.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA

library (HD) Oryza sativa cDNA clone HD--01-D10, mRNA sequence.

ACCESSION CF313171

VERSION CF313171.1 GI:33684932

KEYWORDS EST.

SOURCE Oryza sativa

1..13

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="ABF--08-J13"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="ABF3-overexpressing transgenic rice plasmid

cDNA library (ABF)"

/note="vector: PCR4-TOPO; Site_1: EcoRI; Leaf was dried

for 2hrs. Oligo-capped mRNA was reverse transcribed and

then used for PCR. mRNA was prepared from ABA-responsive

element binding transcription factor 3 overexpression

line."

Query Match 0.9%; Score 13; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1493

|||||

Db 13 AAAAAAAAAAAAAA 1

RESULT 239

CF313171/c

LOCUS 13 bp mRNA linear EST 15-AUG-2003

DEFINITION HD--01-D10.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA

library (HD) Oryza sativa cDNA clone HD--01-D10, mRNA sequence.

ACCESSION CF313171

VERSION CF313171.1 GI:33684932

KEYWORDS EST.

SOURCE Oryza sativa

1..13

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="ABF--08-J13"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="ABF3-overexpressing transgenic rice plasmid

cDNA library (ABF)"

/note="vector: PCR4-TOPO; Site_1: EcoRI; Leaf was dried

for 2hrs. Oligo-capped mRNA was reverse transcribed and

then used for PCR. mRNA was prepared from ABA-responsive

element binding transcription factor 3 overexpression

line."

Query Match 0.9%; Score 13; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1493

|||||

Db 13 AAAAAAAAAAAAAA 1

RESULT 239

CF313171/c

LOCUS 13 bp mRNA linear EST 15-AUG-2003

DEFINITION HD--01-D10.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA

library (HD) Oryza sativa cDNA clone HD--01-D10, mRNA sequence.

ACCESSION CF313171

VERSION CF313171.1 GI:33684932

KEYWORDS EST.

SOURCE Oryza sativa

1..13

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="ABF--08-J13"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="ABF3-overexpressing transgenic rice plasmid

cDNA library (ABF)"

/note="vector: PCR4-TOPO; Site_1: EcoRI; Leaf was dried

for 2hrs. Oligo-capped mRNA was reverse transcribed and

then used for PCR. mRNA was prepared from ABA-responsive

element binding transcription factor 3 overexpression

line."

Query Match 0.9%; Score 13; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1493

|||||

Db 13 AAAAAAAAAAAAAA 1

RESULT 239

CF313171/c

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DEFINITION HD--01-D10.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA

library (HD) Oryza sativa cDNA clone HD--01-D10, mRNA sequence.

ACCESSION CF313171

VERSION CF313171.1 GI:33684932

KEYWORDS EST.

SOURCE Oryza sativa

1..13

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="ABF--08-J13"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="ABF3-overexpressing transgenic rice plasmid

cDNA library (ABF)"

/note="vector: PCR4-TOPO; Site_1: EcoRI; Leaf was dried

for 2hrs. Oligo-capped mRNA was reverse transcribed and

then used for PCR. mRNA was prepared from ABA-responsive

element binding transcription factor 3 overexpression

line."

Query Match 0.9%; Score 13; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1493

|||||

Db 13 AAAAAAAAAAAAAA 1

RESULT 239

CF313171/c

LOCUS 13 bp mRNA linear EST 15-AUG-2003

DEFINITION HD--01-D10.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA

library (HD) Oryza sativa cDNA clone HD--01-D10, mRNA sequence.

ACCESSION CF313171

VERSION CF313171.1 GI:33684932

KEYWORDS EST.

SOURCE Oryza sativa

1..13

/organism="Oryza sativa"

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/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="ABF--08-J13"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="ABF3-overexpressing transgenic rice plasmid

cDNA library (ABF)"

/note="vector: PCR4-TOPO; Site_1: EcoRI; Leaf was dried

for 2hrs. Oligo-capped mRNA was reverse transcribed and

then used for PCR. mRNA was prepared from ABA-responsive

element binding transcription factor 3 overexpression

line."

Query Match 0.9%; Score 13; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1493

|||||

Db 13 AAAAAAAAAAAAAA 1

RESULT 239

CF313171/c

LOCUS 13 bp mRNA linear EST 15-AUG-2003

DEFINITION HD--01-D10.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA

library (HD) Oryza sativa cDNA clone HD--01-D10, mRNA sequence.

ACCESSION CF313171

VERSION CF313171.1 GI:33684932

KEYWORDS EST.

SOURCE Oryza sativa

1..13

/organism="Oryza sativa"

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/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="ABF--08-J13"

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/lab_host="E.coli DH10B"

/clone_lib="ABF3-over

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/clone="HD-02-L01"
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/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

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Query Match 0.9%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1481 AAAAAAAAAAAAAA 1493
    |||||
Db 13 AAAAAAAAAAAAAA 1

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RESULT 241
CF314874/c
LOCUS
DEFINITION
HD--03-J07.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--03-J07, mRNA sequence.
ACCESSION
CF314874
VERSION
CF314874.1 GI:33686635
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 13)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

```

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FEATURES
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            /clone_lib="OshDAC1-overexpressing transgenic rice plasmid
            cDNA library (HD)"
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            treated with ABA(20um) for 1hr. Oligo-capped mRNA was
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            derived from rice Histone Deacetylase overexpression
            line."
Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1481 AAAAAAAAAAAAAA 1493

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    |||||
Db 13 AAAAAAAAAAAAAA 1

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RESULT 241
CF314874/c
LOCUS
DEFINITION
HD--03-J07.g1 OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD) Oryza sativa cDNA clone HD--03-J07, mRNA sequence.
ACCESSION
CF314874
VERSION
CF314874.1 GI:33686635
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 13)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

```

Query Match 0.9%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1481 AAAAAAAAAAAAAA 1493
    |||||
Db 13 AAAAAAAAAAAAAA 1

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RESULT 242
CF315395/c
LOCUS
DEFINITION
HD--04-E20.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--04-E20, mRNA sequence.
ACCESSION
CF315395
VERSION
CF315395.1 GI:33687156
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 13)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

```

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FEATURES
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            /tissue_type="callus"
            /dev_stage="proliferated callus on 2N6 media for 2 weeks"
            /lab_host="E.coli DH10B"
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            cDNA library (HD)"
            /notes="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was
            treated with ABA(20um) for 1hr. Oligo-capped mRNA was
            reverse transcribed and then used for PCR. mRNA was
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            line."
Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1481 AAAAAAAAAAAAAA 1493
    |||||
Db 13 AAAAAAAAAAAAAA 1

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RESULT 243
CF316439/c
LOCUS
DEFINITION
HD--05-l17.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--05-l17, mRNA sequence.
ACCESSION
CF316439
VERSION
CF316439.1 GI:33688200
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 13)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

```

```

FEATURES
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        1..13
            /organism="Oryza sativa"
            /mol_type="mRNA"
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            cDNA library (HD)"
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            treated with ABA(20um) for 1hr. Oligo-capped mRNA was
            reverse transcribed and then used for PCR. mRNA was
            derived from rice Histone Deacetylase overexpression
            line."
Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1481 AAAAAAAAAAAAAA 1493

```

    |||||
Db 13 AAAAAAAAAAAAAA 1

```

of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source

1. .13
/organism="Oryza sativa"
/mol_type="mRNA"
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/lab_host="E.coli DH10B"
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cDNA library (HD)"
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reverse transcribed and then used for PCR. mRNA was
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line."

Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493

Db 13 AAAAAAAAAAAAAA 1

RESULT 244

CF316440

LOCUS

DEFINITION HD--05-L17.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--05-L17, mRNA sequence.

ACCESSION CF316440

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa
Oryza sativa
Rukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 13)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

CONTACT: Nahm B.H.

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of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

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cDNA library (HD)"
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line."

Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493

Db 13 AAAAAAAAAAAAAA 1

RESULT 246

CF318290

LOCUS

DEFINITION HD--08-F19.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--08-F19, mRNA sequence.

ACCESSION CF318290

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa

Oryza sativa

Rukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 13)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

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Unpublished (2003)

CONTACT: Nahm B.H.

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Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

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1. .13
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/lab_host="E.coli DH10B"
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cDNA library (HD)"
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treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493

Db 13 AAAAAAAAAAAAAA 1

RESULT 246

CF318290

LOCUS

DEFINITION HD--08-F19.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--08-F19, mRNA sequence.

ACCESSION CF318290

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa

Oryza sativa

Rukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 13)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

CONTACT: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source

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/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="vector: PCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493

Db 13 AAAAAAAAAAAAAA 1

RESULT 246

CF318290

LOCUS

DEFINITION HD--08-F19.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--08-F19, mRNA sequence.

ACCESSION CF318290

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa

Oryza sativa

Rukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 13)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

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Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source

1. .13
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/cultivar="Nackdong"
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cDNA library (HD)"
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derived from rice Histone Deacetylase overexpression
line."

Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
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QY 1481 AAAAAAAAAAAAAA 1493

Db 13 AAAAAAAAAAAAAA 1

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL

COMMENT Unpublished (2003)

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Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

Location/Qualifiers

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/organism="Oryza sativa"

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/cultivar="Nackdong"

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line."

Query Match

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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1481 AAAAAAAAAAAAAA 1493

Db 13 AAAAAAAAAAAAAA 1

RESULT 247

CF319066/c

LOCUS HD--09-H02.b1 OSHDAc1-overexpressing transgenic rice plasmid cDNA

library (HD) Oryza sativa cDNA clone HD--09-H02, mRNA sequence.

CF319066

CF319066.1 GI:33690827

EST.

KEYWORDS Oryza sativa

SOURCE Oryza sativa

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

1. (bases 1 to 13)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

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Unpublished (2003)

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Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1. .13

/organism="Oryza sativa"

/mol_type="mRNA"

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/db_xref="taxon:4530"

FEATURES

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Location/Qualifiers

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/clone_lib="OSHDAc1-overexpressing transgenic rice plasmid

cDNA library (HD)"

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derived from rice Histone Deacetylase overexpression

line."

Query Match

Best Local Similarity 0.9%; Score 13; DB 1; Length 13;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1481 AAAAAAAAAAAAAA 1493

Db 13 AAAAAAAAAAAAAA 1

RESULT 248

CF319531/c

LOCUS HD--10-B03.b1 OSHDAc1-overexpressing transgenic rice plasmid cDNA

library (HD) Oryza sativa cDNA clone HD--10-B03, mRNA sequence.

CF319531

CF319531.1 GI:33691292

EST.

KEYWORDS Oryza sativa

SOURCE Oryza sativa

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

1. (bases 1 to 13)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

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Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1. .13

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/clone_lib="OSHDAc1-overexpressing transgenic rice plasmid

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/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was

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reverse transcribed and then used for PCR. mRNA was

derived from rice Histone Deacetylase overexpression

line."

Query Match

Best Local Similarity 0.9%; Score 13; DB 1; Length 13;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1481 AAAAAAAAAAAAAA 1493

Db 13 AAAAAAAAAAAAAA 1


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Query Match          0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAA 1493
DB 13 AAAAAAAAAAAAA 1

RESULT 252
CF320018
LOCUS
DEFINITION
HD--10-L20.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--10-L20, mRNA sequence.
ACCESSION
CF320018
VERSION
CF320018.1 GI:33691779
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 13)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source
1..13
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD--10-L20"
/tissue_type="callus"
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/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."
Query Match          0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAA 1493
DB 13 AAAAAAAAAAAAA 1

RESULT 254
CF320938/c
LOCUS
DEFINITION
HD--12-A06.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--12-A06, mRNA sequence.
ACCESSION
CF320938
VERSION
CF320938.1 GI:33692699
KEYWORDS
SOURCE
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 13)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Unpublished (2003)
CONTACT: Nahm B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source
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/dev_stage="proliferated callus on 2N6 media for 2 weeks"
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cDNA library (HD)"
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treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."
Query Match          0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
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QY 1481 AAAAAAAAAAAAA 1493
DB 13 AAAAAAAAAAAAA 13

RESULT 253
CF320143/c
LOCUS
DEFINITION
HD--10-O13.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--10-O13, mRNA sequence.
ACCESSION
CF320143
VERSION
CF320143.1 GI:33691904
KEYWORDS
SOURCE
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 13)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Unpublished (2003)
CONTACT: Nahm B.H.
of Bioscience and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source
1..13
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Contact: Nahm B.H.
of Bioscience and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

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Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAA 1493

DB 13 AAAAAAAAAAAAA 1

RESULT 254

CF320938/c

LOCUS

DEFINITION

HD--12-A06.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA

library (HD) Oryza sativa cDNA clone HD--12-A06, mRNA sequence.

ACCESSION

CF320938

VERSION

CF320938.1 GI:33692699

KEYWORDS

EST.

SOURCE

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

1 (bases 1 to 13)

AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

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Unpublished (2003)

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Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

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/organism="Oryza sativa"

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/db_xref="taxon:4530"

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RT-PCR."

Query Match      0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
Db 13 AAAAAAAAAAAAAA 1

RESULT 258
CF327340
LOCUS
DEFINITION
NACL--01-M15.g1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--01-M15, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 13)
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/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
Db 13 AAAAAAAAAAAAAA 13

RESULT 259
CF327576
LOCUS
DEFINITION
NACL--02-B22.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--02-B22, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
Db 13 AAAAAAAAAAAAAA 1

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DEFINITION
NACL--02-B22.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--02-B22, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 13)
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/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
Db 13 AAAAAAAAAAAAAA 1

RESULT 260
CF327888/c
LOCUS
DEFINITION
NACL--02-122.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--02-122, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Ehrhartoideae; Oryzaceae; Oryza.
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/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
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RT-PCR."

Query Match      0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
Db 13 AAAAAAAAAAAAAA 1

RESULT 260
CF327888/c
LOCUS
DEFINITION
NACL--02-122.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--02-122, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 13)
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 13 AAAAAAAAAAAAAA 1

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Query Match 0.9%; Score 13; DB 1; Length 13;
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 13 AAAAAAAAAAAAAA 1

RESULT 261
CF327939/c

LOCUS
DEFINITION
NACL--02-K02.g1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--02-K02, mRNA sequence.

ACCESSION
CF327939

VERSION
CF327939.1 GI:33804127

KEYWORDS
EST.

SOURCE
Oryza sativa

ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Unpublished (2003)
Contact: Nahm B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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1. .13
/organism="Oryza sativa"
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Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 13 AAAAAAAAAAAAAA 1

RESULT 262
CF328153/c

LOCUS
DEFINITION
NACL--02-O19.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--02-O19, mRNA sequence.

ACCESSION
CF328153

VERSION
CF328153.1 GI:33804556

KEYWORDS
EST.

SOURCE
Oryza sativa

ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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1. .13
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
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Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
|||||
Db 13 AAAAAAAAAAAAAA 1

RESULT 262
CF328153/c

LOCUS
DEFINITION
NACL--02-O19.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--02-O19, mRNA sequence.

ACCESSION
CF328153

VERSION
CF328153.1 GI:33804556

KEYWORDS
EST.

SOURCE
Oryza sativa

ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
|||||
Db 13 AAAAAAAAAAAAAA 1

RESULT 263
CF328228/c

LOCUS
DEFINITION
NACL--03-A13.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--03-A13, mRNA sequence.

ACCESSION
CF328228

VERSION
CF328228.1 GI:33804702

KEYWORDS
EST.

SOURCE
Oryza sativa

ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Unpublished (2003)
Contact: Nahm B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
Location/Qualifiers

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

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RT-PCR."

Query Match      0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
Db 1 AAAAAAAAAAAAAA 13

RESULT 270
CF329800/C
LOCUS
DEFINITION
NACL--05-E04.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--05-E04, mRNA sequence.
CF329800
VERSION
CF329800.1 GI:33807817
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaeae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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/clone_lib="Rice callus plasmid cDNA library (NACL)"
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
Db 1 AAAAAAAAAAAAAA 13

RESULT 272
CF329869/C
LOCUS
DEFINITION
NACL--05-F18.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--05-F18, mRNA sequence.
CF329869
VERSION
CF329869.1 GI:33807959
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaeae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Contact: Nahm B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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1. .13
/organism="Oryza sativa"
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
Db 1 AAAAAAAAAAAAAA 13

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RESULT 271
CF329801
LOCUS
DEFINITION
NACL--05-E04.g1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--05-E04, mRNA sequence.
CF329801
VERSION
CF329801.1 GI:33807819
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaeae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source
1. .13
/organism="Oryza sativa"
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/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
Db 1 AAAAAAAAAAAAAA 13

RESULT 272
CF329869/C
LOCUS
DEFINITION
NACL--05-F18.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--05-F18, mRNA sequence.
CF329869
VERSION
CF329869.1 GI:33807959
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaeae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source
1. .13
/organism="Oryza sativa"
/mol_type="mRNA"
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/clone_lib="Rice callus plasmid cDNA library (NACL)"
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
Db 1 AAAAAAAAAAAAAA 13

```

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Email: bhnamh@gbio.com, bhnamh@bio.myongji.ac.kr.

FEATURES

source

1. .13
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/tissue_type="callus"
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Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493

Db 13 AAAAAAAAAAAAAA 1

RESULT 273

CF329946/c

LOCUS 13 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--05-H12.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--05-H12, mRNA sequence.

ACCESSION CF329946

VERSION CF329946.1

GI:33808114

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 13)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355

Email: bhnamh@gbio.com, bhnamh@bio.myongji.ac.kr.

FEATURES

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Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493

Db 13 AAAAAAAAAAAAAA 1

RESULT 274

CF329988/c

LOCUS 13 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--05-I10.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--05-I10, mRNA sequence.

ACCESSION CF329988

VERSION CF329988.1

GI:33808198

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 13)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355

FEATURES

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1. .13
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Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493

Db 13 AAAAAAAAAAAAAA 1

RESULT 275

CF330023/c

LOCUS 13 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--05-J05.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--05-J05, mRNA sequence.

ACCESSION CF330023

VERSION CF330023.1

GI:33808268

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 13)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source
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 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1481 AAAAAAAAAAAAA 1493
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 Db 13 AAAAAAAAAAAAA 1

RESULT 276

CF330725
 LOCUS
 DEFINITION
 NACL--06-J01.g1 Rice callus plasmid cDNA library (NACL) Oryza
 sativa cDNA clone NACL--06-J01, mRNA sequence.
 CF330725
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 13)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

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 1. .13
 Location/Qualifiers
 /organism="Oryza sativa"
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 /lab_host="E.coli DH10B"
 /clone_lib="Rice callus plasmid cDNA library (NACL)"
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 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1481 AAAAAAAAAAAAA 1493
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Db 1 AAAAAAAAAAAAA 13
 RESULT 277
 CF331041/c
 LOCUS
 DEFINITION
 NACL--07-A04.b1 Rice callus plasmid cDNA library (NACL) Oryza
 sativa cDNA clone NACL--07-A04, mRNA sequence.
 CF331041
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 13)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

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 Location/Qualifiers
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 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Db 13 AAAAAAAAAAAAA 1

RESULT 278

CF331266/c
 LOCUS
 DEFINITION
 NACL--07-F06.b1 Rice callus plasmid cDNA library (NACL) Oryza
 sativa cDNA clone NACL--07-F06, mRNA sequence.
 CF331266
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 13)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University

```

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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source
1. .13
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--07-F06"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
Db 13 AAAAAAAAAAAAAA 1

RESULT 279
LOCUS CF331273
DEFINITION NACL--07-F09.g1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--07-F09, mRNA sequence.
ACCESSION CF331273
VERSION CF331273.1 GI:33810757
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 13)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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1. .13
/organism="Oryza sativa"
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/tissue_type="callus"
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/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
Db 13 AAAAAAAAAAAAAA 1

RESULT 280
LOCUS CF331903/c
DEFINITION NACL--08-D07.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--08-D07, mRNA sequence.
ACCESSION CF331903
VERSION CF331903.1 GI:33812027
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 13)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source
1. .13
/organism="Oryza sativa"
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/db_xref="taxon:4530"
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/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
Db 13 AAAAAAAAAAAAAA 1

RESULT 281
LOCUS CF332079/c
DEFINITION NACL--08-H04.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--08-H04, mRNA sequence.
ACCESSION CF332079
VERSION CF332079.1 GI:33812379
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 13)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source
1. .13
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--07-F09"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
Db 13 AAAAAAAAAAAAAA 1493

```

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Tel: 82 31 330 6193
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Email: bhnamh@bio.com, bhnamh@bio.myongji.ac.kr.

FEATURES

source

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1. .13
/organism="Oryza sativa"
/mol_type="mRNA"
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/tissue_type="callus"
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/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
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with oligoribonucleotides and then used as templates for
RT-PCR."
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Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493

Db 13 AAAAAAAAAAAAAA 1

RESULT 282

CF332695/c

LOCUS

DEFINITION JMT--01-E21.b1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--01-E21, mRNA sequence.

ACCESSION CF332695

VERSION CF332695.1 GI:33813618

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 13)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

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Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnamh@bio.com, bhnamh@bio.myongji.ac.kr.

FEATURES

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1. .13
/organism="Oryza sativa"
/mol_type="mRNA"
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/lab_host="E.coli DH10B"
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/notes="Vector: PCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
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prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."
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Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493

Db 13 AAAAAAAAAAAAAA 1

RESULT 283

CF332696

LOCUS

DEFINITION JMT--01-E21.g1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--01-E21, mRNA sequence.

ACCESSION CF332696

VERSION CF332696.1 GI:33813620

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 13)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

Of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnamh@bio.com, bhnamh@bio.myongji.ac.kr.

FEATURES

source

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1. .13
/organism="Oryza sativa"
/mol_type="mRNA"
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cDNA library (JMT)"
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prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."
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Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493

Db 1 AAAAAAAAAAAAAA 13

RESULT 284

CF333486/c

LOCUS

DEFINITION JMT--02-G11.b1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--02-G11, mRNA sequence.

ACCESSION CF333486

VERSION CF333486.1 GI:33815268

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 13)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,


```

SOURCE      Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 13)
AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL    Unpublished (2003)
COMMENT    Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahmeggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES   Location/Qualifiers
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Query Match      0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAA 1493
Db      13 AAAAAAAAAAAAAA 1

RESULT 289
CF337022/c
LOCUS      CF337022
DEFINITION NACL--01-J16.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--01-J16, mRNA sequence.
ACCESSION  CF337023
VERSION     CF337203.1 GI:33802665
KEYWORDS   EST.
SOURCE      Oryza sativa
ORGANISM    Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 14)
AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL    Unpublished (2003)
COMMENT    Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahmeggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES   Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAA 1493
Db      13 AAAAAAAAAAAAAA 1

RESULT 290
CF301021
LOCUS      CF301021
DEFINITION NACL--01-J16.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--01-J16, mRNA sequence.
ACCESSION  CF337203
VERSION     CF337203.1 GI:33802665
KEYWORDS   EST.
SOURCE      Oryza sativa
ORGANISM    Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 14)
AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL    Unpublished (2003)
COMMENT    Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahmeggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES   Location/Qualifiers
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             /organism="Oryza sativa"
             /mol_type="mRNA"
             /cultivar="Nackdong"

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DEFINITION 7LEAF--05-L10.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--05-L10, mRNA sequence.

ACCESSION CF301021
VERSION CF301021.1 GI:33672782

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 14)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

Location/Qualifiers

1. 14

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/cultivar="Nackdong"

/db_xref="taxon:4530"

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/tissue_type="leaf"

/dev_stage="7 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"

/notes="Vector: PCR4-TOPO; Site 1: EcorI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

Query Match 0.8%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494

||||| |||||

1 AAAAAAAAAAAAAA 14

RESULT 291

CF297251

LOCUS

DEFINITION 30DGS--07-P12.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza

sativa cDNA clone 30DGS--07-P12, mRNA sequence.

ACCESSION CF297251

VERSION CF297251.1 GI:33666284

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 17)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

Location/Qualifiers

1. 17

FEATURES

source

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="30DGS--07-P12"

/tissue_type="leaf"

/dev_stage="30 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"

/notes="Vector: PCR4-TOPO; Site 1: EcorI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

Query Match

Best Local Similarity 82.4%; Score 12.2; DB 1; Length 17;

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1086 TTTTGTGTTTGTCTGA 1102

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1 TTTTGTGTTTGTCTGA 17

RESULT 292

AL048754/c

LOCUS

DEFINITION 18 bp mRNA linear EST 04-SEP-2003

DKFZp566L173.r1 566 (synonym: hfkd2) Homo sapiens cDNA clone

AL048754

ACCESSION AL048754

VERSION AL048754.1 GI:4727825

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 18)

AUTHORS Koehler,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.

EST (Koehler, et al.)

Unpublished (1999)

COMMENT Contact: MIPS

MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES

source

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/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="DKFZp566L173"

/tissue_type="kidney"

/dev_stage="fetal"

/lab_host="X1-2blue"

/clone_lib="566 (synonym: hfkd2)"

/note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

Query Match

Best Local Similarity 82.4%; Score 12.2; DB 1; Length 18;

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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17 TTTTGTGTTTGTCTGA 1

RESULT 293

CF291665

LOCUS

DEFINITION 19 bp mRNA linear EST 14-AUG-2003

14ROOT--02-D01.g1 Rice root plasmid cDNA library (14ROOT) Oryza

sativa cDNA clone 14ROOT--02-D01, mRNA sequence.

ACCESSION CF291665

VERSION CF291665.1 GI:33660698

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 19)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.

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Fax: 82 31 321 6355
Email: bhnamh@bio.com, bhnamh@bio.myongji.ac.kr.

FEATURES

source

1. .19
Location/Qualifiers
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
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/lab_host="E.coli DH108"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: PCR4-TOPO; Site 1: ECORI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.8%; Score 12.2; DB 1; Length 19;
Best Local Similarity 82.4%; Pred. No. 4.5e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1086 TTTTGTGTTGTCCTCA 1102
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Db 3 TTTTGTGTTTCTTCA 19

RESULT 294
BG668943
LOCUS DRN03E05 Rat DRG Library Rattus norvegicus cDNA clone DRN03E05 5',
DEFINITION mRNA sequence.
ACCESSION BG668943
VERSION 1 GI:138990865
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 12)
AUTHORS Xiao,H.S., Huang,Q.H., Zhang,F.X., Bao,L., Lu,Y.J., Guo,C.,
Yang,L., Huang,W.J., Fu,G., Xu,S.H., Cheng,X.P., Yan,Q., Zhu,Z.D.,
Zhang,X., Chen,Z., Han,Z.G. and Zhang,X.
TITLE Identification of gene expression profile of dorsal root ganglion
in the rat peripheral axotomy model of neuropathic pain
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (12), 8360-8366 (2002)
MEDLINE 22056133
PUBMED 12060780
COMMENT Contact: Zhang Xu
Laboratory of Sensory System
Institute of Neuroscience
320 Yue Yang Road, Shanghai 200031, P.R.China
Tel: 86-21-64748700-121
Fax: 86-21-64713446
Email: xu.zhang@ion.ac.cn

This clone is also available at Chinese National Human Genome
Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park,
Pudong New Area, P.R.China. Please contact with Zhang Xu
(xu.zhang@ion.ac.cn) or Han Zeguog (hanzg@chgc.sh.cn)
PCR Primers
FORWARD: T3

BACKWARD: T7
Seq primer: T3
POLYA=No.

FEATURES

source

1. .12
Location/Qualifiers
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="DRN03E05"
/sex="male"
/tissue_type="dorsal root ganglion"
/dev_stage="adult"
/clone_lib="Rat DRG Library"

Query Match 0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAA 1492
|||||
Db 1 AAAAAAAAAA 12

RESULT 295

LOCUS BG582536/c

DEFINITION cDNA clone 024-007-P01-12 bp mRNA linear EST 06-DEC-2002
S013300-024-007-P01-T7 MP12-ADIS-024-inflorescence Beta vulgaris
ACCESSION BG582536
VERSION 1 GI:26112113
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.

REFERENCE 1 (bases 1 to 12)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B

ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851

Email: weisshaar@piz-koeln.mpg.de
Insert Length: 12 Std Error: 0.00
Plate: 7 row: P column: 01
Seq primer: T7; GTAATACGACTCCTACTAGGCG.

FEATURES

source

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/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:184167"
/db_xref="taxon:161934"
/clone="024-007-P01"
/tissue_type="inflorescence"
/lab_host="EMDH108"
/clone_lib="MP12-ADIS-024-inflorescence"

/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatgut AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:

```

Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary Database: http://gabi.rzpd.de"

Query Match      0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAA 1492
Db 12 AAAAAAAAAAAAA 1

RESULT 296
BO588719/c
LOCUS
DEFINITION
CDNA clone 024-014-P24-T7 MP12-ADIS-024-storage root Beta vulgaris
EST.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE
1 (bases 1 to 12)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
22362189
12472698
COMMENT
Contact: Weisshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 12 Std Error: 0.00
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Seq primer: T7; GTAATACGACTCCTACTATAGGC.
FEATURES
source
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/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:187286"
/db_xref="taxon:161934"
/clone="024-014-P24"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MP12-ADIS-024-storage root"
/notes="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCAGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary Database: http://gabi.rzpd.de"

Query Match      0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAA 1492
Db 12 AAAAAAAAAAAAA 1

RESULT 298
CF279278/c
LOCUS
DEFINITION
Oryza sativa cDNA clone 14ETL-05-110, mRNA sequence.
CF279278
ACCESSION

```

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|||||
12 AAAAAAAAAAAAA 1

RESULT 297
BO594698/c
LOCUS
DEFINITION
CDNA clone 024-024-E05-T7 MP12-ADIS-024-developing root Beta vulgaris
EST.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE
1 (bases 1 to 12)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
22362189
12472698
COMMENT
Contact: Weisshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 12 Std Error: 0.00
Plate: 24 row: E column: 05
Seq primer: T7; GTAATACGACTCCTACTATAGGC.
FEATURES
source
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/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
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/db_xref="taxon:161934"
/clone="024-024-E05"
/tissue_type="developing root"
/lab_host="EMDH10B"
/clone_lib="MP12-ADIS-024-developing root"
/notes="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCAGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary Database: http://gabi.rzpd.de"

Query Match      0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAA 1492
Db 12 AAAAAAAAAAAAA 1

RESULT 298
CF279278/c
LOCUS
DEFINITION
Oryza sativa cDNA clone 14ETL-05-110, mRNA sequence.
CF279278
ACCESSION

```

```

CF279278.1 GI:33656664
EST.
SOURCE
ORGANISM
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 12)
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
REFERENCE
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6355
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .12
/organism="Oryza sativa"
/mol type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/db_xref="taxon:4530"
/tissue type="leaf"
/dev stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
Query Match 0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAA 1492
DB 12 AAAAAAAAAA 1

RESULT 299
CF291428
LOCUS 1481 AAAAAAAAAA 1492 bp mRNA linear EST 14-AUG-2003
DEFINITION sativa cDNA clone 14ROOT--01-N14, mRNA sequence.
ACCESSION CF291428
VERSION CF291428.1 GI:33660461
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 12)
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with oligoribonucleotides and then used as templates for
RT-PCR."
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Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAA 1492
DB 12 AAAAAAAAAA 1

RESULT 299
CF291428
LOCUS 1481 AAAAAAAAAA 1492 bp mRNA linear EST 14-AUG-2003
DEFINITION sativa cDNA clone 14ROOT--01-N14, mRNA sequence.
ACCESSION CF291428
VERSION CF291428.1 GI:33660461
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 12)
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
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Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAA 1492
DB 12 AAAAAAAAAA 1

RESULT 299
CF291428
LOCUS 1481 AAAAAAAAAA 1492 bp mRNA linear EST 14-AUG-2003
DEFINITION sativa cDNA clone 14ROOT--01-N14, mRNA sequence.
ACCESSION CF291428
VERSION CF291428.1 GI:33660461
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 12)
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with oligoribonucleotides and then used as templates for
RT-PCR."
Query Match 0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAA 1492
DB 12 AAAAAAAAAA 1

RESULT 299
CF291428
LOCUS 1481 AAAAAAAAAA 1492 bp mRNA linear EST 14-AUG-2003
DEFINITION sativa cDNA clone 14ROOT--01-N14, mRNA sequence.
ACCESSION CF291428
VERSION CF291428.1 GI:33660461
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 12)
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
Query Match 0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAA 1492
DB 12 AAAAAAAAAA 1

RESULT 299
CF291428
LOCUS 1481 AAAAAAAAAA 1492 bp mRNA linear EST 14-AUG-2003
DEFINITION sativa cDNA clone 14ROOT--01-N14, mRNA sequence.
ACCESSION CF291428
VERSION CF291428.1 GI:33660461
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 12)
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with oligoribonucleotides and then used as templates for
RT-PCR."
Query Match 0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAA 1492
DB 12 AAAAAAAAAA 1

RESULT 299
CF291428
LOCUS 1481 AAAAAAAAAA 1492 bp mRNA linear EST 14-AUG-2003
DEFINITION sativa cDNA clone 14ROOT--01-N14, mRNA sequence.
ACCESSION CF291428
VERSION CF291428.1 GI:33660461
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 12)
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
Query Match 0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAA 1492
DB 12 AAAAAAAAAA 1

RESULT 299
CF291428
LOCUS 1481 AAAAAAAAAA 1492 bp mRNA linear EST 14-AUG-2003
DEFINITION sativa cDNA clone 14ROOT--01-N14, mRNA sequence.
ACCESSION CF291428
VERSION CF291428.1 GI:33660461
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 12)
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
Query Match 0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAA 1492
DB 12 AAAAAAAAAA 1

RESULT 299
CF291428
LOCUS 1481 AAAAAAAAAA 1492 bp mRNA linear EST 14-AUG-2003
DEFINITION sativa cDNA clone 14ROOT--01-N14, mRNA sequence.
ACCESSION CF291428
VERSION CF291428.1 GI:33660461
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 12)
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
Query Match 0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAA 1492
DB 12 AAAAAAAAAA 1

RESULT 299
CF291428
LOCUS 1481 AAAAAAAAAA 1492 bp mRNA linear EST 14-AUG-2003
DEFINITION sativa cDNA clone 14ROOT--01-N14, mRNA sequence.
ACCESSION CF291428
VERSION CF291428.1 GI:33660461
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 12)
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
Query Match 0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAA 1492
DB 12 AAAAAAAAAA 1

RESULT 299
CF291428
LOCUS 1481 AAAAAAAAAA 1492 bp mRNA linear EST 14-AUG-2003
DEFINITION sativa cDNA clone 14ROOT--01-N14, mRNA sequence.
ACCESSION CF291428
VERSION CF291428.1 GI:33660461
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 12)
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
Query Match 0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAA 1492
DB 12 AAAAAAAAAA 1

RESULT 299
CF291428
LOCUS 1481 AAAAAAAAAA 1492 bp mRNA linear EST 14-AUG-2003
DEFINITION sativa cDNA clone 14ROOT--01-N14, mRNA sequence.
ACCESSION CF291428
VERSION CF291428.1 GI:33660461
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Eukaryota; Vir
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sativa cDNA clone 14ROOT--02-G04, mRNA sequence.
 CF291801
 VERSION CF291801.1 GI:33660834
 KEYWORDS EST.
 SOURCE
 ORGANISM
 Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 12)
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 CONTACT: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 321 6355
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1. .12
Location/Qualifiers

/organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="14ROOT--02-G04"
 /tissue_type="root"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice root plasmid cDNA library (14ROOT)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.8%; Score 12; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAA 1492

Db 1 AAAAAAAAAAAAA 12

RESULT 302
 CF291805/c
 LOCUS
 DEFINITION 14ROOT--02-I01.b1 Rice root plasmid cDNA library (14ROOT) Oryza
 sativa cDNA clone 14ROOT--02-I01, mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 12)
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 CONTACT: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 321 6355
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1. .12
Location/Qualifiers

/organism="Oryza sativa"
 /mol_type="mRNA"
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 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

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 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAA 1492

Db 1 AAAAAAAAAAAAA 12

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 /clone_lib="Rice root plasmid cDNA library (14ROOT)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.8%; Score 12; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAA 1492

Db 1 AAAAAAAAAAAAA 1

RESULT 303

CF291886

LOCUS
 DEFINITION 14ROOT--02-I01.g1 Rice root plasmid cDNA library (14ROOT) Oryza
 sativa cDNA clone 14ROOT--02-I01, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 12)
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 CONTACT: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 321 6355
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1. .12
Location/Qualifiers

/organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
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 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
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 RT-PCR."

Query Match 0.8%; Score 12; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAA 1492

Db 1 AAAAAAAAAAAAA 12

RESULT 304

CF292107/c

LOCUS

DEFINITION 14ROOT--02-I01.g1 Rice root plasmid cDNA library (14ROOT) Oryza
 sativa cDNA clone 14ROOT--02-I01, mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 12)
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 CONTACT: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 321 6355
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

```

DEFINITION 14ROOT--02-M21.b1 Rice root plasmid cDNA library (14ROOT) Oryza
ACCESSION sativa cDNA clone 14ROOT--02-M21, mRNA sequence.
VERSION CF292107
SOURCE CF292107.1 GI:33661140
KEYWORDS EST.
ORGANISM Oryza sativa
          Oryza sativa
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 12)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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          /dev_stage="14 days after germination"
          /lab_host="E.coli DH10B"
          /clone_lib="Rice root plasmid cDNA library (14ROOT)"
          /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
          with oligoribonucleotides and then used as templates for
          RT-PCR."

Query Match          0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAA 1492
Db 12 AAAAAAAAAA 1

RESULT 305
CF295593/c
LOCUS
DEFINITION 30DGS--05-J18.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
ACCESSION sativa cDNA clone 30DGS--05-J18, mRNA sequence.
VERSION CF295593
KEYWORDS EST.
SOURCE CF295593.1 GI:33664626
ORGANISM Oryza sativa
          Oryza sativa
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 12)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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          /tissue_type="root"
          /dev_stage="14 days after germination"
          /lab_host="E.coli DH10B"
          /clone_lib="Rice root plasmid cDNA library (14ROOT)"
          /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
          with oligoribonucleotides and then used as templates for
          RT-PCR."

Query Match          0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAA 1492
Db 12 AAAAAAAAAA 1

RESULT 305
CF295593/c
LOCUS
DEFINITION 30DGS--05-J18.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
ACCESSION sativa cDNA clone 30DGS--05-J18, mRNA sequence.
VERSION CF295593
KEYWORDS EST.
SOURCE CF295593.1 GI:33664626
ORGANISM Oryza sativa
          Oryza sativa
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 12)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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          /tissue_type="root"
          /dev_stage="14 days after germination"
          /lab_host="E.coli DH10B"
          /clone_lib="Rice root plasmid cDNA library (14ROOT)"
          /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
          with oligoribonucleotides and then used as templates for
          RT-PCR."

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/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="30DGS--05-J18"
/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match          0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAA 1492
Db 12 AAAAAAAAAA 1

RESULT 306
CF298686/c
LOCUS
DEFINITION 7LEAF--02-D15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
ACCESSION sativa cDNA clone 7LEAF--02-D15, mRNA sequence.
VERSION CF298686
KEYWORDS EST.
SOURCE CF298686.1 GI:33670447
ORGANISM Oryza sativa
          Oryza sativa
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 12)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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          /cultivar="Nackdong"
          /db_xref="taxon:4530"
          /clone="7LEAF--02-D15"
          /tissue_type="leaf"
          /dev_stage="7 days after germination"
          /lab_host="E.coli DH10B"
          /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
          /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
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          RT-PCR."

Query Match          0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAA 1492
Db 12 AAAAAAAAAA 1

RESULT 307
CF298672/c

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LOCUS       CF298872               12 bp  mRNA  linear  EST 15-AUG-2003
DEFINITION  7LEAF--02-117.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
ACCESSION   CF298872
VERSION     CF298872.1 GI:33670633
KEYWORDS    EST.
SOURCE      Oryza sativa
            Oryza sativa
ORGANISM    Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 12)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             source
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            /dev_stage="7 days after germination"
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            /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
            /notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
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            RT-PCR."

Query Match      0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAA 1492
Db      12 AAAAAAAAAAAAAA 1

RESULT 308
CF299343
LOCUS       CF299343               12 bp  mRNA  linear  EST 15-AUG-2003
DEFINITION  7LEAF--03-F06.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
ACCESSION   CF299343
VERSION     CF299343.1 GI:33671104
KEYWORDS    EST.
SOURCE      Oryza sativa
            Oryza sativa
ORGANISM    Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 12)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             source
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            /lab_host="E.coli DH10B"
            /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
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            with oligoribonucleotides and then used as templates for
            RT-PCR."

Query Match      0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAA 1492
Db      12 AAAAAAAAAAAAAA 1

RESULT 308
CF299343
LOCUS       CF299343               12 bp  mRNA  linear  EST 15-AUG-2003
DEFINITION  7LEAF--03-F06.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
ACCESSION   CF299343
VERSION     CF299343.1 GI:33671104
KEYWORDS    EST.
SOURCE      Oryza sativa
            Oryza sativa
ORGANISM    Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 12)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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            /lab_host="E.coli DH10B"
            /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
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            with oligoribonucleotides and then used as templates for
            RT-PCR."

Query Match      0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAA 1492
Db      12 AAAAAAAAAAAAAA 1

RESULT 310
CF299514
LOCUS       CF299514               12 bp  mRNA  linear  EST 15-AUG-2003
DEFINITION  7LEAF--03-J03.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
ACCESSION   CF299514
VERSION     CF299514.1 GI:33671275
KEYWORDS    EST.
SOURCE      Oryza sativa
            Oryza sativa
ORGANISM    Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 12)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             source
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            /cultivar="Nackdong"
            /db_xref="taxon:4530"
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            /tissue_type="leaf"
            /dev_stage="7 days after germination"
            /lab_host="E.coli DH10B"
            /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
            /notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
            with oligoribonucleotides and then used as templates for
            RT-PCR."

Query Match      0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAA 1492
Db      12 AAAAAAAAAAAAAA 1

RESULT 310
CF299514/c
LOCUS       CF299514/c            12 bp  mRNA  linear  EST 15-AUG-2003
DEFINITION  7LEAF--03-J03.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
ACCESSION   CF299514
VERSION     CF299514.1 GI:33671275
KEYWORDS    EST.
SOURCE      Oryza sativa
            Oryza sativa
ORGANISM    Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 12)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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            /lab_host="E.coli DH10B"
            /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
            /notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
            with oligoribonucleotides and then used as templates for
            RT-PCR."

Query Match      0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAA 1492
Db      12 AAAAAAAAAAAAAA 1

RESULT 310
CF299514/c

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CF300272/c
LOCUS       CF300272                12 bp    mRNA    linear    EST 15-AUG-2003
DEFINITION   7LEAF--04-J19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
             sativa cDNA clone 7LEAF--04-J19, mRNA sequence.
ACCESSION   CF300272
VERSION     CF300272.1   GI:33672033
KEYWORDS    EST.
SOURCE      Oryza sativa
            Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
             Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 12)
            Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
CONTACT     Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
     source           1..12
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
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                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."
     QUERY MATCH      0.8%; Score 12; DB 1; Length 12;
     BEST LOCAL SIMIL 100.0%; Pred. No. 1.5e+02;
     MATCHES          12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAA 1492
Db      12 AAAAAAAAAA 1

RESULT 312
LOCUS     CF300558/c
DEFINITION 7LEAF--05-B09.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
             sativa cDNA clone 7LEAF--05-B09, mRNA sequence.
ACCESSION   CF300558
VERSION     CF300558.1   GI:33672319
KEYWORDS    EST.
SOURCE      Oryza sativa
            Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
             Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 12)
            Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
CONTACT     Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
     source           1..12
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--04-J19"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."
     QUERY MATCH      0.8%; Score 12; DB 1; Length 12;
     BEST LOCAL SIMIL 100.0%; Pred. No. 1.5e+02;
     MATCHES          12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAA 1492
Db      12 AAAAAAAAAA 1

RESULT 311
LOCUS     CF300420/c
DEFINITION 7LEAF--04-M23.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
             sativa cDNA clone 7LEAF--04-M23, mRNA sequence.
ACCESSION   CF300420
VERSION     CF300420.1   GI:33672181
KEYWORDS    EST.
SOURCE      Oryza sativa
            Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
             Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 12)
            Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
CONTACT     Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

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FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--04-M23"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."
     QUERY MATCH      0.8%; Score 12; DB 1; Length 12;
     BEST LOCAL SIMIL 100.0%; Pred. No. 1.5e+02;
     MATCHES          12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAA 1492
Db      12 AAAAAAAAAA 1

RESULT 312
LOCUS     CF300558/c
DEFINITION 7LEAF--05-B09.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
             sativa cDNA clone 7LEAF--05-B09, mRNA sequence.
ACCESSION   CF300558
VERSION     CF300558.1   GI:33672319
KEYWORDS    EST.
SOURCE      Oryza sativa
            Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
             Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 12)
            Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
CONTACT     Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
     source           1..12
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--05-B09"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."
     QUERY MATCH      0.8%; Score 12; DB 1; Length 12;
     BEST LOCAL SIMIL 100.0%; Pred. No. 1.5e+02;
     MATCHES          12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAA 1492
Db      12 AAAAAAAAAA 1

RESULT 311
LOCUS     CF300420/c
DEFINITION 7LEAF--04-M23.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
             sativa cDNA clone 7LEAF--04-M23, mRNA sequence.
ACCESSION   CF300420
VERSION     CF300420.1   GI:33672181
KEYWORDS    EST.
SOURCE      Oryza sativa
            Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
             Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 12)
            Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
CONTACT     Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

```

```

RESULT 313
CF300881/c
LOCUS
DEFINITION
7LEAF--05-110.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--05-110, mRNA sequence.
ACCESSION
CF300881
VERSION
CF300881.1 GI:33672642
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 12)
/lab_host="E.coli DH10B"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
1..12
Location/Qualifiers
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--05-110"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
Query Match 0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAA 1492
Db 12 AAAAAAAAAAAAA 1

RESULT 314
CF301006/c
LOCUS
DEFINITION
7LEAF--05-102.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--05-102, mRNA sequence.
ACCESSION
CF301006
VERSION
CF301006.1 GI:33672767
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 12)
/lab_host="E.coli DH10B"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
1..12
Location/Qualifiers
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--05-110"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
Query Match 0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAA 1492
Db 12 AAAAAAAAAAAAA 1

RESULT 314
CF301006/c
LOCUS
DEFINITION
7LEAF--05-102.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--05-102, mRNA sequence.
ACCESSION
CF301006
VERSION
CF301006.1 GI:33672767
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 12)
/lab_host="E.coli DH10B"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
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Location/Qualifiers
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--05-110"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
Query Match 0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAA 1492
Db 12 AAAAAAAAAAAAA 1

```

```

Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
1..12
Location/Qualifiers
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--05-102"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
Query Match 0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAA 1492
Db 12 AAAAAAAAAAAAA 1

RESULT 315
CF301075/c
LOCUS
DEFINITION
7LEAF--05-M15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--05-M15, mRNA sequence.
ACCESSION
CF301075
VERSION
CF301075.1 GI:33672836
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 12)
/lab_host="E.coli DH10B"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
1..12
Location/Qualifiers
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--05-M15"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
Query Match 0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAA 1492
Db 12 AAAAAAAAAAAAA 1

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RESULT 316
CF301489/c
LOCUS
DEFINITION
  CF301489 12 bp mRNA linear EST 15-AUG-2003
  sativa cDNA clone 7LEAF--06-G01, mRNA sequence.
ACCESSION
CF301489
VERSION
CF301489.1 GI:33673250
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
  Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
  1 (bases 1 to 12)
  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  Large-scale Sequencing Analysis of Rice ESTs
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  Contact: Nahm B.H.
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  of Bioscience and Bioinformatics, Myongji University
  Yongin, Kyeonggi, Korea
  Tel: 82 31 330 6193
  Fax: 82 31 321 6355
  Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
FEATURES
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  1..12
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    /organism="Oryza sativa"
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    /cultivar="Nackdong"
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    /clone="7LEAF--06-G01"
    /tissue_type="leaf"
    /dev_stage="7 days after germination"
    /lab_host="E.coli DH10B"
    /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
    /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
    with oligoribonucleotides and then used as templates for
    RT-PCR."
  Query Match 0.8%; Score 12; DB 1; Length 12;
  Best Local Similarity 100.0%; Pred. No. 1.5e+02;
  Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1492
Db 12 AAAAAAAAAAAAAA 1

RESULT 318
CF302029/c
LOCUS
DEFINITION
  CF302029 12 bp mRNA linear EST 15-AUG-2003
  sativa cDNA clone 7LEAF--07-C18, mRNA sequence.
ACCESSION
CF302029
VERSION
CF302029.1 GI:33673790
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
  Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
  1 (bases 1 to 12)
  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  Large-scale Sequencing Analysis of Rice ESTs
  Unpublished (2003)
  Contact: Nahm B.H.
  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
  of Bioscience and Bioinformatics, Myongji University
  Yongin, Kyeonggi, Korea
  Tel: 82 31 330 6193
  Fax: 82 31 321 6355
  Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
FEATURES
  source
  1..12
  Location/Qualifiers
    1..12
    /organism="Oryza sativa"
    /mol_type="mRNA"
    /cultivar="Nackdong"
    /db_xref="taxon:4530"
    /clone="7LEAF--07-C18"
    /tissue_type="leaf"
    /dev_stage="7 days after germination"
    /lab_host="E.coli DH10B"
    /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
    /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
    with oligoribonucleotides and then used as templates for
    RT-PCR."
  Query Match 0.8%; Score 12; DB 1; Length 12;
  Best Local Similarity 100.0%; Pred. No. 1.5e+02;
  Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1492
Db 12 AAAAAAAAAAAAAA 1

RESULT 317
CF301940/c
LOCUS
DEFINITION
  CF301940 12 bp mRNA linear EST 15-AUG-2003
  sativa cDNA clone 7LEAF--07-A01, mRNA sequence.
ACCESSION
CF301940
VERSION
CF301940.1 GI:33673701
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
  Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
  1 (bases 1 to 12)
  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  Large-scale Sequencing Analysis of Rice ESTs
  Unpublished (2003)
  Contact: Nahm B.H.
  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
  of Bioscience and Bioinformatics, Myongji University
  Yongin, Kyeonggi, Korea
  Tel: 82 31 330 6193
  Fax: 82 31 321 6355
  Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
FEATURES
  source
  1..12
  Location/Qualifiers
    1..12
    /organism="Oryza sativa"
    /mol_type="mRNA"
    /cultivar="Nackdong"
    /db_xref="taxon:4530"
    /clone="7LEAF--07-A01"
    /tissue_type="leaf"
    /dev_stage="7 days after germination"
    /lab_host="E.coli DH10B"
    /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
    /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
    with oligoribonucleotides and then used as templates for
    RT-PCR."
  Query Match 0.8%; Score 12; DB 1; Length 12;
  Best Local Similarity 100.0%; Pred. No. 1.5e+02;
  Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1492
Db 12 AAAAAAAAAAAAAA 1

RESULT 317
CF301940/c
LOCUS
DEFINITION
  CF301940 12 bp mRNA linear EST 15-AUG-2003
  sativa cDNA clone 7LEAF--07-A01, mRNA sequence.
ACCESSION
CF301940
VERSION
CF301940.1 GI:33673701
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
  Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
  1 (bases 1 to 12)
  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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  Unpublished (2003)
  Contact: Nahm B.H.
  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
  of Bioscience and Bioinformatics, Myongji University
  Yongin, Kyeonggi, Korea
  Tel: 82 31 330 6193
  Fax: 82 31 321 6355
  Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
FEATURES
  source
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    /clone="7LEAF--07-A01"
    /tissue_type="leaf"
    /dev_stage="7 days after germination"
    /lab_host="E.coli DH10B"
    /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
    /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
    with oligoribonucleotides and then used as templates for
    RT-PCR."
  Query Match 0.8%; Score 12; DB 1; Length 12;
  Best Local Similarity 100.0%; Pred. No. 1.5e+02;
  Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1492
Db 12 AAAAAAAAAAAAAA 1

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RESULT 319
CF302122/c
LOCUS
DEFINITION
7LEAF--07-F15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--07-F15, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 12)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

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/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAA 1492
|||||
Db 12 AAAAAAAAAAAAA 1

RESULT 320
CF302289/c
LOCUS
DEFINITION
7LEAF--07-K10.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--07-K10, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 12)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea

Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

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1. .12
/organism="Oryza sativa"
/mol_type="mRNA"
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/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAA 1492
|||||
Db 12 AAAAAAAAAAAAA 1

RESULT 321

CF302486/c
LOCUS
DEFINITION
7LEAF--08-B02.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--08-B02, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 12)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

source
1. .12
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--08-B02"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAA 1492
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Db      12 AAAAAAAAAAAAA 1

RESULT 322
CF308112/c
LOCUS   ABF--01-M19.b1 ABF3-overexpressing transgenic rice plasmid cDNA
DEFINITION library (ABF) Oryza sativa cDNA clone ABF--01-M19, mRNA sequence.
ACCESSION CF308112
VERSION    1
KEYWORDS   EST.
SOURCE     CF308112.1 GI:33679873
          Oryza sativa
          ORGANISM Oryza sativa
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 12)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.

FEATURES             source
          1..12
          /organism="Oryza sativa"
          /mol_type="mRNA"
          /cultivar="Nackdong"
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          /tissue_type="leaf"
          /dev_stage="14 days after germination"
          /lab_host="E.coli DH10B"
          /clone_lib="ABF3-overexpressing transgenic rice plasmid
          cDNA library (ABF)"
          /note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
          for 2hrs. Oligo-capped mRNA was reverse transcribed and
          then used for PCR. mRNA was prepared from ABA-responsive
          element binding transcription factor 3 overexpression
          line."

Query Match          0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAA 1492
          |||||
          Db      12 AAAAAAAAAAAAA 1

RESULT 324
CF311836/c
LOCUS   ABF--07-E11.g1 ABF3-overexpressing transgenic rice plasmid cDNA
DEFINITION library (ABF) Oryza sativa cDNA clone ABF--07-E11, mRNA sequence.
ACCESSION CF311836
VERSION    1
KEYWORDS   EST.
SOURCE     CF311836.1 GI:33683597
          Oryza sativa
          ORGANISM Oryza sativa
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 12)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.

FEATURES             source
          1..12
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          /tissue_type="leaf"
          /dev_stage="14 days after germination"
          /lab_host="E.coli DH10B"
          /clone_lib="ABF3-overexpressing transgenic rice plasmid
          cDNA library (ABF)"
          /note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
          for 2hrs. Oligo-capped mRNA was reverse transcribed and
          then used for PCR. mRNA was prepared from ABA-responsive
          element binding transcription factor 3 overexpression
          line."

Query Match          0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAA 1492
          |||||
          Db      12 AAAAAAAAAAAAA 1

RESULT 323
CF311835/c
LOCUS   ABF--07-E11.b1 ABF3-overexpressing transgenic rice plasmid cDNA
DEFINITION library (ABF) Oryza sativa cDNA clone ABF--07-E11, mRNA sequence.
ACCESSION CF311835
VERSION    1
KEYWORDS   EST.
SOURCE     CF311835.1 GI:33683596
          Oryza sativa
          ORGANISM Oryza sativa
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 12)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)

```

```

COMMENT   Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.

FEATURES             source
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          /mol_type="mRNA"
          /cultivar="Nackdong"
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          /tissue_type="leaf"
          /dev_stage="14 days after germination"
          /lab_host="E.coli DH10B"
          /clone_lib="ABF3-overexpressing transgenic rice plasmid
          cDNA library (ABF)"
          /note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
          for 2hrs. Oligo-capped mRNA was reverse transcribed and
          then used for PCR. mRNA was prepared from ABA-responsive
          element binding transcription factor 3 overexpression
          line."

Query Match          0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAA 1492
          |||||
          Db      12 AAAAAAAAAAAAA 1

RESULT 324
CF311836/c
LOCUS   ABF--07-E11.g1 ABF3-overexpressing transgenic rice plasmid cDNA
DEFINITION library (ABF) Oryza sativa cDNA clone ABF--07-E11, mRNA sequence.
ACCESSION CF311836
VERSION    1
KEYWORDS   EST.
SOURCE     CF311836.1 GI:33683597
          Oryza sativa
          ORGANISM Oryza sativa
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 12)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.

FEATURES             source
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          /tissue_type="leaf"
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          /lab_host="E.coli DH10B"
          /clone_lib="ABF3-overexpressing transgenic rice plasmid
          cDNA library (ABF)"
          /note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
          for 2hrs. Oligo-capped mRNA was reverse transcribed and
          then used for PCR. mRNA was prepared from ABA-responsive
          element binding transcription factor 3 overexpression
          line."

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then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAA 1492
|||||
Db 1 AAAAAAAAAA 12

RESULT 325
CF313356/c
LOCUS
DEFINITION
HD--01-H09.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--01-H09, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE
JOURNAL
COMMENT

Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193
Fax: 82 31 321 6355

Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
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Location/Qualifiers

/organism="Oryza sativa"
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/cultivar="Nackdong"
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/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH108"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAA 1492
|||||
Db 12 AAAAAAAAAA 1

RESULT 326
CF315565/c
LOCUS
DEFINITION
HD--04-I14.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--04-I14, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
EST.

CF315565.1 GI:33687326

SOURCE
ORGANISM

Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE
JOURNAL
COMMENT

Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355

Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
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Location/Qualifiers

/organism="Oryza sativa"
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/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD--04-I14"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH108"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAA 1492
|||||
Db 12 AAAAAAAAAA 1

RESULT 327
CF317551/c

LOCUS
DEFINITION
HD--07-E16.b1 OshDAC1-overexpressing transgenic rice plasmid
library (HD) Oryza sativa cDNA clone HD--07-E16, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CF317551.1 GI:33689312

Oryza sativa
Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE
JOURNAL
COMMENT

Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355

Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
1..12
Location/Qualifiers

/organism="Oryza sativa"
/mol_type="mRNA"

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/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD--07-E16"
/tissue_type="callus"
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/lab_host="E.coli DH10B"
/clone_lib="OSHDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

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Query Match          0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1481 AAAAAAAAAA 1492
Db 12 AAAAAAAAAA 1

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RESULT 328
CF317798/c
LOCUS
DEFINITION
HD--07-J24.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--07-J24, mRNA sequence.

```

```

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

```

```

Oryza sativa
Oryza sativa

```

```

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

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1 (bases 1 to 12)

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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

```

```

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

```

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Location/Qualifiers

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1..12
source

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/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD--07-J24"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OSHDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

```

```

Query Match          0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1481 AAAAAAAAAA 1492
Db 12 AAAAAAAAAA 1

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RESULT 329
CF320426/c

```

```

LOCUS
DEFINITION
HD--11-F02.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--11-F02, mRNA sequence.

```

```

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

```

```

Oryza sativa
Oryza sativa

```

```

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

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1 (bases 1 to 12)

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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

```

```

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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

```

```

Location/Qualifiers

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1..12
source

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/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD--11-F02"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OSHDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

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Query Match          0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1481 AAAAAAAAAA 1492
Db 12 AAAAAAAAAA 1

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RESULT 330
CF324793/c

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LOCUS
DEFINITION
JMT1--01-H22.g1 AtJMT-overexpressing transgenic rice lambda phage
cDNA library (JMT1) Oryza sativa cDNA clone JMT1--01-H22, mRNA
sequence.

```

```

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

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```

Oryza sativa
Oryza sativa

```

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

```

```

1 (bases 1 to 12)

```

```

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Unpublished (2003)

```


COMMENT

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of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

source

Location/Qualifiers

1. .12
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="JMT1-01-H22"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="ATJMT-overexpressing transgenic rice lambda
phage cDNA library (JMT1)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5',
end with EcoRI and 3' end with XhoI site. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match 0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAA 1492

Db 12 AAAAAAAAAAAAA 1

RESULT 331

CF326913/c

LOCUS
DEFINITION
NACL--01-D01.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--01-D01, mRNA sequence.

ACCESSION CF326913

VERSION CF326913.1 GI:33802082

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 12)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

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Fax: 82 31 321 6355

Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

source

Location/Qualifiers

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/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAA 1492

Db 12 AAAAAAAAAAAAA 1

RESULT 332

CF327376/c

LOCUS
DEFINITION
NACL--01-N10.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--01-N10, mRNA sequence.

ACCESSION CF327376

VERSION CF327376.1 GI:33803011

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 12)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

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Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

source

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/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAA 1492

Db 12 AAAAAAAAAAAAA 1

RESULT 333

CF327962/c

LOCUS
DEFINITION
NACL--02-K14.g1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--02-K14, mRNA sequence.

ACCESSION CF327962

VERSION CF327962.1 GI:33804174

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 12)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES Location/Qualifiers

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/clone_lib="Rice callus plasmid cDNA library (NACL)"
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with oligoribonucleotides and then used as templates for
RT-PCR."
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAA 1492
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Db 12 AAAAAAAAAAAAA 1

RESULT 334

CF328229 12 bp mRNA linear EST 18-AUG-2003
LOCUS NACL--03-A13.g1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION sativa cDNA clone NACL--03-A13, mRNA sequence.

ACCESSION CF328229
VERSION CF328229.1 GI:33804704

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

REFERENCE 1 (bases 1 to 12)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES source

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/organism="Oryza sativa"
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/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
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RT-PCR."

Query Match 0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAA 1492
|||||
Db 1 AAAAAAAAAAAAA 12

RESULT 335

CF329141/c

LOCUS NACL--04-F18.b1 Rice callus plasmid cDNA library (NACL) Oryza

DEFINITION sativa cDNA clone NACL--04-F18, mRNA sequence.

ACCESSION CF329141

VERSION CF329141.1 GI:33806519

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

REFERENCE 1 (bases 1 to 12)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES source

```

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/organism="Oryza sativa"
/mol_type="mRNA"
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RT-PCR."
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAA 1492
|||||
Db 12 AAAAAAAAAAAAA 1

RESULT 336

CF329142

LOCUS NACL--04-F18.g1 Rice callus plasmid cDNA library (NACL) Oryza

DEFINITION sativa cDNA clone NACL--04-F18, mRNA sequence.

ACCESSION CF329142

VERSION CF329142.1 GI:33806520

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

REFERENCE 1 (bases 1 to 12)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.


```

REFERENCE
AUTHORS      Ehrhartoideae; Oryzeae; Oryza.
              1 (bases 1 to 12)
              Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
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              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
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  RT-PCR."

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Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1481 AAAAAAAAAAAAA 1492
Db      12 AAAAAAAAAAAAA 1

RESULT 341
LOCUS      CF331858
DEFINITION NACL--08-C08-g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa CDNA clone NACL--08-C08, mRNA sequence.
ACCESSION  CF331858
VERSION     CF331858.1 GI:33811939
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 12)
AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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JOURNAL    Unpublished (2003)
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
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  /organism="Oryza sativa"
  /mol_type="mRNA"
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  /clone_lib="Rice callus plasmid cDNA library (NACL)"
  /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
  with oligoribonucleotides and then used as templates for
  RT-PCR."

Query Match      0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1481 AAAAAAAAAAAAA 1492
Db      1 AAAAAAAAAAAAA 12

RESULT 342
LOCUS      CF331904
DEFINITION NACL--08-D07-g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa CDNA clone NACL--08-D07, mRNA sequence.
ACCESSION  CF331904
VERSION     CF331904.1 GI:33812029
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

REFERENCE
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, MyongJi University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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  /organism="Oryza sativa"
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Query Match      0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1481 AAAAAAAAAAAAA 1492
Db      12 AAAAAAAAAAAAA 1

RESULT 340
LOCUS      CF331241/C
DEFINITION NACL--07-E15.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa CDNA clone NACL--07-E15, mRNA sequence.
ACCESSION  CF331241
VERSION     CF331241.1 GI:33810705
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 12)
AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL    Unpublished (2003)
COMMENT    Contact: Nahm B.H.
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            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
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Query Match      0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1481 AAAAAAAAAAAAA 1492
Db      12 AAAAAAAAAAAAA 1

RESULT 341
LOCUS      CF331858
DEFINITION NACL--08-C08-g1 Rice callus plasmid cDNA library (NACL) Oryza
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ACCESSION  CF331858
VERSION     CF331858.1 GI:33811939
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 12)
AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
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            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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  /mol_type="mRNA"
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  RT-PCR."

Query Match      0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1481 AAAAAAAAAAAAA 1492
Db      1 AAAAAAAAAAAAA 12

RESULT 342
LOCUS      CF331904
DEFINITION NACL--08-D07-g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa CDNA clone NACL--08-D07, mRNA sequence.
ACCESSION  CF331904
VERSION     CF331904.1 GI:33812029
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.
 1 (bases 1 to 12)
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
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 Unpublished (2003)
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 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

source

1. .12
 Location/Qualifiers
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="NACL--08-D07"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 30 days"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice callus plasmid cDNA library (NACL)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.8%; Score 12; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAA 1492

Db 1 AAAAAAAAAAAAA 12

RESULT 343

CF331950/c

LOCUS CF331950 12 bp mRNA linear EST 18-AUG-2003
 DEFINITION NACL--08-E07.b1 Rice callus plasmid cDNA library (NACL) Oryza
 sativa cDNA clone NACL--08-E07, mRNA sequence.

ACCESSION CF331950

VERSION CF331950.1 GI:33812121

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 12)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

source

1. .12
 Location/Qualifiers
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="NACL--08-E07"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 30 days"
 /lab_host="E.coli DH10B"

Query Match 0.8%; Score 12; DB 1; Length 12;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

/clone lib="Rice callus plasmid cDNA library (NACL)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.8%; Score 12; DB 1; Length 12;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAA 1492

Db 12 AAAAAAAAAAAAA 1

RESULT 344

CF332993/c

LOCUS

DEFINITION

JMT--01-L10.g1 AtJMT-overexpressing transgenic rice plasmid cDNA

library (JMT) Oryza sativa cDNA clone JMT--01-L10, mRNA sequence.

ACCESSION CF332993

VERSION CF332993.1 GI:33814228

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 12)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

source

1. .12
 Location/Qualifiers
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="JMT--01-L10"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="AtJMT-overexpressing transgenic rice plasmid
 cDNA library (JMT)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
 was reverse transcribed and then used for PCR. mRNA was
 prepared from Arabidopsis Jasmonate Carboxyl
 methyltransferase overexpression line."

Query Match 0.8%; Score 12; DB 1; Length 12;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAA 1492

Db 12 AAAAAAAAAAAAA 1

RESULT 345

CF333992/c

LOCUS

DEFINITION

JMT--03-B22.b1 AtJMT-overexpressing transgenic rice plasmid cDNA

library (JMT) Oryza sativa cDNA clone JMT--03-B22, mRNA sequence.

ACCESSION CF333992

VERSION CF333992.1 GI:33816288

KEYWORDS EST.

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SOURCE
ORGANISM      Oryza sativa
              Oryza sativa
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL       Unpublished (2003)
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnamh@bio.com, bhnamh@bio.myongji.ac.kr.

FEATURES
source
1..12
    /organism="Oryza sativa"
    /mol_type="mRNA"
    /cultivar="Nackdong"
    /db_xref="taxon:4530"
    /clone="JMT--03-B22"
    /tissue_type="leaf"
    /dev_stage="14 days after germination"
    /lab_host="E.coli DH10B"
    /clone_lib="AtUMT-overexpressing transgenic rice plasmid
    cDNA library (JMT)"
    /notes="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
    was reverse transcribed and then used for PCR. mRNA was
    prepared from Arabidopsis Jasmonate Carboxyl
    methyltransferase overexpression line."

Query Match      0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAA 1492
Db       12 AAAAAAAAAA 1

RESULT 346
BQ591949/c
LOCUS      BQ591949
DEFINITION BQ591949
            14 bp mRNA linear EST 06-DEC-2002
            cDNA clone 024-016-C15 5-PRIME, mRNA sequence.
ACCESSION  BQ591949
VERSION     BQ591949
KEYWORDS    EST.
SOURCE      Beta vulgaris
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Anaranthaceae; Beta.
            1 (bases 1 to 14)
            Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
            Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
            Plant J. 32 (5), 845-857 (2002)
            22362189
            12472698
            Contact: Weisshaar B
            ADIS DNA core facility at MPZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaar@mpiz-koeln.mpg.de
            Insert Length: 14 Std Error: 0.00
            Plate: 16 row: C column: 15

SOURCE
ORGANISM      Oryza sativa
              Oryza sativa
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL       Unpublished (2003)
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnamh@bio.com, bhnamh@bio.myongji.ac.kr.

FEATURES
source
1..14
    /organism="Oryza sativa"
    /mol_type="mRNA"
    /cultivar="Nackdong"
    /db_xref="taxon:4530"
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    /tissue_type="callus"
    /dev_stage="proliferated callus on 2N6 media for 30 days"
    /lab_host="E.coli DH10B"
    /clone_lib="Rice callus plasmid cDNA library (NACL)"
    /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
    with oligoribonucleotides and then used as templates for
    RT-PCR."

Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
Location/Qualifiers
1..14
    /organism="Beta vulgaris"
    /mol_type="mRNA"
    /cultivar="KWS2320 (double haploid, monogerm breeding
    line)"
    /db_xref="GABI:188168"
    /db_xref="taxon:161934"
    /clone="024-016-C15"
    /tissue_type="storage root"
    /lab_host="EMDH10B"
    /clone_lib="MP1Z-ADIS-024-storage root"
    /note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
    cDNA library from sugar beet. Library provided by KWS
    Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
    b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
    orientation:
    SP6-Sali-CCACGGGTCCG-SPRime-cDNA-polyA-CC-NotI-T7; Note:
    Sequencing granted in the context of the GABI-Best
    project, local PI: Dr. Katharina Schneider, coordinator:
    Prof. Christian Jung; Sequence submission managed by
    RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      0.8%; Score 12; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAA 1492
Db       13 AAAAAAAAAA 2

RESULT 347
CF330198/c
LOCUS      CF330198
DEFINITION CF330198
            14 bp mRNA linear EST 18-AUG-2003
            sativa cDNA clone NACL--05-N04, mRNA sequence.
ACCESSION  CF330198
VERSION     CF330198
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
            1 (bases 1 to 14)
            Song,S.I., Kim,J.K., Kim,Y.-K., Lee,T.H., Shin,Y.C.,
            Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H.,
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnamh@bio.com, bhnamh@bio.myongji.ac.kr.

FEATURES
source
1..14
    /organism="Oryza sativa"
    /mol_type="mRNA"
    /cultivar="Nackdong"
    /db_xref="taxon:4530"
    /clone="NACL--05-N04"
    /tissue_type="callus"
    /dev_stage="proliferated callus on 2N6 media for 30 days"
    /lab_host="E.coli DH10B"
    /clone_lib="Rice callus plasmid cDNA library (NACL)"
    /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
    with oligoribonucleotides and then used as templates for
    RT-PCR."

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Query Match      0.8%; Score 12; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAA 1492
Db 14 AAAAAAAAAA 3

RESULT 348
LOCUS CF299997 17 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF-04-D19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
ACCESSION CF299997
VERSION CF299997.1 GI:33671758
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 17)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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Location/Qualifiers
1..17
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF-04-D19"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.8%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 4.3e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1086 TTTTGTGTTTGTCT 1100
Db 3 TTTTGTGTTTGTCT 17

RESULT 349
LOCUS CF300456 18 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF-04-N23.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
ACCESSION CF300456
VERSION CF300456.1 GI:33672217
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

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Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..18
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF-04-N23"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.8%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 4.7e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1086 TTTTGTGTTTGTCT 1100
Db 4 TTTTGTGTTTGTCT 18

RESULT 350
LOCUS CF329285 18 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--04-122.b1 Rice callus plasmid cDNA library (NACL) Oryza
ACCESSION CF329285
VERSION CF329285.1 GI:33806806
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..18
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL-04-122"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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Query Match 0.8%; Score 11.8; DB 1; Length 18;
 Best Local Similarity 86.7%; Pred. No. 4.7e+02;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1086 TTTTGTGTTTGTCT 1100
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 Db 3 TTTTGTGTTTGTCT 17

RESULT 351
 CF298591 18 bp mRNA linear EST 15-AUG-2003
 DEFINITION 7LEAF--02-A20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
 sativa cDNA clone 7LEAF--02-A20, mRNA sequence.

ACCESSION CF298591 GI:33670352
 VERSION
 KEYWORDS
 SOURCE

ORGANISM Oryza sativa
 Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 18)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)

TITLE Contact: Nahm B.H.
 JOURNAL Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 COMMENT of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea

FEATURES
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 1..18
 Location/Qualifiers
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="7LEAF--02-A20"
 /tissue_type="leaf"
 /dev_stage="7 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
 /notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.8%; Score 11.6; DB 1; Length 18;
 Best Local Similarity 77.8%; Pred. No. 4.9e+02;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1086 TTTTGTGTTTGTCTGAA 1103
 |||||
 Db 1 TTTTGTGTTTGTCTGAA 18

RESULT 352
 AZ345795/c 19 bp DNA linear GSS 29-SEP-2000
 LOCUS 1M0520P13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC1M0080H09 R, genomic survey sequence.

ACCESSION AZ345795 GI:10425032
 VERSION
 KEYWORDS
 SOURCE

ORGANISM Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 19)

REFERENCE Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 AUTHORS Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,

Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
 Plate: 0080 row: H column: 09

Seq primer: CACACAGGNAACAGCTATGACC
 Class: plasmid ends

High quality sequence stop: 19.
 Location/Qualifiers

FEATURES
 source

1..19
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0080H09"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWB42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.8%; Score 11.6; DB 1; Length 19;
 Best Local Similarity 77.8%; Pred. No. 5.1e+02;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1086 TTTTGTGTTTGTCTGAA 1103
 |||||
 Db 18 TTTTGTGTTTGTCTGAA 1

RESULT 353
 AZ650575/c 19 bp DNA linear GSS 14-DEC-2000
 LOCUS 1M0520P13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC1M0520P13 R, genomic survey sequence.

ACCESSION AZ650575 GI:11785200
 VERSION
 KEYWORDS
 SOURCE

ORGANISM Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 19)

REFERENCE Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 AUTHORS Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0520 row: P column: 13
Seq primer: CACACAGGAACACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES source

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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0520P13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWP42 (GI|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.8%; Score 11.6; DB 1; Length 19;
Best Local Similarity 77.8%; Pred. No. 5.1e+02;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1086 TTTTGTGTTTGTCTGAA 1103
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Db 18 TTTTGTGTTTGTCTGAA 1

RESULT 354
AZ849506/c
LOCUS
DEFINITION
2M0150P21R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0150P21 R, genomic survey sequence.

ACCESSION
AZ849506
VERSION
AZ849506.1 GI:13033596
KEYWORDS
GSS.

SOURCE
Mus musculus (house mouse)

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)

REFERENCE
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

TITLE JOURNAL COMMENT

Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0150 row: P column: 21
Seq primer: CACACAGGAACACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.

FEATURES source

1. 20
/organism="Mus musculus"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
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/sex="Male"
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWP42 (GI|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.8%; Score 11.6; DB 1; Length 20;
Best Local Similarity 77.8%; Pred. No. 5.1e+02;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1086 TTTTGTGTTTGTCTGAA 1103
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Db 18 TTTTGTGTTTGTCTGAA 1

RESULT 355
CF291168

LOCUS
DEFINITION
14ROOT--01-H20.g1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa cDNA clone 14ROOT--01-H20, mRNA sequence.

ACCESSION
CF291168
VERSION
CF291168.1 GI:33660201
KEYWORDS
EST.

SOURCE
Oryza sativa

ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
1 (bases 1 to 13)

AUTHORS
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs

JOURNAL
COMMENT

Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

Location/Qualifiers
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/organism="Oryza sativa"
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/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
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Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
Db 1 AAAAAAAAAAAAAA 13

RESULT 356

CF327120

LOCUS 13 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--01-H14.g1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--01-H14, mRNA sequence.

ACCESSION CF327120.1 GI:33802495
VERSION EST.
KEYWORDS

SOURCE

ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs

JOURNAL

COMMENT

Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

Location/Qualifiers
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/db_xref="taxon:4530"
/clone="NACL--01-H14"
/issue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match

0.8%; Score 11.4; DB 1; Length 13;

Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
Db 1 AAAAAAAAAAAAAA 13

RESULT 357

BQ590207

LOCUS 16 bp mRNA linear EST 06-DEC-2002
DEFINITION E012843-024-019-015-T7 MP12-ADIS-024-storage root Beta vulgaris
cDNA clone 024-019-015 3-PRIME, mRNA sequence.

ACCESSION BQ590207
VERSION BQ590207.1 GI:26119790
KEYWORDS EST.
SOURCE

ORGANISM

Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.

REFERENCE

1 (bases 1 to 16)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruick,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.

TITLE

Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Weisshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weisshaar@mpiz-koeln.mpg.de

Insert Length: 16 Std Error: 0.00

Plate: 19 row: 0 column: 15

Seq primer: T7; GTAATACGACTCACTATAGGCG.

FEATURES

source

Location/Qualifiers
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/cultivar="KWS2320 (double haploid, monogerm breeding
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/db_xref="taxon:161934"
/clone="024-019-015"
/issue_type="storage root"
/lab_host="EMDH108"
/clone_lib="MP1Z-ADIS-024-storage root"
/note="Vector: PCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kwa.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCGG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.7%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 4.8e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1086 TTTTGTGTTTGTCTG 1101
Db 1 TTTTGTGTTTGTCTG 16

RESULT 358

CF318894

LOCUS CF318894 16 bp mRNA linear EST 15-AUG-2003
 DEFINITION HD--09-D06.g1 OshDACL1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--09-D06, mRNA sequence.
 ACCESSION CF318894
 VERSION CF318894.1 GI:33690655
 KEYWORDS EST.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Oryza sativa
 Oryza sativa
 Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
 REFERENCE 1 (bases 1 to 16)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source
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 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
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 /lab_host="E.coli DH10B"
 /clone_lib="OshDACL1-overexpressing transgenic rice plasmid cDNA library (HD)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.7%; Score 11.2; DB 1; Length 16;
 Best Local Similarity 81.2%; Pred. No. 4.8e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1086 TTTTGTGTTTGTCTG 1101
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 Db 1 TTTTGTGTTTGTCTG 16

RESULT 359
 CF327923 16 bp mRNA linear EST 18-AUG-2003
 LOCUS NACL--02-J18.g1 Rice callus plasmid cDNA library (NACL) Oryza
 DEFINITION sativa cDNA clone NACL--02-J18, mRNA sequence.
 ACCESSION CF327923
 VERSION CF327923.1 GI:33804096
 KEYWORDS EST.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
 REFERENCE 1 (bases 1 to 16)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193

Fax: 82 31 321 6355
 Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
 Location/Qualifiers
 source
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 /mol_type="mRNA"
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 /db_xref="taxon:4530"
 /clone="NACL--02-J18"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 30 days"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice callus plasmid cDNA library (NACL)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.7%; Score 11.2; DB 1; Length 16;
 Best Local Similarity 81.2%; Pred. No. 4.8e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1086 TTTTGTGTTTGTCTG 1101
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 Db 1 TTTTGTGTTTGTCTG 16

RESULT 360

CF328223 16 bp mRNA linear EST 18-AUG-2003
 LOCUS NACL--03-A10.g1 Rice callus plasmid cDNA library (NACL) Oryza
 DEFINITION sativa cDNA clone NACL--03-A10, mRNA sequence.
 ACCESSION CF328223
 VERSION CF328223.1 GI:33804692
 KEYWORDS EST.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
 REFERENCE 1 (bases 1 to 16)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

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 /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.7%; Score 11.2; DB 1; Length 16;
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 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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 Db 1 TTTTGTGTTTGTCTG 16

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RESULT 361
CF295807
LOCUS
DEFINITION
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  sativa cDNA clone 30DGS--05-012, mRNA sequence.
ACCESSION
  CF295807
VERSION
  CF295807.1 GI:33664840
KEYWORDS
  EST.
SOURCE
  Oryza sativa
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Eukaryota; Magnoliophyta; Liliopsida; Poales; Poaceae;
    Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
  1 (bases 1 to 17)
  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  Large-scale Sequencing Analysis of Rice ESTs
  Unpublished (2003)
  Contact: Nahm B.H.
  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
  of Bioscience and Bioinformatics, Myongji University
  Yongin, Kyeonggi, Korea
  Tel: 82 31 330 6193
  Fax: 82 31 321 6355
  Email: bhnam@bio.com, bhnam@bio.myongji.ac.kr.
FEATURES
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  Db 2 TTTTGTGTTTGTCTG 17

RESULT 362
CF299639
LOCUS
DEFINITION
  CF299639 17 bp mRNA linear EST 15-AUG-2003
  sativa cDNA clone 7LEAF--03-L20, mRNA sequence.
ACCESSION
  CF299639
VERSION
  CF299639.1 GI:33671400
KEYWORDS
  EST.
SOURCE
  Oryza sativa
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
    Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
  1 (bases 1 to 17)
  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  Large-scale Sequencing Analysis of Rice ESTs
  Unpublished (2003)
  Contact: Nahm B.H.
  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
  of Bioscience and Bioinformatics, Myongji University
  Yongin, Kyeonggi, Korea
  Tel: 82 31 330 6193
  Fax: 82 31 321 6355
  Email: bhnam@bio.com, bhnam@bio.myongji.ac.kr.
FEATURES
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    /dev_stage="30 days after germination"
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    /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
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RESULT 363
CF298341
LOCUS
DEFINITION
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  sativa cDNA clone 7LEAF--01-K24, mRNA sequence.
ACCESSION
  CF298341
VERSION
  CF298341.1 GI:33670102
KEYWORDS
  EST.
SOURCE
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  ORGANISM
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    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
    Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
  1 (bases 1 to 17)
  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  Large-scale Sequencing Analysis of Rice ESTs
  Unpublished (2003)
  Contact: Nahm B.H.
  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
  of Bioscience and Bioinformatics, Myongji University
  Yongin, Kyeonggi, Korea
  Tel: 82 31 330 6193
  Fax: 82 31 321 6355
  Email: bhnam@bio.com, bhnam@bio.myongji.ac.kr.
FEATURES
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    /issue_type="leaf"
    /dev_stage="7 days after germination"
    /lab_host="E.coli DH10B"
    /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
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  Query Match
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    Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
  QY 1086 TTTTGTGTTTGTCTG 1101
  Db 2 TTTTGTGTTTGTCTG 17

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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@bio.com, bhnam@bio.myongji.ac.kr.
FEATURES
  source
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    /organism="Oryza sativa"
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    /lab_host="E.coli DH10B"
    /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
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    with oligoribonucleotides and then used as templates for
    RT-PCR."
  Query Match
    Best Local Similarity 0.7%; Score 11.2; DB 1; Length 17;
    Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
  QY 1086 TTTTGTGTTTGTCTG 1101
  Db 2 TTTTGTGTTTGTCTG 17

RESULT 363
CF298341
LOCUS
DEFINITION
  CF298341 17 bp mRNA linear EST 15-AUG-2003
  sativa cDNA clone 7LEAF--01-K24, mRNA sequence.
ACCESSION
  CF298341
VERSION
  CF298341.1 GI:33670102
KEYWORDS
  EST.
SOURCE
  Oryza sativa
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
    Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
  1 (bases 1 to 17)
  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  Large-scale Sequencing Analysis of Rice ESTs
  Unpublished (2003)
  Contact: Nahm B.H.
  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
  of Bioscience and Bioinformatics, Myongji University
  Yongin, Kyeonggi, Korea
  Tel: 82 31 330 6193
  Fax: 82 31 321 6355
  Email: bhnam@bio.com, bhnam@bio.myongji.ac.kr.
FEATURES
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    /mol_type="mRNA"
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    /db_xref="taxon:4530"
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    /issue_type="leaf"
    /dev_stage="7 days after germination"
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    /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
    /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
    with oligoribonucleotides and then used as templates for
    RT-PCR."
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    Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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  Db 2 TTTTGTGTTTGTCTG 1101

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Db      4  |||| |||| |||| ||||
         4  TTTT TTTT TTTT TTTG 19

RESULT 367
CF327587
LOCUS   NACL--02-C04.b1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION
sativa cDNA clone NACL--02-C04, mRNA sequence.
ACCESSION   CF327587
VERSION     CF327587.1 GI:33803426
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM   Oryza sativa
REFERENCE   1 (bases 1 to 19)
AUTHORS    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
TITLE      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL    Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
COMMENT    Unpublished (2003)
Contact: Nam B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             source
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            /mol_type="cDNA"
            /cultivar="Nackdong"
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with oligoribonucleotides and then used as templates for
RT-PCR."

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Best Local Similarity 81.3%; Pred. No. 5.4e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1086 TTTTGTGTTTGTCTG 1101
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RESULT 368
BQ589109
LOCUS   S013715-024-015-B24-T7 MP1Z-ADIS-024-storage root Beta vulgaris
DEFINITION
cDNA clone 024-015-B24 3-PRIME, mRNA sequence.
ACCESSION   BQ589109
VERSION     BQ589109.1 GI:26118692
KEYWORDS    EST.
SOURCE      Beta vulgaris
ORGANISM   Beta vulgaris
REFERENCE   1 (bases 1 to 11)
AUTHORS    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
TITLE      Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Insert Length: 11 Std Error: 0.00
Plate: 19 row: D column: 02

JOURNAL    Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weissaha@mpiz-koeln.mpg.de

MEDLINE 22362189
PUBMED 12472698
COMMENT  Contact: Weisshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weissaha@mpiz-koeln.mpg.de
Insert Length: 11 Std Error: 0.00
Plate: 15 row: B column: 24
Seq primer: T7; GTAATACGACTCACTATAGGCG.

FEATURES             source
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            /tissue_type="storage root"
            /lab_host="EMDH10B"
            /clone_lib="MP1Z-ADIS-024-storage root"
            /note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCG-Sprime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
Project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      0.7%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAA 1491
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Db      1  AAAAAAAAAA 11

RESULT 369
BQ590590/c
LOCUS   E012846-024-019-D02-T7 MP1Z-ADIS-024-storage root Beta vulgaris
DEFINITION
cDNA clone 024-019-D02 3-PRIME, mRNA sequence.
ACCESSION   BQ590590
VERSION     BQ590590.1 GI:26120173
KEYWORDS    EST.
SOURCE      Beta vulgaris
ORGANISM   Beta vulgaris
REFERENCE   1 (bases 1 to 11)
AUTHORS    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
TITLE      Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Insert Length: 11 Std Error: 0.00
Plate: 19 row: D column: 02

JOURNAL    Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weissaha@mpiz-koeln.mpg.de

```

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FEATURES
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Seq primer: T7; GTAATACGACTCTACTATAGGC.
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    Location/Qualifiers
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      /mol_type="mRNA"
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      line)"
      /db_xref="GABI:189530"
      /db_xref="taxon:161934"
      /clone="024-019-D02"
      /tissue_type="storage root"
      /lab_host="EMDH10B"
      /clone_lib="MP1Z-ADIS-024-storage root"
      /notes="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
      cDNA library from sugar beet, library provided by KWS
      Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
      b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
      orientation:
      SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
      Sequencing granted in the context of the GABI-Beet
      project, local PI: Dr. Katharina Schneider, coordinator:
      Prof. Christian Jung; Sequence submission managed by
      RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      0.7%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAA 1491
Db 11 AAAAAAAAAA 1

RESULT 370
BO595827/c
LOCUS
DEFINITION
  BO595827 11 bp mRNA linear EST 06-DEC-2002
  cDNA clone 024-021-P01 3-PRIME, mRNA sequence.
ACCESSION
  BO595827
VERSION
  BO595827.1 GI:26125410
KEYWORDS
  EST.
SOURCE
  Beta vulgaris
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
    Caryophyllales; Amaranthaceae; Beta.
  1 (bases 1 to 11)
  Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
  Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
  and Radelof,U.
REFERENCE
  AUTHORS
    Construction of a 'unigene' cDNA clone set by oligonucleotide
    fingerprinting allows access to 25 000 potential sugar beet genes
    Plant J. 32 (5), 845-857 (2002)
  22362189
  12472698
  COMMENT
    Contact: Weisshaar B
    ADIS DNA core facility at MP1Z
    Max-Planck-Institute for Plant Breeding Research
    Carl-von-Linne Weg 10, 50829 Koeln, Germany
    Fax: 00492215062851
    Email: weisshaar@mpiz-koeln.mpg.de
    Insert Length: 11 Std Error: 0.00
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    Seq primer: T7; GTAATACGACTCTACTATAGGC.
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FEATURES
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Seq primer: T7; GTAATACGACTCTACTATAGGC.
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      /clone="024-019-D02"
      /tissue_type="storage root"
      /lab_host="EMDH10B"
      /clone_lib="MP1Z-ADIS-024-storage root"
      /notes="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
      cDNA library from sugar beet, library provided by KWS
      Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
      b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
      orientation:
      SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
      Sequencing granted in the context of the GABI-Beet
      project, local PI: Dr. Katharina Schneider, coordinator:
      Prof. Christian Jung; Sequence submission managed by
      RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      0.7%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAA 1491
Db 11 AAAAAAAAAA 1

RESULT 370
BO595827/c
LOCUS
DEFINITION
  BO595827 11 bp mRNA linear EST 06-DEC-2002
  cDNA clone 024-021-P01 3-PRIME, mRNA sequence.
ACCESSION
  BO595827
VERSION
  BO595827.1 GI:26125410
KEYWORDS
  EST.
SOURCE
  Beta vulgaris
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
    Caryophyllales; Amaranthaceae; Beta.
  1 (bases 1 to 11)
  Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
  Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
  and Radelof,U.
REFERENCE
  AUTHORS
    Construction of a 'unigene' cDNA clone set by oligonucleotide
    fingerprinting allows access to 25 000 potential sugar beet genes
    Plant J. 32 (5), 845-857 (2002)
  22362189
  12472698
  COMMENT
    Contact: Weisshaar B
    ADIS DNA core facility at MP1Z
    Max-Planck-Institute for Plant Breeding Research
    Carl-von-Linne Weg 10, 50829 Koeln, Germany
    Fax: 00492215062851
    Email: weisshaar@mpiz-koeln.mpg.de
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      /tissue_type="storage root"
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      /clone_lib="MP1Z-ADIS-024-storage root"
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      Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
      b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
      orientation:
      SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
      Sequencing granted in the context of the GABI-Beet
      project, local PI: Dr. Katharina Schneider, coordinator:
      Prof. Christian Jung; Sequence submission managed by
      RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      0.7%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAA 1491
Db 11 AAAAAAAAAA 1

RESULT 370
BO595827/c
LOCUS
DEFINITION
  BO595827 11 bp mRNA linear EST 06-DEC-2002
  cDNA clone 024-021-P01 3-PRIME, mRNA sequence.
ACCESSION
  BO595827
VERSION
  BO595827.1 GI:26125410
KEYWORDS
  EST.
SOURCE
  Beta vulgaris
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
    Caryophyllales; Amaranthaceae; Beta.
  1 (bases 1 to 11)
  Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
  Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
  and Radelof,U.
REFERENCE
  AUTHORS
    Construction of a 'unigene' cDNA clone set by oligonucleotide
    fingerprinting allows access to 25 000 potential sugar beet genes
    Plant J. 32 (5), 845-857 (2002)
  22362189
  12472698
  COMMENT
    Contact: Weisshaar B
    ADIS DNA core facility at MP1Z
    Max-Planck-Institute for Plant Breeding Research
    Carl-von-Linne Weg 10, 50829 Koeln, Germany
    Fax: 00492215062851
    Email: weisshaar@mpiz-koeln.mpg.de
    Insert Length: 11 Std Error: 0.00
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    Seq primer: T7; GTAATACGACTCTACTATAGGC.
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        /mol_type="mRNA"
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        /notes="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
        cDNA library from sugar beet, library provided by KWS
        Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
        b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
        orientation:
        SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
        Sequencing granted in the context of the GABI-Beet

```



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/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.7%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAA 1491
Db 1 AAAAAAAAAA 11

RESULT 375
CF291453/c
LOCUS      11 bp      mRNA      linear      EST 14-AUG-2003
DEFINITION 14ROOT--01-004.b1 Rice root plasmid cDNA library (14ROOT) Oryza
ACCESSION  CF291453
VERSION     CF291453.1 GI:33660486
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE  1 (bases 1 to 11)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnamh@gbio.com, bhnamh@bio.myongji.ac.kr.

FEATURES             source
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     /notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.7%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAA 1491
Db 1 AAAAAAAAAA 11

RESULT 376
CF291454/c
LOCUS      11 bp      mRNA      linear      EST 14-AUG-2003
DEFINITION 14ROOT--01-004.g1 Rice root plasmid cDNA library (14ROOT) Oryza
ACCESSION  CF291454
VERSION     CF291454.1 GI:33660487
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE  1 (bases 1 to 11)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnamh@gbio.com, bhnamh@bio.myongji.ac.kr.

FEATURES             source
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     /tissue_type="root"
     /dev_stage="14 days after germination"
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.7%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAA 1491
Db 1 AAAAAAAAAA 11

RESULT 376
CF291454/c
LOCUS      11 bp      mRNA      linear      EST 14-AUG-2003
DEFINITION 14ROOT--01-004.g1 Rice root plasmid cDNA library (14ROOT) Oryza
ACCESSION  CF291454
VERSION     CF291454.1 GI:33660487
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE  1 (bases 1 to 11)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnamh@gbio.com, bhnamh@bio.myongji.ac.kr.

FEATURES             source
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     /clone lib="Rice root plasmid cDNA library (14ROOT)"
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with oligoribonucleotides and then used as templates for
RT-PCR."

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ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE  1 (bases 1 to 11)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnamh@gbio.com, bhnamh@bio.myongji.ac.kr.

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VERSION     CF292150.1 GI:33661183
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SOURCE     Oryza sativa
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE  1 (bases 1 to 11)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
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Email: bhnamh@gbio.com, bhnamh@bio.myongji.ac.kr.

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VERSION        CF292151.1 GI:33661184
KEYWORDS       EST.
SOURCE         Oryza sativa
ORGANISM       Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 11)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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DEFINITION      14ROOT--02-P21.g1 Rice root plasmid cDNA library (14ROOT) Oryza
ACCESSION      CF292236
VERSION        CF292236.1 GI:33661269
KEYWORDS       EST.

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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Db 11 AAAAAAAAAA 11

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VERSION        CF297318.1 GI:33666351
KEYWORDS       EST.
SOURCE         Oryza sativa
ORGANISM       Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 11)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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RESULT 381
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ORGANISM        Oryza sativa
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
AUTHORS        Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE          Large-scale Sequencing Analysis of Rice ESTs
JOURNAL        Unpublished (2003)
COMMENT        Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

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REFERENCE
AUTHORS        Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE          Large-scale Sequencing Analysis of Rice ESTs
JOURNAL        Unpublished (2003)
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Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

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Db 11 AAAAAAAAAA 1

RESULT 382
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LOCUS
DEFINITION      11 bp mRNA linear EST 15-AUG-2003
sativa cDNA clone 7LEAF--02-G21, mRNA sequence.
ACCESSION      CF298806
VERSION        CF298806.1 GI:33670567
KEYWORDS
SOURCE
ORGANISM        Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
AUTHORS        Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE          Large-scale Sequencing Analysis of Rice ESTs
JOURNAL        Unpublished (2003)
COMMENT        Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
AUTHORS        Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE          Large-scale Sequencing Analysis of Rice ESTs
JOURNAL        Unpublished (2003)
COMMENT        Contact: Nahm B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
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Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

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Db 11 AAAAAAAAAA 1

RESULT 383
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ORGANISM        Oryza sativa
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
AUTHORS        Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE          Large-scale Sequencing Analysis of Rice ESTs
JOURNAL        Unpublished (2003)
COMMENT        Contact: Nahm B.H.
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Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

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QY 1481 AAAAAAAAAA 1491
DB 11 AAAAAAAAAA 1

RESULT 384
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CF299849
VERSION    CF299849.1 GI:33671610
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ORGANISM
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Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 11)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
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Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

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RESULT 385
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CF300174
VERSION    CF300174.1 GI:33673049
KEYWORDS
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ORGANISM
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Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 11)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
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Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

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DB 11 AAAAAAAAAA 1

RESULT 386
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CF301288
VERSION    CF301288.1 GI:33673049
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Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 11)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source
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/mol_type="mRNA"
/cultivar="Nackdong"

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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 11)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAA 1491
DB 11 AAAAAAAAAA 1

RESULT 386
CF301288/c
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DEFINITION 7LEAF--06-B16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--06-B16, mRNA sequence.
CF301288
VERSION    CF301288.1 GI:33673049
KEYWORDS
SOURCE      Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 11)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
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FEATURES
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with oligoribonucleotides and then used as templates for
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Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 11 AAAAAAAAAA 1

RESULT 387
CF301713
LOCUS      11 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--06-K21.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--06-K21, mRNA sequence.
ACCESSION  CF301713
VERSION     CF301713.1 GI:33673474
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE  1 (bases 1 to 11)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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/tissue_type="leaf"
/dev_stage="7 days after germination"
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/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.7%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAA 1491
Db 11 AAAAAAAAAA 1

RESULT 388
CF301744/c
LOCUS      11 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--06-L14.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--06-L14, mRNA sequence.
ACCESSION  CF301744
VERSION     CF301744.1 GI:33673505
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE  1 (bases 1 to 11)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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Location/Qualifiers
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/db_xref="taxon:4530"
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/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.7%; Score 11; DB 1; Length 11;
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Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAA 1491
Db 11 AAAAAAAAAA 1

RESULT 389
CF302896/c
LOCUS      11 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--08-N07.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--08-N07, mRNA sequence.
ACCESSION  CF302896
VERSION     CF302896.1 GI:33674657
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE  1 (bases 1 to 11)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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RT-PCR."

Query Match      0.7%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAA 1491
Db 11 AAAAAAAAAA 1

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ACCESSION  CF301744
VERSION     CF301744.1 GI:33673505
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE  1 (bases 1 to 11)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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/tissue_type="leaf"
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/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
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Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAA 1491
Db 11 AAAAAAAAAA 1

RESULT 389
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LOCUS      11 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--08-N07.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--08-N07, mRNA sequence.
ACCESSION  CF302896
VERSION     CF302896.1 GI:33674657
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE  1 (bases 1 to 11)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
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TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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/organism="Oryza sativa"
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RT-PCR."

Query Match      0.7%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
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Db 11 AAAAAAAAAA 1

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RT-PCR."

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Query Match 0.7%; Score 11; DB 1; Length 11;
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 Db 11 AAAAAAAAAA 1

RESULT 390
 CF307845/c
 LOCUS
 DEFINITION ABF--01-G20.b1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa cDNA clone ABF--01-G20, mRNA sequence.

ACCESSION CF307845
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzoae; Oryza.

REFERENCE
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL
 COMMENT Unpublished (2003)

Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
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element binding transcription factor 3 overexpression
line."

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Query Match 0.7%; Score 11; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAA 1491
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 Db 11 AAAAAAAAAA 1

RESULT 391

CF309987/c
 LOCUS
 DEFINITION

ACCESSION CF309987
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzoae; Oryza.

REFERENCE
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL
 COMMENT Unpublished (2003)

Contact: Nahm B.H.
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 Fax: 82 31 321 6355
 Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
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/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

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Query Match 0.7%; Score 11; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAA 1491
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 Db 11 AAAAAAAAAA 1

RESULT 392
 CF311911/c

LOCUS
 DEFINITION ABF--07-G06.b1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa cDNA clone ABF--07-G06, mRNA sequence.

ACCESSION CF311911
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzoae; Oryza.

REFERENCE
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL
 COMMENT Unpublished (2003)

Contact: Nahm B.H.
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Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnamh@gbio.com, bhnamh@bio.myongji.ac.kr.

FEATURES

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 /clone="ABF--07-G06"
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 /clone_lib="ABF3-overexpressing transgenic rice plasmid
 cDNA library (ABF)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
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 then used for PCR. mRNA was prepared from ABA-responsive
 element binding transcription factor 3 overexpression
 line."

Query Match 0.7%; Score 11; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAA 1491
 11 AAAAAAAAAA 1

RESULT 393

CF311912
 LOCUS
 DEFINITION
 ABF--07-G06.g1 ABF3-overexpressing transgenic rice plasmid cDNA
 library (ABF) Oryza sativa cDNA clone ABF--07-G06, mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Oryza sativa
 Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
 1 (bases 1 to 11)
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
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 Fax: 82 31 321 6355
 Email: bhnamh@gbio.com, bhnamh@bio.myongji.ac.kr.

FEATURES

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 /db_xref="taxon:4530"
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 /tissue_type="leaf"
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 /clone_lib="ABF3-overexpressing transgenic rice plasmid
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 /note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
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 element binding transcription factor 3 overexpression
 line."

Query Match 0.7%; Score 11; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAA 1491
 11 AAAAAAAAAA 11

RESULT 394

CF314533/c
 LOCUS
 DEFINITION
 HD--03-B13.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
 library (HD) Oryza sativa cDNA clone HD--03-B13, mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Oryza sativa
 Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
 1 (bases 1 to 11)
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 Large-scale Sequencing Analysis of Rice ESTs
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 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnamh@gbio.com, bhnamh@bio.myongji.ac.kr.

FEATURES

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 1. 11
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="HD--03-B13"
 /tissue_type="callus"
 /dev_host="proliferated callus on 2N6 media for 2 weeks"
 /lab_hosts="E.coli DH10B"
 /clone_lib="OSHDAC1-overexpressing transgenic rice plasmid
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 /note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was
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 line."

Query Match 0.7%; Score 11; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAA 1491
 11 AAAAAAAAAA 1

RESULT 395

CF318741/c
 LOCUS
 DEFINITION
 HD--08-P20.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
 library (HD) Oryza sativa cDNA clone HD--08-P20, mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Oryza sativa
 Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

REFERENCE
 1 (bases 1 to 11)
 AUTHORS
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE
 Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL
 Unpublished (2003)
 COMMENT
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

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 Db 11 AAAAAAAAAA 1

RESULT 396
 CF326997/c
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 sativa cDNA clone NACL--01-E20, mRNA sequence.
 CF326997
 VERSION
 CF326997.1 GI:33802249
 EST.
 SOURCE
 Oryza sativa

ORGANISM
 Oryza sativa
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 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.
 1 (bases 1 to 11)
 AUTHORS
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 CF326998
 VERSION
 CF326998.1 GI:33802251
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 SOURCE
 Oryza sativa

ORGANISM
 Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.
 1 (bases 1 to 11)
 AUTHORS
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RESULT 398
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 LOCUS
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 CF327885
 ACCESSION
 CF327885.1 GI:33804018
 VERSION
 EST.


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SOURCE
ORGANISM
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 11)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

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Db 11 AAAAAAAAAA 1

RESULT 400
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sativa cDNA clone NACL--03-J20, mRNA sequence.
ACCESSION
CF328618.1 GI:33805485
VERSION
CF328618.1
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
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AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Db 1 AAAAAAAAAA 1

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NACL--03-J20.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--03-J20, mRNA sequence.
ACCESSION
CF328618
VERSION
CF328618.1 GI:33805485
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 11)
AUTHORS
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Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
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Db 1 AAAAAAAAAA 1

RESULT 401
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LOCUS
DEFINITION
NACL--04-H23.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--04-H23, mRNA sequence.
ACCESSION
CF329242
VERSION
CF329242.1 GI:33806721

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KEYWORDS
SOURCE      Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 11)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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JOURNAL     Unpublished (2003)
COMMENT     Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
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RESULT 402
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LOCUS      CF329344
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ACCESSION  CF329344
VERSION     CF329344.1 GI:33806925
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 11)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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Db      11 AAAAAAAAAA 1

RESULT 402
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ACCESSION  CF329344
VERSION     CF329344.1 GI:33806925
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 11)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
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Db      11 AAAAAAAAAA 1

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ACCESSION  CF329345
VERSION     CF329345.1 GI:33806926
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SOURCE     Oryza sativa
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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REFERENCE   1 (bases 1 to 11)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Db      1 AAAAAAAAAA 11

RESULT 404
CF331049/c
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ACCESSION  CF331049

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CF331049.1 GI:33810315
EST.
SOURCE
ORGANISM
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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REFERENCE
AUTHORS
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Email: bnhahm@bio.myongji.ac.kr.

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ACCESSION
VERSION
CF331066.1 GI:33810350
KEYWORDS
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ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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with oligoribonucleotides and then used as templates for
RT-PCR."

AUTHORS
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TITLE
JOURNAL
COMMENT

FEATURES
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Db 11 AAAAAAAAAA 1

RESULT 405
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LOCUS
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NACL--07-A17.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--07-A17, mRNA sequence.
ACCESSION
VERSION
CF331066.1 GI:33810350
KEYWORDS
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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RT-PCR."

AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6355
Fax: 82 31 321 6355
Email: bnhahm@bio.myongji.ac.kr.

TITLE
JOURNAL
COMMENT

FEATURES
source
1..11
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--07-A17"
/tissue_type="callus"
/dev_host="E.coli DH10B"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.7%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAA 1491
|||||
Db 11 AAAAAAAAAA 1

RESULT 407
CF331815
LOCUS
DEFINITION
NACL--08-B09.g1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--08-B09, mRNA sequence.
ACCESSION
VERSION
CF331815.1 GI:33811850
KEYWORDS
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 11)
/dev_host="E.coli DH10B"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--08-B09"
/tissue_type="callus"
/dev_host="E.coli DH10B"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
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RT-PCR."

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Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAA 1491
|||||
Db 11 AAAAAAAAAA 1

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LOCUS
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sativa cDNA clone NACL--08-B09, mRNA sequence.
ACCESSION
VERSION
CF331815.1 GI:33811850
KEYWORDS
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 11)
/dev_host="E.coli DH10B"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
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TITLE
JOURNAL
COMMENT

FEATURES
source
1..11
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--08-B09"
/tissue_type="callus"
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/clone_lib="Rice callus plasmid cDNA library (NACL)"
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Query Match 0.7%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAA 1491
|||||
Db 11 AAAAAAAAAA 1

RESULT 407
CF331815
LOCUS
DEFINITION
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ACCESSION
VERSION
CF331815.1 GI:33811850
KEYWORDS
SOURCE
Oryza sativa
ORGANISM
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/dev_stage="proliferated callus on 2N6 media for 30 days"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
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TITLE
JOURNAL
COMMENT

FEATURES
source
1..11
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--08-B09"
/tissue_type="callus"
/dev_host="E.coli DH10B"
/dev
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ACCESSION CF331815
VERSION CF331815.1 GI:33811852
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
REFERENCE 1 (bases 1 to 11)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
1..11
Location/Qualifiers
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--08-B09"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
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/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.7%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAA 1491
|||||
Db 1 AAAAAAAAAA 11

Search completed: April 21, 2004, 11:00:02
Job time : 7 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 15, 2004, 09:12:59 ; Search time 252 Seconds
(without alignments)
337.159 Million cell updates/sec

Title: US-10-006-430-76

Perfect score: 20

Sequence: 1 acggagtcaggatgttga 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 3185356

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	9	ADC35604 Human CD8
2	20	100.0	50	6	ABZ04679 Human leu
3	14.2	71.0	20	3	AAG66532 Dog genom
4	14.2	71.0	20	3	AAG66614 Dog genom
5	13.8	69.0	38	2	AAV04408 Primer us
6	13.8	69.0	38	5	AAP57868 Murine OP
7	13.4	67.0	25	8	ACK17461 Human mic
8	13.4	67.0	31	4	AAI10957 Human sin
9	13.4	67.0	50	6	ABZ01461 Human leu
10	13.4	67.0	50	6	ABZ01133 Human leu
11	13.4	67.0	50	6	ABZ01467 Human leu
12	13.4	67.0	50	9	ADD93328 Ptl1 gene
13	13.2	66.0	50	6	ABZ05433 Human leu
14	13	65.0	25	8	ACI35316 Human mic
15	12.8	64.0	17	7	ACD52070 HEV inozoy
16	12.8	64.0	17	7	ACD50650 HEV genom
17	12.8	64.0	20	2	AAT08244 p204, PCR
18	12.8	64.0	20	2	AAT93430 Primer 2
19	12.8	64.0	20	2	AAI17855 Primer #2
20	12.8	64.0	20	3	AAV78308 Human Ig
21	12.8	64.0	24	2	AAV30090 DNA seque
22	12.8	64.0	24	9	ADC33472 Gnt-V rel
23	12.8	64.0	25	8	ACI69449 Human mic

c	24	12.8	64.0	25	8	ACI27699	Human mic
c	25	12.8	64.0	25	8	ACK13687	Human mic
c	26	12.8	64.0	25	8	ACI81271	Human mic
c	27	12.8	64.0	25	8	ACH56433	DNA tatge
c	28	12.8	64.0	27	2	AAQ26429	Human bet
c	29	12.8	64.0	27	3	AAQ38967	Human G p
c	30	12.8	64.0	29	2	AAQ86771	PCR prime
c	31	12.8	64.0	30	2	AAQ72887	Primer #2
c	32	12.8	64.0	30	3	AAZ98292	P. vivax
c	33	12.8	64.0	30	3	AAZ98292	P. vivax
c	34	12.8	64.0	30	6	AAZ44259	Mutant ta
c	35	12.8	64.0	31	7	ACD43663	Human gen
c	36	12.8	64.0	34	7	ACC69768	Human H-F
c	37	12.8	64.0	36	2	AAQ84796	Spinocere
c	38	12.8	64.0	50	6	ABA95147	P. vivax
c	39	12.8	64.0	50	6	ABZ02100	Human leu
c	40	12.6	63.0	25	8	ACK05147	Human mic
c	41	12.6	63.0	25	8	ACI11455	Human mic
c	42	12.6	63.0	25	8	ACK27387	Human mic
c	43	12.6	63.0	25	8	ACI60529	Human mic
c	44	12.6	63.0	25	8	ACI17517	Human mic
c	45	12.6	63.0	25	8	ACK16092	Human mic

ALIGNMENTS

RESULT 1

ADC35604
ID ADC35604 standard; DNA; 20 BP.

XX

AC ADC35604;

DT 18-DEC-2003 (first entry)

DE Human CD81/TAPA-1 antisense oligonucleotide #64.

XX Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
KW cocaine addiction; autoimmune disorder; antinflammatory; antibacterial;
KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.

XX Homo sapiens.

XX Key Location/Qualifiers

FT modified_base 1..20

FT /tag= b

FT /mod_base= OTHER

FT /note= "phosphorothioate backbone and all cytidines are 5'-methyl cytidines"

FT modified_base 1..5

FT /tag= a

FT /mod_base= OTHER

FT /note= "2'-methoxyethyl nucleotide"

FT modified_base 16..20

FT /tag= c

FT /mod_base= OTHER

FT /note= "2'-methoxyethyl nucleotide"

US2003113914-A1.

19-JUN-2003.

XX 10-DEC-2001; 2001US-00006430.

XX 10-DEC-2001; 2001US-00006430.

XX (ISIS-) ISIS PHARM INC.

XX Graham MJ, Dobie K;

XX WPI; 2003-810907/76.

PT Novel compound hybridizing with nucleic acid molecule encoding CD81 and
 PT inhibiting the expression of CD81, useful for treating infections and
 PT disease associated with expression of CD81 such as inflammation disorder.

XX Claim 3; SEQ ID NO 76; 55pp; English.

XX The invention relates to a compound (antisense oligonucleotide)
 CC hybridising with the eighth nucleobase portion of an active site on a
 CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
 CC and inhibiting the expression of CD81. Also included is a composition
 CC comprising the antisense oligonucleotide and a carrier or a diluent. The
 CC antisense oligonucleotide is useful for inhibiting the expression of CD81
 CC in cells or tissues. The antisense oligonucleotide is also useful for
 CC treating infections preferably viral, bacterial and parasitic and
 CC diseases such as inflammatory disorders and autoimmune disorders. The
 CC disease or condition is characterised by chemical dependency (e.g.
 CC cocaine addiction). The present sequence is a CD81 antisense
 CC oligonucleotide of the invention.

SQ Sequence 20 BP; 5 A; 2 C; 8 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 9; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.6;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACGGAGTCAGGATGTTGTA 20

DB 1 ACGGAGTCAGGATGTTGTA 20

RESULT 2

ID ABZ04679/c

ID ABZ04679 standard; DNA; 50 BP.

AC ABZ04679;

XX 09-JAN-2003 (first entry)

DE Human leukocyte gene expression profiling probe SEQ ID NO 4670.

XX T7; leukocyte; gene expression profiling; allograft rejection;
 KW atherosclerosis; congestive heart failure; systemic lupus erythematosus;
 KW rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
 KW ss.

OS Homo sapiens.

XX WO200257414-A2.

XX 25-JUL-2002.

XX 22-OCT-2001; 2001WO-US047856.

XX 20-OCT-2000; 2000US-0241994P.

PR 08-JUN-2001; 2001US-0296764P.

XX (BIOC-) BIOCARDIA INC.

XX Wohlgemuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;
 PI Ly N, Woodward R, Quettermous T, Johnson F;

DR WPI; 2002-636525/68.

XX New system for leukocyte expression profiling, diagnosing a disease, or
 PT monitoring (the rate of) progression of a disease, e.g. atherosclerosis
 PT or congestive heart failure, comprises diagnostic oligonucleotides.

PS Claim 1; Page 477; Opp; English.

XX The invention relates to a system for detecting gene expression, which
 CC comprises one or two isolated DNA molecules that detect expression of a
 CC gene, where the gene corresponds to any of 8143 oligonucleotides
 CC (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful

CC for leukocyte expression profiling. It is particularly useful for
 CC diagnosing a disease, monitoring (rate of) progression of a disease,
 CC predicting therapeutic outcome, determining prognosis for a patient,
 CC predicting disease complications in an individual or monitoring response
 CC to treatment in an individual. The diseases include cardiac allograft
 CC rejection, kidney allograft rejection, liver allograft rejection,
 CC atherosclerosis, congestive heart failure, systemic lupus erythematosus,
 CC rheumatoid arthritis, osteoarthritis or cytomegalovirus infection

SQ Sequence 50 BP; 13 A; 17 C; 5 G; 15 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 50;

Best Local Similarity 100.0%; Pred. No. 2.9;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACGGAGTCAGGATGTTGTA 20

DB 46 ACGGAGTCAGGATGTTGTA 27

RESULT 3

AAA66532

ID AAA66532 standard; DNA; 20 BP.

AC AAA66532;

XX 09-OCT-2000 (first entry)

DE Dog genomic marker oligonucleotide sequence SEQ ID NO:394.

XX Dog; genome; genomic marker; radiation hybrid map; identification;
 KW chromosome location; gene marker; polymorphic microsatellite marker;
 KW phenotype; behaviour; pedigree; ss.

OS Canis familiaris.

XX WO200029615-A2.

XX 25-MAY-2000.

XX 15-NOV-1999; 99WO-IB001907.

XX 13-NOV-1998; 98US-0108193P.

XX (CNRS) CNRS CENT NAT RECH SCI.

XX Galibert F, Andre C;

XX WPI; 2000-387821/33.

XX New radiation hybrid map of the dog, Canine familiaris, genome, useful
 PT for e.g. identifying genes implicated in phenotypic and behavioral traits
 PT or in genetic diseases and for studying dog pedigrees.

PS Claim 1; Page 70; 87pp; English.

XX The present invention describes a radiation hybrid map of the dog (Canine
 CC familiaris) genome comprising the genome location of a marker selected
 CC from AAA66139 to AAA66942. The radiation hybrid map is useful for
 CC identifying and localising dog genes, since it covers approximately 80 %
 CC of the dog genome and provides a dense map integrating different types
 CC (i.e. Type I and Type II) of markers. The map and the dog genome markers
 CC (or complementary sequences) are especially useful to identify genes
 CC responsible for phenotypic and behavioural traits in dogs, to identify
 CC morbid genes, to analyse diseases and identify implicated genes in such
 CC diseases and their alleles, and to study dog pedigrees. They may also be
 CC useful for isolating corresponding human gene sequences e.g. genes
 CC involved in genetic diseases

SQ Sequence 20 BP; 6 A; 2 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 71.0%; Score 14.2; DB 3; Length 20;

Best Local Similarity 84.2%; Pred. No. 2.1e+03;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CGGAGTCAGATGTTGCA 20
 ||||| ||||| |||||
 Db 1 CGGAGACTGATGATGCA 19

RESULT 4
 AA66614 standard; DNA; 20 BP.
 ID AA66614 standard; DNA; 20 BP.
 XX
 AC AAA66614;
 XX
 DT 09-OCT-2000 (first entry)
 XX
 DE Dog genomic marker oligonucleotide sequence SEQ ID NO:476.
 XX
 KM Dog; genome; genomic marker; radiation hybrid map; identification;
 KM chromosome location; gene marker; polymorphic microsatellite marker;
 KM phenotype; behaviour; pedigree; ss.
 OS
 XX Canis familiaris.
 XX
 PN WO200029615-A2.
 XX
 PD 25-MAY-2000.
 XX
 PF 15-NOV-1999; 99WO-IB001907.
 XX
 PR 13-NOV-1998; 98US-0108193P.
 XX
 PA (CNRS) CNRS CENT NAT RECH SCI.
 XX
 PI Galibert F, Andre C;
 XX
 DR WPI; 2000-387821/33.
 XX
 PT New radiation hybrid map of the dog, Canine familiaris, genome, useful
 PT for e.g. identifying genes implicated in phenotypic and behavioral traits
 PT or in genetic diseases and for studying dog pedigrees.
 XX
 PS Claim 1; Page 73; 87pp; English.
 XX
 CC The present invention describes a radiation hybrid map of the dog (Canine
 CC familiaris) genome comprising the genome location of a marker selected
 CC from AA66613 to AA66942. The radiation hybrid map is useful for
 CC identifying and localising dog genes, since it covers approximately 80 %
 CC of the dog genome and provides a dense map integrating different types
 CC (i.e. Type I and Type II) of markers. The map and the dog genome markers
 CC (or complementary sequences) are especially useful to identify genes
 CC responsible for phenotypic and behavioural traits in dogs, to identify
 CC morbid genes, to analyse diseases and identify implicated genes in such
 CC diseases and their alleles, and to study dog pedigrees. They may also be
 CC useful for isolating corresponding human gene sequences e.g. genes
 CC involved in genetic diseases
 XX
 SQ Sequence 20 BP; 6 A; 2 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 71.0%; Score 14.2; DB 3; Length 20;
 Best Local Similarity 84.2%; Pred. No. 2.1e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CGGAGTCAGATGTTGCA 20
 ||||| ||||| |||||
 Db 1 CGGAGACTGATGATGCA 19

RESULT 5
 AA664408
 ID AA664408 standard; DNA; 38 BP.
 XX
 AC AA664408;
 XX

DT 20-APR-1998 (first entry)
 XX
 DE Primer used in preparation of osteoprotegerin products.
 XX
 KM Osteoprotegerin; antibody; diagnosis; affinity purification;
 KM recombinant production; transgenic animal; treatment; prevention;
 KM antisense oligonucleotide; probe; detection; screening; bone disease;
 KM osteoporosis; Paget's disease; hypercalcaemia; hyperparathyroidism;
 KM rheumatoid arthritis; osteomyelitis; osteolytic metastasis;
 KM periodontal bone loss; bone necrosis; osteopaenia; PCR primer; ss.
 XX
 OS Synthetic.
 XX
 PN DE19654610-A1.
 XX
 PD 26-JUN-1997.
 XX
 PF 20-DEC-1996; 96DE-01054610.
 XX
 PR 22-DEC-1995; 95US-00577788.
 PR 03-SEP-1996; 96US-00706945.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Boyle WJ, Lacey DL, Calzone FU, Chang M;
 XX
 DR WPI; 1997-334271/31.
 XX
 PT Nucleic acid encoding osteoprotegerin - useful for treatment of diseases
 PT involving excessive bone loss, e.g. osteoporosis.
 XX
 PS Example 9; Page 52; 182pp; German.
 XX
 CC The present sequence is a primer, which was used in the preparation of
 CC osteoprotegerin (OPG) products. Anti-OPG antibodies can be used in OPG
 CC diagnostic assays, and as affinity purification materials. The OPG cDNA
 CC can be used to express recombinant OPG and to generate transgenic
 CC animals. It can also be used to regulate the level of OPG in mammals,
 CC specifically to increase OPG levels, however the use of antisense
 CC sequences is also contemplated. Fragments of the cDNA can be used as
 CC probes to detect OPG expressing cells and tissue, and to screen cDNA
 CC libraries for related sequences. OPG can be used to treat or prevent bone
 CC diseases, specifically excessive bone loss, e.g. osteoporosis, Paget's
 CC disease, hypercalcaemia, hyperparathyroidism, rheumatoid arthritis,
 CC osteomyelitis, osteolytic metastases, periodontal bone loss, bone
 CC necrosis and osteopaenia
 XX
 SQ Sequence 38 BP; 6 A; 9 C; 11 G; 12 T; 0 U; 0 Other;

Query Match 69.0%; Score 13.8; DB 2; Length 38;
 Best Local Similarity 88.2%; Pred. No. 3.5e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GAGTCAGATGTTGCA 20
 ||||| ||||| |||||
 Db 9 GAGTCAGATGTTTCA 25

RESULT 6
 AA57868
 ID AA57868 standard; DNA; 38 BP.
 XX
 AC AA57868;
 XX
 DT 19-APR-2001 (first entry)
 XX
 DE Murine OPG mutagenic PCR primer #18.
 XX
 KM Bone loss; osteoprotegerin; OPG; rheumatoid arthritis; hyperalgesia;
 KM multiple sclerosis; osteoporosis; osteomyelitis; asthma; inflammation;
 KM systemic lupus erythematosus; graft-versus-host disease; septic shock;
 KM acute pancreatitis; Alzheimer's disease; anorexia; atherosclerosis; pain;
 KM coronary condition; myocardial infarction; cancer; diabetes; psoriasis;

KW endometriosiis; fever; glomerulonephritis; inflammatory bowel disease;
XX ischaemia; Parkinson's disease; PCR primer; ss.
OS Mus sp.
XX WO200103719-A2.
PN 18-JAN-2001.
PD 07-JUL-2000; 2000MO-US018667.
PF 09-UTL-1999; 99US-00350670.
PR 09-DEC-1999; 99US-00457647.
XX (AMGE-) AMGEN INC.
XX Boyle WJ, Lacey DL, Calzone FJ, Chang M, Senaldi G;
XX MPI; 2001-103031/11.
XX
XX Treating conditions leading to bone loss such as rheumatoid arthritis,
PT multiple sclerosis and asthma, comprises administering an osteoprotegerin
PT protein in conjunction with e.g. inhibitors of interleukin and tumor
PT necrosis factor alpha.
XX
XX Example 9; Page 145; 316pp; English.
XX
XX The present invention relates to a method for treating conditions leading
CC to bone loss. The method comprises administering a purified and isolated
CC osteoprotegerin (OPG) protein (AAFS783c-AAFS7838 and AAB66974-AAB66976)
CC in conjunction with other substances such as tumor necrosis factor-alpha
CC (TNF-alpha) inhibitors, interleukin (IL)-6, -8 and -18 inhibitors, ICE
CC modulators, fibroblast growth factor (FGF)1-10 modulators and/or platelet
CC activating factor (PAF) antagonists. The method is useful for treating
CC conditions leading to bone loss such as rheumatoid arthritis, multiple
CC sclerosis, osteoporosis, osteomyelitis and asthma. The method is also
CC useful for treating inflammation, systemic lupus erythematosus (SLE) and
CC graft-versus-host disease (GVHD). Other diseases that can be treated
CC include acute pancreatitis, Alzheimer's disease, anorexia,
CC atherosclerosis, coronary conditions (e.g. myocardial infarction),
CC cancer, diabetes, endometriosis, fever, glomerulonephritis, hyperalgesia,
CC inflammatory bowel disease, ischaemia, pain, Parkinson's disease,
CC psoriasis and septic shock. The present sequence is a PCR primer used in
CC the present invention
XX
SQ Sequence 38 BP; 6 A; 9 C; 11 G; 12 T; 0 U; 0 Other;
Query Match 69.0%; Score 13.8; DB 5; Length 38;
Best Local Similarity 88.2%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 GAGTCAGAGATGTTGTA 20
| | | | | | | | | | | | | | | | | | | | | |
Db 9 GAGTCAGAGATGTTTCA 25

RESULT 7
ACK17461
ID ACK17461 standard; DNA; 25 BP.
XX
AC ACK17461;
XX
DT 14-OCT-2003 (first entry)
XX
DE Human microarray DNA oligonucleotide SEQ ID NO 117442.
XX
XX EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; biallelic marker; polymorphism; human;
XX cross-species comparison.
OS Homo sapiens.
XX
PN US2003104410-A1.

XX
PD 05-JUN-2003.
XX
XX 15-MAR-2002; 2002US-00098263.
PF
XX 16-MAR-2001; 2001US-0276759P.
PR
XX (AFFY-) AFFYMETRIX INC.
XX
PA Miltmann MP;
XX
PI MPI; 2003-567953/53.
XX
XX
XX New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.
XX
XX Claim 1; SEQ ID NO 117442; 9pp; English.
XX
XX The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridisation to a DNA library,
CC in analysis of genetic variation or in hybridisation of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridising at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridisation. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying biallelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in in situ hybridisation, in Southern, Northern or dot-
CC blot hybridisation to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' terminus of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html
XX
SQ Sequence 25 BP; 7 A; 6 C; 7 G; 5 T; 0 U; 0 Other;
Query Match 67.0%; Score 13.4; DB 8; Length 25;
Best Local Similarity 93.3%; Pred. No. 5.4e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ACGGAGTCAGAGATGT 15
| | | | | | | | | | | | | | | | | | | | | |
Db 1 ACGGAGTCAGAAATGT 15

RESULT 8
AA130957/c
ID AA130957 standard; DNA; 31 BP.
XX
AC AA130957;
XX
DT 18-OCT-2001 (first entry)
XX
DE Human single nucleotide polymorphism (SNP) HIVEP1 6.
XX
XX Human; resequence; genotype; disease; forensic; paternity testing;
KW single nucleotide polymorphism; SNP; ss.
XX
OS Homo sapiens.
XX
XX Key location/Qualifiers
FT Variation replace(16,T)
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"

XX MO20016680-A2.
 XX
 PD 13-SEP-2001.
 XX
 PF 07-MAR-2001; 2001MO-US007268.
 XX
 PR 07-MAR-2000; 2000US-0187510P.
 XX
 PR 22-MAY-2000; 2000US-0206129P.
 XX
 PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
 XX
 PI Cargill M, Ireland JS, Lander ES;
 XX
 DR MPI, 2001-522952/57.
 XX
 PT Nucleic acid molecules from the human genome which include polymorphic
 PT sites, useful in methods for predicting the presence, absence or severity
 PT of a particular phenotype or disorder (e.g. diabetes) associated with a
 PT particular genotype.
 XX
 PS Claim 1; Page 119; 145bp; English.
 XX
 CC The invention relates to the identification of nucleic acid molecules
 CC (AAI29513-AAI31314) from the human genome which include polymorphic sites
 CC which can predispose individuals to disease. Various genes from a number
 CC of individuals were resequenced and single nucleotide polymorphisms
 CC (SNPs) in these genes discovered. The method is useful for predicting the
 CC presence, absence or severity of a particular phenotype or disorder (e.g.
 CC diabetes) associated with a particular genotype. The nucleic acids
 CC containing the polymorphic sites may be useful in forensics and paternity
 CC testing
 XX
 SQ Sequence 31 BP; 5 A; 12 C; 6 G; 8 T; 0 U; 0 Other;

Query Match 67.0%; Score 13.4; DB 4; Length 31;
 Best Local Similarity 93.3%; Pred. No. 5.5e+03;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 GTCAGAGTGTGTGA 20
 |||||
 DB 31 GTCAGAGTGTGTGA 17

RESULT 9
 AB201461
 ID AB201461 standard; DNA; 50 BP.
 XX
 AC AB201461;
 XX

DT 09-JAN-2003 (first entry)
 XX

DE Human leukocyte gene expression profiling probe SEQ ID NO 1452.
 XX

XX T7; leukocyte; gene expression profiling; allograft rejection;
 KM atherosclerosis; congestive heart failure; systemic lupus erythematosus;
 KM rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
 KM ss.
 XX

OS Homo sapiens.
 XX

PN MO200257414-A2.
 XX

PD 25-JUL-2002.
 XX

PF 22-OCT-2001; 2001MO-US047856.
 XX

PR 20-OCT-2000; 2000US-0241994P.
 XX

PR 08-JUN-2001; 2001US-0296764P.
 XX

PA (BIOC-) BIOCARDIA INC.
 XX

PI Wohlgemuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;

PI Ly N, Woodward R, Quertermous T, Johnson F;
 XX
 DR MPI; 2002-636525/68.
 XX
 PT New system for leukocyte expression profiling, diagnosing a disease, or
 PT monitoring (the rate of) progression of a disease, e.g. atherosclerosis
 PT or congestive heart failure, comprises diagnostic oligonucleotides.
 XX
 PS Claim 1; Page 371; Opp; English.

XX The invention relates to a system for detecting gene expression, which
 CC comprises one or two isolated DNA molecules that detect expression of a
 CC gene, where the gene corresponds to any of 8143 oligonucleotides
 CC (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful
 CC for leukocyte expression profiling. It is particularly useful for
 CC diagnosing a disease, monitoring (rate of) progression of a disease,
 CC predicting therapeutic outcome, determining prognosis for a patient,
 CC predicting disease complications in an individual or monitoring response
 CC to treatment in an individual. The diseases include cardiac allograft
 CC rejection, kidney allograft rejection, liver allograft rejection,
 CC atherosclerosis, congestive heart failure, systemic lupus erythematosus,
 CC rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
 XX

Query Match 67.0%; Score 13.4; DB 6; Length 50;
 Best Local Similarity 93.3%; Pred. No. 5.7e+03;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGAGTCAGATGTG 17
 |||||
 DB 20 GGAGTCAGATGTG 34

RESULT 10
 AB201133
 ID AB201133 standard; DNA; 50 BP.
 XX
 AC AB201133;
 XX

DT 09-JAN-2003 (first entry)
 XX

DE Human leukocyte gene expression profiling probe SEQ ID NO 1124.
 XX

XX T7; leukocyte; gene expression profiling; allograft rejection;
 KM atherosclerosis; congestive heart failure; systemic lupus erythematosus;
 KM rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
 KM ss.
 XX

OS Homo sapiens.
 XX

PN MO200257414-A2.
 XX

PD 25-JUL-2002.
 XX

PF 22-OCT-2001; 2001MO-US047856.
 XX

PR 20-OCT-2000; 2000US-0241994P.
 XX

PR 08-JUN-2001; 2001US-0296764P.
 XX

PA (BIOC-) BIOCARDIA INC.
 XX

PI Wohlgemuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;
 XX

DR MPI; 2002-636525/68.
 XX

PT New system for leukocyte expression profiling, diagnosing a disease, or
 PT monitoring (the rate of) progression of a disease, e.g. atherosclerosis
 PT or congestive heart failure, comprises diagnostic oligonucleotides.
 XX

PS Claim 1; Page 360; Opp; English.

CC atherosclerosis, congestive heart failure, systemic lupus erythematosus,
CC rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
XX

SQ Sequence 50 BP; 8 A; 11 C; 12 G; 19 T; 0 U; 0 Other;

QY Query Match 67.0%; Score 13.4; DB 6; Length 50;
Best Local Similarity 93.3%; Pred. No. 5.7e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 20 GGACTCTGAGTGTGG 34

QY 3 GGACTCAGATGTTG 17
|||||
|||

RESULT 12
ADD93328
ID ADD93328 standard; DNA; 50 BP.
XX
AC ADD93328;
XX
DT 29-JAN-2004 (first entry)
XX
DE Flt1 gene fragment, target for antisense phosphoramidate morpholino.
XX Zebrafish, flt1; angiogenesis; antisense; ds.
XX
KM Danio rerio.
OS
PN MO200307976-A2.
XX
PD 02-OCT-2003.
XX
PE 25-MAR-2003; 2003MO-EP003089.
PF
PR 27-MAR-2002; 2002US-0368616P.
PA (ARTE-) ARTEMIS PHARM GMBH.
PI Habeck HA, Schulte-Merker S;
DR WPI; 2003-779157/73.
XX
XX New engineered mutant telost embryo having reduced flt1 activity, useful
PT in forward and reverse screens to identify interacting genes in the flt1
PT pathway, and screening for pharmaceutical agents capable of altering flt1
PT phenotype.

PS Claim 17, Page 33; 34pp; English.

CC The present sequence is a 50-nucleotide fragment of a zebrafish gene,
CC denoted flt1 AD93315, that is required for sprouting angiogenesis.
CC Claimed antisense phosphoramidate morpholinos (PMOs) of the invention
CC specifically inactivate a teleost flt1 gene, and comprise a sequence of
CC 10-50 nucleotides that is complementary to contiguous nucleotides within
CC a sequence selected from a group consisting of the present sequence,
CC those given in AD93317 and nucleotides 1-400 of flt1 AD93315.
CC Claimed engineered mutant zebrafish telost embryos have reduced flt1
CC activity, which causes a phenotype of normal assembly of main circulatory
CC routes and a reduction in sprouted vessels. The flt1 phenotype may be
CC caused by an exogenously added nucleic acid inhibitor that specifically
CC inhibits flt1, such as one of the claimed PMOs. The mutant telost
CC embryos are used in genetic and compound screens to identify members of
CC the flt1 signaling pathway and compounds that affect sprouting
CC angiogenesis.

SQ Sequence 50 BP; 15 A; 6 C; 12 G; 17 T; 0 U; 0 Other;

QY Query Match 67.0%; Score 13.4; DB 9; Length 50;
Best Local Similarity 93.3%; Pred. No. 5.7e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 GTCAAGATTGTGA 20
|||||

DB 26 GTGAGGATGTTGTGA 40

RESULT 13
AB205433
ID AB205433 standard; DNA; 50 BP.
XX
AC AB205433;
XX
DT 09-JUN-2003 (first entry)
XX
DE Human leukocyte gene expression profiling probe SEQ ID NO 5424.
XX
KM T7; leukocyte; gene expression profiling; allograft rejection;
KM atherosclerosis; congestive heart failure; systemic lupus erythematosus;
KM rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
KM ss.
XX
OS Homo sapiens.
XX
PN WO200257414-A2.
XX
PD 25-JUL-2002.
XX
PF 22-OCT-2001; 2001WO-US047856.
XX
PR 20-OCT-2000; 2000US-0241994P.
XX
PR 08-JUN-2001; 2001US-0296764P.
XX
PA (BIOC-) BIOCARDIA INC.
XX
PI Wohlgemuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;
PI Ly N, Woodward R, Quertermous T, Johnson F;
XX
DR MPI; 2002-636525/68.
XX
PT New system for leukocyte expression profiling, diagnosing a disease, or
PT monitoring (the rate of) progression of a disease, e.g. atherosclerosis
PT or congestive heart failure, comprises diagnostic oligonucleotides.
XX
PS Claim 1; Page 503; 0pp; English.
XX
CC The invention relates to a system for detecting gene expression, which
CC comprises one or two isolated DNA molecules that detect expression of a
CC gene, where the gene corresponds to any of 8143 oligonucleotides
CC (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful
CC for leukocyte expression profiling. It is particularly useful for
CC diagnosing a disease, monitoring (rate of) progression of a disease,
CC predicting therapeutic outcome, determining prognosis for a patient,
CC predicting disease complications in an individual or monitoring response
CC to treatment in an individual. The diseases include cardiac allograft
CC rejection, kidney allograft rejection, liver allograft rejection,
CC atherosclerosis, congestive heart failure, systemic lupus erythematosus,
CC rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
XX
SQ Sequence 50 BP; 17 A; 5 C; 20 G; 8 T; 0 U; 0 Other;
XX
Query Match 66.0%; Score 13.2; DB 6; Length 50;
Best Local Similarity 83.3%; Pred. No. 7.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
QY 3 GGAGTCAGGATGTTGTGA 20
DB 6 GAAGTCAGGAAAGTTTGA 23

RESULT 14
AC135316/c
ID AC135316 standard; DNA; 25 BP.
XX
AC AC135316;
XX
DT 13-OCT-2003 (first entry)
XX

XX
DE Human microarray DNA oligonucleotide SEQ ID NO 35307.
XX
KM EST; ss; probe; expressed sequence tag; microarray; gene expression;
KM genetic variation; biallelic marker; polymorphism; human;
KM cross-species comparison.
XX
OS Homo sapiens.
XX
PN US2003104410-A1.
XX
PD 05-JUN-2003.
XX
PF 15-MAR-2002; 2002US-00098263.
XX
PR 16-MAR-2001; 2001US-0276759P.
XX
PA (AFFY-) AFFYMETRIX INC.
XX
PI Miltmann MP;
XX
DR MPI; 2003-567953/53.
XX
PT New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.
XX
PS Claim 1; SEQ ID NO 35307; 9pp; English.
XX
CC The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridization to a DNA library,
CC in analysis of genetic variation or in hybridization of tag-labeled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridizing at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridization. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying biallelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in in situ hybridization, in Southern, Northern or dot-
CC blot hybridization to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html
XX
SQ Sequence 25 BP; 7 A; 6 C; 6 G; 6 T; 0 U; 0 Other;
XX
Query Match 65.0%; Score 13; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 6 GTCAGGATGTTGT 18
DB 19 GTCAGGATGTTGT 7

RESULT 15
ACD52070/c
ID ACD52070 standard; RNA; 17 BP.
XX
AC ACD52070;
XX
DT 24-SEP-2003 (first entry)
XX
DE HBV inozyme substrate sequence #200.

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 15, 2004, 10:46:21 ; Search time 2007 Seconds
(without alignments)
297.580 Million cell updates/sec

Title: US-10-006-430-76

Perfect score: 20
Sequence: 1 acgagatcagatgtgtga 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 138346

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_estbm:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_ping:*
27: em_gss_vrt:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.4	72.0	48	28	AZ318461
2	14.2	71.0	33	12	BM398979
3	12.8	64.0	45	28	BH619838
4	12.6	63.0	40	9	AI642028

5	12.6	63.0	50	9	AU103832
6	12.6	63.0	50	28	AZ817361
7	12.2	61.0	36	28	AZ487594
8	12.2	61.0	50	9	AU102676
9	12	60.0	43	28	AZ346681
10	12	60.0	43	28	AZ807113
11	12	60.0	50	9	AU105073
12	12	60.0	50	9	AU105086
13	11.8	59.0	30	14	CP333773
14	11.8	59.0	41	29	DR17N10T
15	11.8	59.0	43	12	B0528597
16	11.6	58.0	40	9	A1080507
17	11.6	58.0	40	28	AQ072891
18	11.6	58.0	42	12	B039854
19	11.6	58.0	43	9	AA096781
20	11.6	58.0	47	28	AZ341255
21	11.6	58.0	47	28	AZ767804
22	11.4	57.0	37	9	AU256480
23	11.4	57.0	41	28	AZ412439
24	11.2	56.0	42	9	AI833018
25	11.2	56.0	43	9	AA972845
26	11.2	56.0	43	28	AZ464392
27	11.2	56.0	45	28	AZ480635
28	11.2	56.0	48	29	AL765485
29	11.2	56.0	50	9	AU102678
30	11.2	56.0	50	9	AU103858
31	11.2	56.0	50	9	AU103858
32	11.2	56.0	50	9	AU103914
33	11.2	56.0	50	28	BZ286230
34	11.2	56.0	32	12	B1818900
35	11.2	56.0	32	12	B1824853
36	11.2	56.0	35	14	U44207
37	11.2	56.0	37	14	R36016
38	11.2	56.0	39	29	CG12794
39	11.2	56.0	41	14	CF312745
40	11.2	56.0	43	9	AA911375
41	11.2	56.0	43	29	AL948959
42	11.2	56.0	44	28	AZ787976
43	11.2	56.0	45	12	B066342
44	11.2	56.0	46	14	T98810
45	11.2	56.0	48	28	BH621788

ALIGNMENTS

RESULT 1
LOCUS AZ318461 48 bp DNA linear GSS 29-SEP-2000
DEFINITION IM0037A17R Mouse 10kb plasmid UGCLIM library Mus musculus genomic
VERSION AZ318461
KEYWORDS AZ318461.1 GI:10368252
SOURCE GSS
ORGANISM Mus musculus (house mouse)
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 48)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beaorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausen, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
 Insert Length: 1000 Std Error: 0.00
 Plate: 0037 row: A column: 17
 Seq primer: CACACAGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 48.

FEATURES

source

1..48
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="U0810037A17"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1ib="Mouse 10kb plasmid U0810037A17"
 /note="Vector: PMD42ny, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF12072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 72.0%; Score 14.4; DB 28; Length 48;
 Best Local Similarity 93.8%; Pred. No. 2e+04;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 AGTCAGATGTTGTGA 20
 |||||
 14 AGTTAGATGTTGTGA 29

RESULT 2

BM398979/c

LOCUS BM398979 33 bp mRNA linear EST 17-JAN-2002
 DEFINITION 5009-0-51-D10.t.1 Chilcoat/Turkewitz cDNA (large fraction)
 Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION

BM398979

VERSION BM398979.1 GI:18199032
 EST.

KEYWORDS

SOURCE

ORGANISM

Tetrahymena thermophila
 Tetrahymena thermophila
 Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
 Hymenostomatida; Tetrahymenina; Tetrahymena.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 33)
 EST from Tetrahymena thermophila, strain CU428.1, growing cells
 Unpublished (2002)
 Contact: Turkewitz AP
 Molecular Genetics and Cell Biology
 University of Chicago
 920 E. 58th Street, Chicago, IL 60637, USA
 Tel: 773 702 4374
 Fax: 773 702 3172
 Email: apturkew@midway.uchicago.edu
 Seq primer: T3

FEATURES

source

Location/Qualifiers
 1..33

/organism="Tetrahymena thermophila"
 /mol_type="mRNA"
 /strain="CU428.1"
 /db_xref="taxon:5911"
 /clone_1ib="Chilcoat/Turkewitz cDNA (large fraction)"
 /note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN

Query Match 71.0%; Score 14.2; DB 12; Length 33;
 Best Local Similarity 84.2%; Pred. No. 2.2e+04;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CGGAGTCAGATGTTGTGA 20
 |||||
 25 CGGAGTCAGCTTGTGTGA 7

RESULT 3

BH619838

LOCUS

DEFINITION

ACCESSION

BH619838

VERSION

BH619838.1 GI:18431010

KEYWORDS

SOURCE

ORGANISM

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoidae; Andropogoneae; Zea.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Maize genomic sequences found using engineered Rescemu transposon
 Unpublished (2001)
 Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Very probable ligation site of ends cut by single endonuclease.
 Reverse complemented post-ligation sequence from source sequence.
 Plate: 1007063 column: 18
 Class: transposon-tagged.

FEATURES

source

1..45
 Location/Qualifiers
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /cultivar="mixed background W23/A188/B73"
 /db_xref="taxon:4577"
 /tissue_type="leaf"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_1ib="1007 - Rescemu Grid H"
 /note="Organ: leaf; Vector: Rescemu (engineered from
 pBluescript backbone); Site_1: BamHI, Site_2: BglII;
 Rescemu is a 4.9 kb, modified maize Mu transposon
 designed to allow plasmid rescue from total genomic DNA.
 Mu elements insert preferentially into transcription
 units. For more information on Rescemu, go to the web
 site 'www.zmdb.iastate.edu' and follow the links for
 'Rescemu'. Grid H was grown at Berkeley in 2001. DNA
 was extracted from leaf punches, double digested using
 BamHI and BglII, and ligated to form circular plasmids.
 DH10B cells were transformed and then screened on LB
 plates with ampicillin."

ORIGIN

Query Match 64.0%; Score 12.8; DB 28; Length 45;
 Best Local Similarity 87.5%; Pred. No. 1e+05;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CGAGTCAGGATGTTG 17
 |||||
 Db 3 CGAGTCAGGATGTTG 18

RESULT 4
 A1642028 40 bp mRNA linear EST 29-APR-1999
 ub74h04.x1 Soares mammary_gland_NMLMG Mus musculus cDNA clone
 LOCUS A1642028
 DEFINITION IMAGE:183511.3; similar to SW:UCP3_MOUSE P56501 MITOCHONDRIAL UNCOUPLING PROTEIN 3; mRNA sequence.

ACCESSION A1642028
 VERSION A1642028.1 GI:4720503
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 40)
 NCI-CCGAP http://www.ncbi.nlm.nih.gov/ccgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaabs@mail.nih.gov
 This clone is available royalty-free through LML; contact the IMAGE Consortium (info@image.lnl.gov) for further information.
 MGI:905979
 This clone was previously sequenced on the 5' end only, this new data is from the 3' end
 Possible reversed clone; similarity on wrong strand
 High quality sequence stop: 1.
 Location/Qualifiers
 1..40
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="IMAGE:183511"
 /sex="female (lactating)"
 /tissue_type="mammary gland"
 /lab_host="DH10B"
 /clone_lib="Soares mammary gland_NMLMG"
 /note="Vector: p7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from mammary gland tissue from a lactating female, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptor (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN
 Query Match 63.0%; Score 12.6; DB 9; Length 40;
 Best Local Similarity 78.9%; Pred. No. 1.2e+05;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ACGAGTCAGGATGTTG 19
 |||||
 Db 24 AAGGACTCAGGCGCTTGTG 6

RESULT 5
 AUI03832 50 bp mRNA linear EST 30-AUG-2001
 LOCUS AUI03832
 DEFINITION HRC10538, Suguano Homo sapiens cDNA library Homo sapiens cDNA clone
 ACCESSION AUI03832
 VERSION AUI03832.1 GI:13553353
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
 Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
 EMBO Rep. 2 (5), 388-393 (2001)

JOURNAL MEDLINE
 PUBMED 21270072
 11375928
 CONTACT: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minato-ku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp
 Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
 source location/Qualifiers
 1..50
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="HRC10538"
 /clone_lib="Suguano Homo sapiens cDNA library"

ORIGIN
 Query Match 63.0%; Score 12.6; DB 9; Length 50;
 Best Local Similarity 78.9%; Pred. No. 1.3e+05;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ACGAGTCAGGATGTTG 19
 |||||
 Db 32 ACGTAGTCAGGCTTGTG 50

RESULT 6
 A2817361 50 bp DNA linear GSS 20-FEB-2001
 LOCUS A2817361
 DEFINITION 2M0086K21R Mouse 10kb plasmid UGCGM library Mus musculus genomic clone UGCG2M0086K21 R, genomic survey sequence.

ACCESSION A2817361
 VERSION A2817361.1 GI:12987365
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 50)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 CONTACT: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert length: 1000 Std Error: 0.00
 Plate: 0086 row: K column: 21
 Seq primer: CACACAGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 50.
 Location/Qualifiers
 1..50

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG2M0086K21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1ib="Mouse 10kb plasmid UGCGIM library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 63.0%; Score 12.6; DB 28; Length 50;
Best Local Similarity 78.9%; Pred. No. 1.3e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 CCGAGTCAGATGTTGTGA 20
| ||| ||||| |||||
Db 25 CTGAGCGAGATGATGTAA 43

RESULT 7
AZ487594/c 36 bp DNA linear GSS 05-OCT-2000
LOCUS 1M0317B1F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
DEFINITION clone UGCGIM0317B21 F, genomic survey sequence.
ACCESSION AZ487594
VERSION AZ487594.1 GI:10655481
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 36)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

JOURNAL Contact: Robert B. Weiss
COMMENT University of Utah Genome Center

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0317 row: B column: 21
Seq primer: CGTTGTAACGACGCGCAGT
Class: plasmid ends

High quality sequence stop: 36.
Location/Qualifiers
1. .36

FEATURES
source

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0317B21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1ib="Mouse 10kb plasmid UGCGIM library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 61.0%; Score 12.2; DB 28; Length 36;
Best Local Similarity 82.4%; Pred. No. 1.8e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CCGAGTCAGATGTTGT 18
| ||| ||||| |||||
Db 30 CCGACTCATGATGTTGT 14

RESULT 8
AUI02676/c 50 bp mRNA linear EST 30-APR-2001
LOCUS AUI02676 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION HS101211, mRNA sequence.
ACCESSION AUI02676
VERSION AUI02676.1 GI:13552197
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 50)

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)

JOURNAL MEDLINE
COMMENT 21270072
11375928

Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokane-dai, Minato-ku, Tokyo 108-8639, Japan

Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

Location/Qualifiers
1. .50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

FEATURES
source

ORIGIN
/clone="HS101211"
/clone_lib="Sugano Homo sapiens cDNA library"

Query Match 61.0%; Score 12.2; DB 9; Length 50;
Best Local Similarity 82.4%; Pred. No. 2e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GGAGTCAGATGTTGTG 19
|||||
DB 18 GGAGTCAGCTGTTGTG 2

RESULT 9
AZ346681/c 43 bp DNA linear GSS 29-SEP-2000
LOCUS
DEFINITION 1M0082G01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0082G01 F, genomic survey sequence.
ACCESSION AZ346681
VERSION
KEYWORDS
AZ346681.1 GI:10425918
GSS.

SOURCE
Mus musculus (house mouse)

REFERENCE
AUTHORS

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0082 row: G column: 01
Seq primer: CCGTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 43.
Location/Qualifiers

FEATURES
source
1. 43
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0082G01"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (GI|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapored mouse DNA was annealed to
adapored vector DNA, and transformed into

ORIGIN

chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 60.0%; Score 12; DB 28; Length 43;
Best Local Similarity 75.0%; Pred. No. 2.4e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ACGAGTCAGATGTTGTGA 20
|||||
DB 25 AAGAGTCAGAGAGGGGTGA 6

RESULT 10
AZ807113/c 43 bp DNA linear GSS 20-FEB-2001
LOCUS
DEFINITION 2M0069G09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0069G09 R, genomic survey sequence.
ACCESSION AZ807113
VERSION
KEYWORDS
AZ807113.1 GI:12971138
GSS.

SOURCE
Mus musculus (house mouse)

REFERENCE
AUTHORS

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0063 row: G column: 02
Seq primer: CAACAAGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 43.
Location/Qualifiers

FEATURES
source
1. 43
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0069G09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (GI|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapored mouse DNA was annealed to
adapored vector DNA, and transformed into

/note="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis thaliana Carboxyl methyltransferase overexpression line."

ORIGIN

Query Match 59.0%; Score 11.8; DB 14; Length 30;
Best Local Similarity 86.7%; Pred. No. 2.9e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GTCAGAGTGTGTGA 20
DB 13 GTCAGATTTTGTGA 27

RESULT 14
DRI7N10T/c 41 bp DNA linear GSS 21-NOV-2002
LOCUS Dario rerio genomic clone DKEY-17N10, genomic survey sequence.
DEFINITION
ACCESSION AL733216
VERSION AL733216.1 GI:21342233
KEYWORDS
SOURCE
ORGANISM

Dario rerio (zebrafish)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.

REFERENCE
AUTHORS Humphrey, S.J., Huckle, E. and Hunt, S.E.
TITLE Direct Submission
JOURNAL Submitted (06-JUN-2002) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact: humquerry@sanger.ac.uk Unpublished
This sequence was generated from the T7 end of BAC 17N10. 17N10 is part of the Daniokey BAC library created by R. Plaetzer and N.V. Keygene.

COMMENT
Further details: http://www.sanger.ac.uk/Projects/D_rerio/.
Location/Qualifiers

FEATURES
source
1..41
/organism="Dario rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-17N10"
/issue_type="Testis"
/note="Vector pindigobAC-536"

ORIGIN

Query Match 59.0%; Score 11.8; DB 29; Length 41;
Best Local Similarity 86.7%; Pred. No. 2.9e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CGGAGTCAGAGTGT 16
DB 36 CGAGTCAGAGTGT 22

RESULT 15
BJ052697 43 bp mRNA linear EST 29-SEP-2003
LOCUS BJ052697 NIBB Mochii normalized Xenopus neurula library Xenopus
DEFINITION laevis cDNA clone XL042f11 3', mRNA sequence.
ACCESSION BJ052697
VERSION BJ052697.1 GI:17498743
KEYWORDS
SOURCE
ORGANISM

Xenopus laevis (African clawed frog)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
Xenopodinae; Xenopus.

REFERENCE
AUTHORS Kitayama, A., Teraoka, C., Mochii, M., Ueno, N., Shin-I, T. and Kohara, Y.
TITLE Expressed genes in X. laevis embryo

JOURNAL

Unpublished (2001)
Contact: Tadao Shin-i

COMMENT

Center for Genetic Resource Information
National Institute of Genetics
111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@genes.nig.ac.jp
The information of this clone is available through the following URL.
<http://xenopus.nibb.ac.jp/>

FEATURES

source
1..43
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="XL042f11"
/issue_type="whole embryo"
/dev_stage="stage 15"
/clone_1ib="NIBB Mochii normalized Xenopus neurula library"

ORIGIN

Query Match 59.0%; Score 11.8; DB 12; Length 43;
Best Local Similarity 86.7%; Pred. No. 2.9e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 AGTCAGAGTGTGTG 19
DB 22 AGTCAGAGTGTGTG 36

Search completed: April 15, 2004, 12:51:29
Job time : 2008 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 15, 2004, 10:50:39 ; Search time 1731 Seconds
(without alignments)
500.786 Million cell updates/sec

Title: US-10-006-430-76

Perfect score: 20

Sequence: 1 acgagatcagatgtgtgca 20

Scoring table: IDENTITY NUC

Gap0 10.0 , Gapext 1.0

Searched: 3470272 seqs, 2167151695 residues

Total number of hits satisfying chosen parameters: 1603530

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

```

1: gb_ba:*
2: gb_ba:*
3: gb_in:*
4: gb_in:*
5: gb_ov:*
6: gb_ov:*
7: gb_ph:*
8: gb_ph:*
9: gb_pl:*
10: gb_pl:*
11: gb_ro:*
12: gb_ro:*
13: gb_un:*
14: gb_un:*
15: gb_vl:*
16: gb_vl:*
17: em_fun:*
18: em_fun:*
19: em_mu:*
20: em_mu:*
21: em_or:*
22: em_or:*
23: em_ov:*
24: em_ov:*
25: em_ph:*
26: em_ph:*
27: em_pl:*
28: em_pl:*
29: em_ro:*
30: em_ro:*
31: em_un:*
32: em_un:*
33: em_vl:*
34: em_vl:*
35: em_ba:*
36: em_ba:*
37: em_in:*
38: em_in:*
39: em_ov:*
40: em_ov:*
41: em_ph:*

```

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.2	71.0	20	6	BD230525
2	14.2	71.0	20	6	BD230525 Total gen
3	13.8	69.0	38	6	AX076651
4	13.4	67.0	31	6	AX249366
5	13.4	67.0	50	6	AX249366 Sequence
6	13.2	66.0	28	6	E05487
7	13.2	66.0	32	6	E05487 PCR primer.
8	12.8	64.0	20	6	E40736
9	12.8	64.0	24	6	E16132
10	12.8	64.0	27	6	E17990
11	12.8	64.0	29	6	E26920
12	12.8	64.0	30	6	AR064721
13	12.8	64.0	30	6	AR089162
14	12.8	64.0	30	6	AR153238
15	12.8	64.0	47	6	AR291326
16	12.8	64.0	50	6	AX377926
17	12.6	63.0	41	6	AX515735
18	12.6	63.0	41	6	AX518330
19	12.6	63.0	47	6	AR288483
20	12.4	62.0	20	6	AR212002
21	12.4	62.0	20	6	AR315163
22	12.4	62.0	21	6	AR049055
23	12.4	62.0	21	6	AX095333
24	12.4	62.0	23	6	E59205
25	12.4	62.0	23	6	E64386
26	12.2	62.0	26	6	BD168169
27	12.2	61.0	18	6	AR295893
28	12.2	61.0	21	6	BD177428
29	12.2	61.0	21	6	BD226172
30	12.2	61.0	25	6	AR242533
31	12.2	61.0	26	6	AX201524
32	12.2	61.0	27	6	AX752019
33	12.2	61.0	28	6	AR283917
34	12.2	61.0	28	6	BD005489
35	12.2	61.0	31	6	AR090075
36	12.2	61.0	31	6	AR197110
37	12.2	61.0	31	6	AR259264
38	12.2	61.0	33	6	AR261271
39	12.2	61.0	33	6	AR400534
40	12.2	61.0	33	6	AR405801
41	12.2	61.0	33	6	AX201048
42	12.2	61.0	33	6	AX267847
43	12.2	61.0	34	6	AR142300
44	12.2	61.0	34	6	I27173
45	12.2	61.0	34	6	I32754

ALIGNMENTS

RESULT 1
BD230525
LOCUS BD230525 20 bp DNA linear PAT 17-JUL-2003
DEFINITION Total genome radiation hybrid map of canine genome and its use for
identification of interesting genes.
ACCESSION BD230525
VERSION BD230525.1 GI:33040295
KEYWORDS JP 2002530091-A/394.
SOURCE
ORGANISM
Canis familiaris
Canis familiaris (dog)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
1 (bases 1 to 20)
AUTHORS
Galibert, F. and Andre, C.
TITLE
Total genome radiation hybrid map of canine genome and its use for

JOURNAL
Identification of interesting genes
Patent: JP 2002530091-A 394 17-SEP-2002;
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE
OS Canis familiaris (dog)
PN JP 2002530091-A/394
PD 17-SEP-2002
PF 15-NOV-1999 JP 2000582596
PR 13-NOV-1998 US 60/108193
PI FRANCIS GALIBERT, CATHERINE ANDRE
PC C12N15/09, C12Q1/68, C12N15/00
CC B00237R
FH Key
FT source
Location/Qualifiers
1..20
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/mol_type="genomic DNA"
/db_xref="taxon:9615"

ORIGIN
source
Location/Qualifiers
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/db_xref="taxon:9615"

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DB 1 CGGAGACTGATGATGTGA 19

RESULT 2
BD30607
LOCUS BD30607 20 bp DNA linear PAT 17-JUL-2003
DEFINITION Total genome radiation hybrid map of canine genome and its use for
identification of interesting genes.
ACCESSION BD230607.1 GI:33040377
KEYWORDS JP 2002530091-A/476.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis;
1|baees 1 to 20
Galibert, F. and Andre, C.
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE
OS Canis familiaris (dog)
PN JP 2002530091-A/476
PD 17-SEP-2002
PF 15-NOV-1999 JP 2000582596
PR 13-NOV-1998 US 60/108193
PI FRANCIS GALIBERT, CATHERINE ANDRE
PC C12N15/09, C12Q1/68, C12N15/00
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FH Key
FT source
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Location/Qualifiers
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Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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|||||
DB 1 CGGAGACTGATGATGTGA 19

RESULT 3
AX076651 38 bp DNA linear PAT 06-FEB-2001
LOCUS AX076651
DEFINITION Sequence 167 from Patent WO0103719.
ACCESSION AX076651
VERSION AX076651.1 GI:12711188
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
Boyle, W.J., Lacey, D.L., Calzone, F.J., Chang, M.S. and Senaldi, G.
Patent: WO 0103719-A 167 18-JAN-2001;
Amgen Inc. (US)
Location/Qualifiers
1..38
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="PCR primer for deletion mutant."

ORIGIN
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Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="PCR primer for deletion mutant."

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Best Local Similarity 69.0%; Score 13.8; DB 6; Length 38;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GAGTCAGGATGTTGTA 20
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DB 9 GAGTCAGGATGTTTCA 25

RESULT 4
AX249366/c 31 bp DNA linear PAT 28-SEP-2001
LOCUS AX249366
DEFINITION Sequence 1445 from Patent WO0166800.
ACCESSION AX249366
VERSION AX249366.1 GI:15863989
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS
TITLE
JOURNAL
Cargill, M., Ireland, J.S. and Lander, E.S.
Human single nucleotide polymorphisms
Patent: WO 0166800-A 1445 13-SEP-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
Location/Qualifiers
1..31
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
source
Location/Qualifiers
1..31
/organism="Homo sapiens"
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Query Match
Best Local Similarity 67.0%; Score 13.4; DB 6; Length 31;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 GTCAGGATGTTGTA 20
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DB 31 GTCAGGATGTTGTA 17

RESULT 5
AX923380 50 bp DNA linear PAT 18-DEC-2003
LOCUS AX923380
DEFINITION Sequence 14 from Patent WO03079776.
ACCESSION AX923380
VERSION AX923380.1 GI:40216429
KEYWORDS

SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Haback,H.A. and Schulte-Merker,S.
TITLE Identification of the flt1 gene required for angiogenesis in zebrafish, and uses thereof
JOURNAL Patent: WO 03079776-A 14 02-Oct-2003;
Exelixis Deutschland GmbH (DE)
FEATURES
source
1..50
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/note="Description of Artificial Sequence: PMO 12"

ORIGIN

Query Match 67.0%; Score 13.4; DB 6; Length 50;
Best Local Similarity 93.3%; Pred. No. 2.6e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GTGAGATGTTGTGA 20
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Db 26 GTGAGATGTTGTGA 40

RESULT 6
E05487
LOCUS PCR primer. 28 bp DNA 1linear PAT 29-SEP-1997
DEFINITION E05487
ACCESSION E05487
VERSION E05487.1 GI:2173676
KEYWORDS JP 1993244982-A/15.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
1 (bases 1 to 28)

REFERENCE 1
AUTHORS Nakatani,T., Gomi,H., Jiyon,W. and Noguchi,H.
TITLE ANTHROPOMORPHISM B-B10
JOURNAL Patent: JP 1993244982-A 15 24-SEP-1993;
SUMITOMO CHEM CO LTD, SUMITOMO PHARMACEUT CO LTD, BIOTEST AG,
INOTERAPII LAB
COMMENT OS Artificial gene
OC Artificial sequence; Genes.
FN JP 1993244982-A/15
PD 24-SEP-1993
PF 06-DEC-1991 JP 1991323319
PI NAKATANI TOMOSUKE, GOMI HIDEYUKI, JIYON WAIDENESU, PI
NOGUCHI HIROSHI
PC C12P21/08,A61K39/395//C12N5/10,C12N15/13,G01N33/577; CC
Strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
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Location/Qualifiers
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ORIGIN

Query Match 66.0%; Score 13.2; DB 6; Length 28;
Best Local Similarity 83.3%; Pred. No. 3.5e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ACCGATCAGATGTTGT 18
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Db 1 ACTGATCAGAGATGT 18

RESULT 7
I07146/c
LOCUS 107146 32 bp DNA 1linear PAT 02-DEC-1994

DEFINITION Sequence 5 from Patent EP 0341892.
ACCESSION I07146
VERSION I07146.1 GI:589824
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1
AUTHORS Ingolia,T.D., Kovacevic,S., Miller,J.R. and Skatrud,P.L.
TITLE Recombinant DNA expression vectors and DNA compounds that encode deacetoxycephalosporin C synthetase
JOURNAL Patent: EP 0341892-A1 5 15-NOV-1989;
FEATURES
source
1..32
Location/Qualifiers
/organism="unknown"
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ORIGIN

Query Match 65.0%; Score 13; DB 6; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.6e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 ACTCAGATGTTG 17
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Db 18 ACTCAGATGTTG 6

RESULT 8
E40736
LOCUS 20 bp DNA 1linear PAT 31-JAN-2002
DEFINITION E40736
ACCESSION E40736
VERSION E40736.1 GI:18627325
KEYWORDS JP 2000154149-A/107.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
1 (bases 1 to 20)

REFERENCE 1
AUTHORS Serizawa,N., Hanyama,H., Takahashi,W., Nakahara,K. and Yonehara,S.
TITLE Antihuman Fas humanized antibody-containing antirheumatic
JOURNAL Patent: JP 2000154149-A 107 06-JUN-2000;
SANKYO CO LTD
COMMENT OS Artificial Sequence
FN JP 2000154149-A/107
PD 06-JUN-2000
PF 17-SEP-1999 JP 1999263984
PI NOBUKI SERIZAWA,HIDEYUKI HANYAMA,WATARU TAKAHASHI, PI KAORI
NAKAHARA,
PI SHIN YONEHARA
PC A61K39/395,A61P29/00,C12N15/09//C07K16/28,C12P21/02,C12N15/00
CC
FH Key
FT source
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ORIGIN

Query Match 64.0%; Score 12.8; DB 6; Length 20;
Best Local Similarity 87.5%; Pred. No. 6.1e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 ACTCAGATGTTGTGA 20
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Db 4 AGTGGGATGTTGTGA 19

RESULT 9
E16132

LOCUS E16132 24 bp DNA linear PAT 28-JUL-1999
DEFINITION Sequence of Ets-1-binding motif.
ACCESSION E16132
VERSION E16132.1 GI:5710815
KEYWORDS JP 1998137000-A/1.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 24)
AUTHORS Taniguchi, N.
TITLE SCREENING OF METASTASIS SUPPRESSOR
JOURNAL Patent: JP 198137000-A 1 28-MAY-1998;
SUNTORY LTD, TANIGUCHI NAOYUKI
COMMENT OS None
OC Artificial sequences.
PN JP 1998137000-A/1
PD 26-MAY-1998
PF 01-NOV-1998 JP 1996305486
PI TANIGUCHI NAOYUKI
PC C12Q1/68, G01N33/15, G01N33/50, G01N33/566//C12N15/09;
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CC topology: linear;
CC hypothetical: No;
FH key Location/Qualifiers
FT source 1..24
Location/Qualifiers
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/organism="unidentified"
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Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGAGTCAGATGTTGT 18
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Db 2 GGAGTCAGATGTTGT 17
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RESULT 10
LOCUS 157990 27 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 6 from patent US 5610137.
ACCESSION 157990
VERSION 157990.1 GI:2483054
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 27)
AUTHORS Townes, T.M. and McCune, S.L.
TITLE Transgenic, cross-linked hemoglobin
JOURNAL Patent: US 5610137-A 6 11-MAR-1997;
FEATURES
source 1..27
Location/Qualifiers
/organism="unknown"
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ORIGIN
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Best Local Similarity 87.5%; Pred. No. 6e+04; 2; Indels 0; Gaps 0;
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QY 3 GGAGTCAGATGTTGT 18
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Db 23 GGAGTCAGATGTTGT 8
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RESULT 11

E26920
LOCUS E26920 29 bp DNA linear PAT 18-JUN-2001
DEFINITION Mutant secretory device enzyme capable of efficiently secreting
protein into medium in coryneform bacterium.
ACCESSION E26920
VERSION E26920.1 GI:13026340
KEYWORDS JP 199169182-A/11.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 29)
AUTHORS Takashi, K., Yoko, A. and Hideaki, Y.
TITLE Mutant secretory device enzyme capable of efficiently secreting
protein into medium in coryneform bacterium
JOURNAL Patent: JP 199169182-A 11 29-JUN-1999;
MITSUBISHI CHEM CORP
COMMENT OS Unidentified
PN JP 199169182-A/11
PD 29-JUN-1999
PF 10-DEC-1997 JP 1997361768
PI TAKASHI KOBAYASHI, YOKO ASAI, HIDEAKI YUKAWA
PC C12N15/09, C12N1/21, C12P21/02//C12N15/09, C12R1:13, (C12N1/21,
PC C12R1:19), (C12N1/21, C12R1:13), (C12P21/02, C12R1:19), C12N15/00, (C12N15/00,
PC C12R1:13)
CC Strandedness: Single;
CC Topology: linear;
FH key Location/Qualifiers
FT source 1..29
Location/Qualifiers
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source 1..29
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/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN
Query Match 64.0%; Score 12.8; DB 6; Length 29;
Best Local Similarity 87.5%; Pred. No. 6e+04; 2; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACCGAGTCAGATGTT 16
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Db 14 ACCGAGTCAGATGTT 29
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RESULT 12
LOCUS AR064721 30 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 37 from patent US 5849306.
ACCESSION AR064721
VERSION AR064721.1 GI:5994937
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Sim, K.lee., Chitnis, C., Miller, L.H., Peterson, D.S., Su, X.-Z. and
Wellens, T.B.
TITLE Binding domains from Plasmodium vivax and Plasmodium falciparum
erythrocyte binding proteins
JOURNAL Patent: US 5849306-A 37 15-DEC-1998;
FEATURES
source 1..30
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/organism="unknown"
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Db      30 ACTCAGAGAGTGTGTA 15

RESULT 13
LOCUS   AR089162
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Sequence 20 from patent US 5993827.
ACCESSION AR089162
VERSION   AR089162.1 GI:10015919
KEYWORDS
SOURCE   Unknown.
ORGANISM Unclassified.
REFERENCE
1 (bases 1 to 30)
AUTHORS Sim,K.Lee., Chitlins,C., Miller,L.H., Peterson,D.S., Su,X.-Z. and
Willems,T.E.
TITLE    Binding domains from plasmodium vivax and plasmodium falciparum
JOURNAL Patent: US 5993827-A 20 30-NOV-1999;
FEATURES
Location/Qualifiers
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Db      30 ACTCAGAGAGTGTGTA 15

RESULT 14
LOCUS   AR153238
DEFINITION
Sequence 240 from patent US 6235480.
ACCESSION AR153238
VERSION   AR153238.1 GI:15120770
KEYWORDS
SOURCE   Unknown.
ORGANISM Unclassified.
REFERENCE
1 (bases 1 to 30)
AUTHORS Shultz,U.William., Lewis,M.K., Leippe,D., Mandrekar,M., Kephart,D.,
Rhodes,R.Byron., Andrews,C.Ann., Hartnett,J.Robert., Gu,T.,
Olson,R.J., Wood,K.V. and Welch,R.
TITLE    Detection of nucleic acid hybrids
JOURNAL Patent: US 6235480-A 240 22-MAY-2001;
FEATURES
Location/Qualifiers
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/organism="unknown"
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ORIGIN
Query Match 64.0%; Score 12.8; DB 6; Length 30;
Best Local Similarity 87.5%; Pred. No. 6e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      5 AGTCAGAGATGTTGTGA 20
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Db      2 AGTCAGAGAGTGTGTA 17

RESULT 15
LOCUS   AR291326
DEFINITION
Sequence 3061 from patent US 6537751.
ACCESSION AR291326
VERSION   AR291326.1 GI:31678610

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KEYWORDS
SOURCE   Unknown.
ORGANISM Unclassified.
REFERENCE
1 (bases 1 to 47)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE    Biallelic markers for use in constructing a high density
JOURNAL Patent: US 6537751-A 3061 25-MAR-2003;
FEATURES
Location/Qualifiers
1..47
/mol_type="genomic DNA"

ORIGIN
Query Match 64.0%; Score 12.8; DB 6; Length 47;
Best Local Similarity 77.8%; Pred. No. 5.9e+04;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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Db      37 ACCGGGTCAGAGTGTCT 20

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GenCore version 5.1.6
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(without alignments)
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Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

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SUMMARIES

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4	13.8	69.0	38	11	US-09-405-032-167
5	13.4	67.0	25	14	US-10-098-263B-117442
6	13.4	67.0	31	9	US-09-801-274-1445
7	13.4	67.0	50	15	US-10-402-365-14
8	13.4	67.0	50	15	US-10-131-827-1124
9	13.4	67.0	50	15	US-10-131-827-1452
10	13.4	67.0	50	15	US-10-131-827-1458
11	13.2	66.0	50	15	US-10-131-827-3424
12	13	65.0	25	14	US-10-098-263B-35307
13	12.8	64.0	25	14	US-10-098-263B-35307
14	12.8	64.0	17	10	US-09-877-478-901
15	12.8	64.0	17	12	US-10-342-902-200

c 16	12.8	64.0	17	12	US-10-342-902-901	Sequence 901, App
c 17	12.8	64.0	18	9	US-09-969-373-1732	Sequence 1732, Ap
c 18	12.8	64.0	25	14	US-10-215-112-5569	Sequence 5569, Ap
c 19	12.8	64.0	25	14	US-10-098-263B-27690	Sequence 27690, A
c 20	12.8	64.0	25	14	US-10-098-263B-69440	Sequence 69440, A
c 21	12.8	64.0	25	14	US-10-098-263B-81262	Sequence 81262, A
c 22	12.8	64.0	25	14	US-10-098-263B-113668	Sequence 113668, A
c 23	12.8	64.0	30	9	US-09-790-417-240	Sequence 240, App
c 24	12.8	64.0	30	13	US-10-153-273-37	Sequence 37, App1
c 25	12.8	64.0	31	10	US-09-912-263-97	Sequence 97, App1
c 26	12.8	64.0	47	15	US-10-345-143-3061	Sequence 3061, Ap
c 27	12.8	64.0	50	15	US-10-131-827-2091	Sequence 2091, Ap
c 28	12.6	63.0	25	14	US-10-098-263B-11446	Sequence 11446, A
c 29	12.6	63.0	25	14	US-10-098-263B-17508	Sequence 17508, A
c 30	12.6	63.0	25	14	US-10-098-263B-60520	Sequence 60520, A
c 31	12.6	63.0	25	14	US-10-098-263B-105128	Sequence 105128, A
c 32	12.6	63.0	25	14	US-10-098-263B-116073	Sequence 116073, A
c 33	12.6	63.0	25	14	US-10-098-263B-127368	Sequence 127368, A
c 34	12.6	63.0	47	15	US-10-349-143-218	Sequence 218, App
c 35	12.6	63.0	50	15	US-10-131-827-7202	Sequence 7202, App
c 36	12.4	62.0	20	15	US-10-289-762-5700	Sequence 5700, Ap
c 37	12.4	62.0	21	9	US-09-753-143-44	Sequence 44, App1
c 38	12.4	62.0	25	14	US-10-098-263B-44418	Sequence 44418, A
c 39	12.4	62.0	26	12	US-10-398-877-76	Sequence 76, App1
c 40	12.4	62.0	29	12	US-10-231-079-58	Sequence 58, App1
c 41	12.4	62.0	50	15	US-10-131-827-1177	Sequence 1177, Ap
c 42	12.4	62.0	50	15	US-10-131-827-1178	Sequence 1178, Ap
c 43	12.2	61.0	17	10	US-09-877-478-201	Sequence 201, App
c 44	12.2	61.0	17	12	US-10-342-902-201	Sequence 201, App
c 45	12.2	61.0	18	15	US-10-349-143-7628	Sequence 7628, Ap

ALIGNMENTS

RESULT 1

US-10-006-430-76

Sequence 76, Application US/10006430

GENERAL INFORMATION:

APPLICANT: Mark J. Graham

APPLICANT: Kenneth Dobie

TITLE OF INVENTION: ANTISENSE MODULATION OF CD81 EXPRESSION

FILE REFERENCE: RTS-0341

CURRENT APPLICATION NUMBER: US/10/006,430

CURRENT FILING DATE: 2001-12-10

NUMBER OF SEQ ID NOS: 90

SEQ ID NO 76

LENGTH: 20

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Antisense Oligonucleotide

US-10-006-430-76

Query Match 100.0%; Score 20; DB 14; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.6;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAGGATCAGATGTTGTA 20

DB 1 ACAGGATCAGATGTTGTA 20

RESULT 2

US-10-131-827-4670/c

Sequence 4670, Application US/1011827

GENERAL INFORMATION:

APPLICANT: Wohlgemuth, Jay

APPLICANT: Fry, Kirk

APPLICANT: Woodward, Robert

APPLICANT: Ly, Ngoc

```
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
/ FILE REFERENCE: 506612000120
/ CURRENT APPLICATION NUMBER: US/10/131,827
/ CURRENT FILING DATE: 2002-09-06
/ PRIOR APPLICATION NUMBER: US 10/006,290
/ PRIOR FILING DATE: 2001-10-22
/ PRIOR APPLICATION NUMBER: US 60/296,764
/ PRIOR FILING DATE: 2001-06-08
/ NUMBER OF SEQ ID NOS: 9090
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 4670
/ LENGTH: 50
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-131-827-4670

Query Match          100.0%; Score 20; DB 15; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACGGAGTCAGATGTTGTA 20
DB 46 ACGGAGTCAGATGTTGTA 27

RESULT 3
US-10-170-097-1178/c
/ Sequence 1178, Application US/10170097
/ Publication No. US20030228582A1
/ GENERAL INFORMATION:
/ APPLICANT: Blumenfeld, Marita
/ APPLICANT: Bouquelere, Lydie
/ APPLICANT: Chumakov, Ilya
/ APPLICANT: Cohen, Amick
/ TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
/ FILE REFERENCE: GEN-114XC2D1
/ CURRENT APPLICATION NUMBER: US/10/170,097
/ CURRENT FILING DATE: 2002-06-10
/ PRIOR APPLICATION NUMBER: US 09/641,638
/ PRIOR FILING DATE: 2000-08-16
/ PRIOR APPLICATION NUMBER: US 09/502,330
/ PRIOR FILING DATE: 2000-02-11
/ PRIOR APPLICATION NUMBER: US 60/133,200
/ PRIOR FILING DATE: 1999-05-07
/ PRIOR APPLICATION NUMBER: US 09/275,267
/ PRIOR FILING DATE: 1999-03-23
/ PRIOR APPLICATION NUMBER: US 60/119,917
/ PRIOR FILING DATE: 1999-02-12
/ NUMBER OF SEQ ID NOS: 1304
/ SOFTWARE: Patent.pm
/ SEQ ID NO 1178
/ LENGTH: 47
/ TYPE: DNA
/ ORGANISM: Homo Sapiens
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 24
/ OTHER INFORMATION: 10-298-122 : polymorphic base C or T
US-10-170-097-1178

Query Match          77.0%; Score 15.4; DB 15; Length 47;
Best Local Similarity 84.2%; Pred. No. 4e+02;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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/ Sequence 167, Application US/09405032
/ Publication No. US20030207827A1
/ GENERAL INFORMATION:
/ APPLICANT: Amgen Inc.
/ TITLE OF INVENTION: OSTEOPROTEGERIN
/ NUMBER OF SEQUENCES: 168
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Amgen Inc.
/ STREET: 1840 Dehavenland Drive
/ CITY: Thousand Oaks
/ STATE: California
/ COUNTRY: United States
/ ZIP: 91320
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/405,032
/ FILING DATE: 24-Sep-1999
/ CLASSIFICATION: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Winter, Robert B.
/ REFERENCE/DOCKET NUMBER: A-378-CIP2
/ INFORMATION FOR SEQ ID NO: 167:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 38 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ SEQUENCE DESCRIPTION: SEQ ID NO: 167:
US-09-405-032-167

Query Match          69.0%; Score 13.8; DB 11; Length 38;
Best Local Similarity 88.2%; Pred. No. 2.7e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GAGTCAGATGTTGTA 20
DB 9 GAGTCAGATGTTGTA 25

RESULT 5
US-10-098-263B-117442
/ Sequence 117442, Application US/10098263B
/ Publication No. US20030104410A1
/ GENERAL INFORMATION:
/ APPLICANT: Miltman, Michael
/ TITLE OF INVENTION: Human Microarray
/ FILE REFERENCE: 3118.1
/ CURRENT APPLICATION NUMBER: US/10/098,263B
/ CURRENT FILING DATE: 2003-01-08
/ PRIOR APPLICATION NUMBER: 60/276,759
/ PRIOR FILING DATE: 2001-03-16
/ NUMBER OF SEQ ID NOS: 131066
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 117442
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-10-098-263B-117442

Query Match          67.0%; Score 13.4; DB 14; Length 25;
Best Local Similarity 93.3%; Pred. No. 4.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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RESULT 6
US-09-801-274-1445/C
; Sequence 1445, Application US/09801274
; Patent No. US20020032319A1
; GENERAL INFORMATION:
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Lander, Eric S.
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: 2825.2009-001
; CURRENT APPLICATION NUMBER: US/09/801,274
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 60/187,510
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 60/206,129
; PRIOR FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 1802
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1445
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-801-274-1445

Query Match      67.0%; Score 13.4; DB 9; Length 31;
Best Local Similarity 93.3%; Pred. No. 4.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 GTCAGAGTGTGTGA 20
DB      31 GTCAGAGTGTGTGA 17

RESULT 7
US-10-402-365-14
; Sequence 14, Application US/10402365
; Patent No. US20030229913A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS DEUTSCHLAND GMBH
; TITLE OF INVENTION: Identification of the FLT1 Gene Required for Angiogenesis in
; FILE REFERENCE: AR03-003C
; CURRENT APPLICATION NUMBER: US/10/402,365
; CURRENT FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: US 60/368,616
; PRIOR FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Synthetic
US-10-402-365-14

Query Match      67.0%; Score 13.4; DB 15; Length 50;
Best Local Similarity 93.3%; Pred. No. 4.4e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 GTCAGAGTGTGTGA 20
DB      26 GTCAGAGTGTGTGA 40

RESULT 8
US-10-131-827-1124
; Sequence 1124, Application US/10131827
; Patent No. US20040009479A1
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
```

```
; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1124
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-1124

Query Match      67.0%; Score 13.4; DB 15; Length 50;
Best Local Similarity 93.3%; Pred. No. 4.4e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 GGAGTCAGAGTGTG 17
DB      20 GGAGTCAGAGTGTG 34

RESULT 9
US-10-131-827-1452
; Sequence 1452, Application US/10131827
; Patent No. US20040009479A1
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1452
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-1452

Query Match      67.0%; Score 13.4; DB 15; Length 50;
Best Local Similarity 93.3%; Pred. No. 4.4e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 GGAGTCAGAGTGTG 17
DB      20 GGAGTCAGAGTGTG 34

RESULT 10
US-10-131-827-1458
; Sequence 1458, Application US/10131827
; Patent No. US20040009479A1
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
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; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1458
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-1458
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Query Match          67.0%; Score 13.4; DB 15; Length 50;
Best Local Similarity 93.3%; Pred. No. 4.4e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY      3 GGAGTCAGAGATGTTG 17
        |||||
Db      20 GGAGTCAGAGATGTTG 34
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```
RESULT 11
US-10-131-827-5424
; Sequence 5424, Application US/10131827
; Publication No. US20040009479A1
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5424
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-5424
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Query Match          66.0%; Score 13.2; DB 15; Length 50;
Best Local Similarity 83.3%; Pred. No. 5.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      3 GGAGTCAGAGATGTTGCA 20
        |||||
Db      6 GAAGTCAGAGAGATTGCA 23
```

```
RESULT 12
US-10-098-263B-35307/C
; Sequence 35307, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 35307
; LENGTH: 25
```

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; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-35307
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Query Match          65.0%; Score 13; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.7e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      6 GTCAGAGATGTTGT 18
        |||||
Db      19 GTCAGAGATGTTGT 7
```

```
RESULT 13
US-09-877-478-200/C
; Sequence 200, Application US/09877478
; Publication No. US20030068301A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: MBHB00-845-H (400/029)
; CURRENT APPLICATION NUMBER: US/09/877,478
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1993-05-14
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 08/433,993
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 08/434,504
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 200
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B virus
US-09-877-478-200
```

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Query Match          64.0%; Score 12.8; DB 10; Length 17;
Best Local Similarity 87.5%; Pred. No. 8.2e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      3 GGAGTCAGAGATGTTGT 18
        |||||
Db      17 GGAGTCAGAGATGTTGT 2
```

```
RESULT 14
US-09-877-478-901/C
; Sequence 901, Application US/09877478
; Publication No. US20030068301A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: MBHB00-845-H (400/029)
; CURRENT APPLICATION NUMBER: US/09/877,478
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Query Match	64.0%	Score 12.8	DB 12	Length 17
Best Local Similarity	87.5%	Pred. No. 8.2e+03		
Matches 14; Conservative	0	Mismatches 2	Indels 0	Gaps 0

Search completed: April 15, 2004, 13:24:37
Job time : 235 secs

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OM nucleic - nucleic search, using sw model

Run on: April 15, 2004, 12:23:31 ; Search time 51 seconds
(without alignments)
217.628 Million cell updates/sec

Title: US-10-006-430-76

Perfect score: 20

Sequence: 1 acgagtcagatgtgtga 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 segs, 277475446 residues

Total number of hits satisfying chosen parameters: 839752

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 3: /cgn2_6/prodata/2/ina/6A_COMB.seq:*
- 4: /cgn2_6/prodata/2/ina/6B_COMB.seq:*
- 5: /cgn2_6/prodata/2/ina/PCTUS_COMB.seq:*
- 6: /cgn2_6/prodata/2/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	15.4	77.0	47	4	US-09-641-638-1178 Sequence 1178, Ap
C 2	13.2	66.0	28	2	US-08-232-081B-25 Sequence 25, Appl
C 3	12.8	64.0	20	2	US-08-623-906A-55 Sequence 55, Appl
C 4	12.8	64.0	27	1	US-08-100-465-6 Sequence 6, Appl1
C 5	12.8	64.0	30	2	US-08-568-459A-37 Sequence 37, Appl
C 6	12.8	64.0	30	2	US-08-487-826B-20 Sequence 20, Appl
C 7	12.8	64.0	30	3	US-09-358-972-240 Sequence 240, App
C 8	12.8	64.0	30	3	US-09-430-615-9 Sequence 9, Appl1
C 9	12.8	64.0	30	4	US-09-210-288-37 Sequence 37, Appl
C 10	12.8	64.0	47	4	US-09-422-978-3061 Sequence 3061, Ap
C 11	12.6	63.0	47	4	US-09-422-978-218 Sequence 218, App
C 12	12.4	62.0	20	4	US-09-798-096-58 Sequence 58, Appl
C 13	12.4	62.0	20	4	US-09-198-452A-5700 Sequence 5700, Ap
C 14	12.4	62.0	21	1	US-08-559-303B-44 Sequence 44, Appl
C 15	12.4	62.0	21	3	US-09-175-828-44 Sequence 44, Appl
C 16	12.2	61.0	18	4	US-09-422-978-7628 Sequence 7628, Ap
C 17	12.2	61.0	20	4	US-09-495-714C-128 Sequence 128, App
C 18	12.2	61.0	25	4	US-09-645-629-6 Sequence 6, Appl1
C 19	12.2	61.0	28	4	US-09-603-613-1-1 Sequence 1, Appl1
C 20	12.2	61.0	31	2	US-08-859-998-195 Sequence 195, App
C 21	12.2	61.0	31	4	US-09-225-928-195 Sequence 195, App
C 22	12.2	61.0	31	4	US-09-225-201B-195 Sequence 195, App
C 23	12.2	61.0	33	4	US-09-636-215-821 Sequence 821, Appl
C 24	12.2	61.0	33	4	US-09-685-166A-821 Sequence 821, Appl
C 25	12.2	61.0	34	1	US-08-437-841-28 Sequence 28, Appl
C 26	12.2	61.0	34	1	US-08-286-521-28 Sequence 28, Appl
C 27	12.2	61.0	34	1	US-08-436-175-28 Sequence 28, Appl

C 28	12.2	61.0	34	3	US-08-943-682-28 Sequence 28, Appl
C 29	12.2	61.0	34	5	PCT-US95-09464-28 Sequence 28, Appl
C 30	12.2	61.0	36	1	US-08-437-841-29 Sequence 29, Appl
C 31	12.2	61.0	36	1	US-08-286-521-29 Sequence 29, Appl
C 32	12.2	61.0	36	1	US-08-436-175-29 Sequence 29, Appl
C 33	12.2	61.0	36	3	US-08-943-682-29 Sequence 29, Appl
C 34	12.2	61.0	36	5	PCT-US95-09464-29 Sequence 29, Appl
C 35	12.2	61.0	47	4	US-09-671-317-576 Sequence 576, App
C 36	12.2	61.0	47	4	US-09-422-978-3049 Sequence 3049, Ap
C 37	12	60.0	20	4	US-09-601-144-16 Sequence 16, Appl
C 38	12	60.0	22	1	US-08-388-779A-6 Sequence 6, Appl1
C 39	12	60.0	22	1	US-08-591-070A-6 Sequence 6, Appl1
C 40	12	60.0	22	2	US-08-927-855-6 Sequence 6, Appl1
C 41	12	60.0	25	3	US-09-173-914-34 Sequence 34, Appl
C 42	12	60.0	28	4	US-08-997-685A-21 Sequence 21, Appl
C 43	12	60.0	38	4	US-09-371-772B-8016 Sequence 8016, Ap
C 44	11.8	59.0	20	2	US-08-117-952-693 Sequence 693, App
C 45	11.8	59.0	20	3	US-09-487-445-87 Sequence 87, Appl

ALIGNMENTS

```
RESULT 1
US-09-641-638-1178/C
; Sequence 1178, Application US/09641638
; Patent No. 6432648
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Bougenlefer, Lydie
; APPLICANT: Chumakov, Ilya
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
; FILE REFERENCE: GENSET.051CPI
; CURRENT APPLICATION NUMBER: US/09/641, 638
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: US 09/502,330
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: US 60/133,200
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 09/275,267
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: US 60/119,917
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 1304
; SOFTWARE: Patent.pm
; SEQ ID NO 1178
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 10-298-122 : polymorphic base C or T
US-09-641-638-1178

Query Match          77.0% Score 15.4; DB 4; Length 47;
Best Local Similarity 84.2% Pred. No. 43;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1  ACCGAGTCAGATGTGTG 19
Db      37  ACCGAGTCAGATGTGTG 19

RESULT 2
US-08-232-081B-25
; Sequence 25, Application US/08232081B
; Patent No. 5886152
; GENERAL INFORMATION:
; APPLICANT: NAKATANI, TOMOYUKI
; APPLICANT: GOMI, HIDEYUKI
```

APPLICANT: WIJENES, JOHN
APPLICANT: NOGUCHI, HIROSHI
TITLE OF INVENTION: HUMANIZED B-B10
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSER: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,081B
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SVENSSON, LEONARD R
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 20-3484
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-232-081B-25

Query Match 66.0%; Score 13.2; DB 2; Length 28;
Best Local Similarity 83.3%; Pred. No. 5.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGGAGTCAGATGTGT 18
DB 1 ACTGAGTCAGAGAGATG 18

RESULT 3
US-08-623-906A-55
Sequence 55, Application US/08623906A
Patent No. 5874217
GENERAL INFORMATION:
APPLICANT: Stevenson, Tamara
APPLICANT: Dvorak, Jan
APPLICANT: Halverson, Joy
TITLE OF INVENTION: Microsatellite Sequences for Canine
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSER: FLEHR, HOBRACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: US
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/623,906A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: Sherwood, Pamela J.
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: A-62282/BIR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-623-906A-55

Query Match 64.0%; Score 12.8; DB 2; Length 20;
Best Local Similarity 87.5%; Pred. No. 8.4e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GAGTCAGATGTGTG 19
DB 1 GACTCATGATGTGTG 16

RESULT 4
US-08-100-465-6/c
Sequence 6, Application US/08100465
Patent No. 5610137
GENERAL INFORMATION:
APPLICANT: TOWNES, TIM M., ET AL.
TITLE OF INVENTION: TRANSGENIC, CROSS-LINKED
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSER: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: Wordperfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/100,465
FILING DATE: 30-JUL-1993
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER: 07/630,825
FILING DATE: DECEMBER 20, 1990
ATTORNEY/AGENT INFORMATION:
NAME: CLARK, PAUL T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 004005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 27
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-100-465-6
Query Match 64.0%; Score 12.8; DB 1; Length 27;
Best Local Similarity 87.5%; Pred. No. 8.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 23 GGAGTCAGCATGCTGT 8

RESULT 5

US-08-568-459A-37/c
Sequence 37, Application US/08568459A
Patent No. 5849306

GENERAL INFORMATION:

APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
COUNTRY: US
ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/568,459A

FILING DATE: 07-DEC-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Israelisen, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH121.001CP1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176

INFORMATION FOR SEQ ID NO: 37:

SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs

TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: CDNA

HYPOTHETICAL: NO
ANTI-SENSE: NO

FRAGMENT TYPE:
ORIGINAL SOURCE:

US-08-568-459A-37
Query Match Best Local Similarity 64.0%; Score 12.8; DB 2; Length 30;
Pred. No. 9e+02; 2; Indels 0; Gaps 0;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 5 AGTCAGGATGTTGTGA 20
Db 30 ACTCAGGAAGTTGTGA 15

RESULT 6

US-08-487-826B-20/c
Sequence 20, Application US/08487826B
Patent No. 593827

GENERAL INFORMATION:

APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun

APPLICANT: Wellens, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
COUNTRY: US
ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826B

FILING DATE: 10-SEP-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Israelisen, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH121.001CP1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176

INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs

TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: CDNA

HYPOTHETICAL: NO
ANTI-SENSE: NO

FRAGMENT TYPE:
ORIGINAL SOURCE:

US-08-487-826B-20

Query Match Best Local Similarity 64.0%; Score 12.8; DB 2; Length 30;
Pred. No. 9e+02; 2; Indels 0; Gaps 0;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 5 AGTCAGGATGTTGTGA 20
Db 30 ACTCAGGAAGTTGTGA 15

RESULT 7

US-09-358-972-240
Sequence 240, Application US/09358972
Patent No. 6235480

GENERAL INFORMATION:

APPLICANT: Shultz, John W.
APPLICANT: Lewis, Martin K.
APPLICANT: Lapepe, Donna
APPLICANT: Mandrekar, Michelle
APPLICANT: Kephart, Daniel
APPLICANT: Rhodes, Richard B.
APPLICANT: Andrews, Christine A.
APPLICANT: Hartnett, James R.
APPLICANT: Gu, Trent
APPLICANT: Olson, Ryan J.
APPLICANT: Wood, Keith W.
APPLICANT: Welch, Roy

TITLE OF INVENTION: Nucleic Acid Detection
FILE REFERENCE: Pro-103 6868/75528

CURRENT APPLICATION NUMBER: US/09/358,972
CURRENT FILING DATE: 1999-07-22

EARLIER APPLICATION NUMBER: 09/252,436
EARLIER FILING DATE: 1999-02-18
EARLIER APPLICATION NUMBER: 09/042,287

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/ EARLIER FILING DATE: 1998-03-13
/ NUMBER OF SEQ ID NOS: 290
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 240
/ LENGTH: 30
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:mutant target
US-09-358-972-240

Query Match          64.0%; Score 12.8; DB 3; Length 30;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      5 AGTCAGGAGTTGTGA 20
Db      2 AGTCAGCAGCTTGTGA 17

RESULT 8
US-09-430-615-9
/ Sequence 9, Application US/09430615
/ Patent No. 6277578
/ GENERAL INFORMATION:
/ APPLICANT: Lewis, Martin K.
/ APPLICANT: Leippe, Donna
/ APPLICANT: Mandrekar, Michelle
/ APPLICANT: Andrews, Christine Ann
/ APPLICANT: Hartnett, James Robert
/ APPLICANT: Welch, Roy
/ APPLICANT: Shultz, John William
/ TITLE OF INVENTION: Method for Amplified Nucleic Acid Detection
/ FILE REFERENCE:
/ CURRENT APPLICATION NUMBER: US/09/430,615
/ PRIOR FILING DATE: 1999-10-29
/ PRIOR APPLICATION NUMBER: 09/358,972
/ PRIOR FILING DATE: 1999-07-21
/ PRIOR APPLICATION NUMBER: 09/252,436
/ PRIOR FILING DATE: 1999-02-18
/ PRIOR APPLICATION NUMBER: 09/042,287
/ PRIOR FILING DATE: 1998-03-13
/ NUMBER OF SEQ ID NOS: 69
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 9
/ LENGTH: 30
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:mutant target
US-09-430-615-9

Query Match          64.0%; Score 12.8; DB 3; Length 30;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      5 AGTCAGGAGTTGTGA 20
Db      2 AGTCAGCAGCTTGTGA 17

RESULT 9
US-09-210-288-37/c
/ Sequence 37, Application US/09210288
/ Patent No. 6392026
/ GENERAL INFORMATION:
/ APPLICANT: Sim, Kim L.
/ APPLICANT: Chitnis, Chetan
/ APPLICANT: Miller, Louis H.
/ APPLICANT: Peterson, David S.
/ APPLICANT: Su, Xin-zhaun
/ APPLICANT: Wellem, Thomas E.
/ TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
```

```
/ TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
/ NUMBER OF SEQUENCES: 37
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Knobbe Martens Olson & Bear
/ STREET: 620 Newport Center Drive 16th floor
/ CITY: Newport Beach
/ STATE: California
/ COUNTRY: US
/ ZIP: 92660
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/210,288
/ FILING DATE:
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Fuller, Michael
/ REGISTRATION NUMBER: 36,516
/ REFERENCE/DOCKET NUMBER: NIH121.1FMDV1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (619) 235-0176
/ TELEFAX: (619) 235-8550
/ INFORMATION FOR SEQ ID NO: 37:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 30 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ FRAGMENT TYPE:
/ ORIGINAL SOURCE:
US-09-210-288-37

Query Match          64.0%; Score 12.8; DB 4; Length 30;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      5 AGTCAGGAGTTGTGA 20
Db      30 ACTCAGGAAGTTGTGA 15

RESULT 10
US-09-422-978-3061/c
/ Sequence 3061, Application US/09422978
/ Patent No. 6537751
/ GENERAL INFORMATION:
/ APPLICANT: Cohen, Daniel
/ APPLICANT: Blumenfeld, Marta
/ APPLICANT: Chumakov, Ilya
/ TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
/ FILE REFERENCE: GENSET.020CPI
/ CURRENT APPLICATION NUMBER: US/09/422,978
/ CURRENT FILING DATE: 1999-10-20
/ EARLIER APPLICATION NUMBER: US 09/298,850
/ EARLIER FILING DATE: 1999-04-21
/ EARLIER APPLICATION NUMBER: US 60/109,732
/ EARLIER FILING DATE: 1998-11-23
/ EARLIER APPLICATION NUMBER: US 60/082,614
/ EARLIER FILING DATE: 1998-04-21
/ NUMBER OF SEQ ID NOS: 11796
/ SEQ ID NO 3061
/ LENGTH: 47
/ TYPE: DNA
/ ORGANISM: Homo Sapiens
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 24
```

OTHER INFORMATION: 99-21921-338 : polymorphic base T or C
US-09-422-978-3061

Query Match 64.0%; Score 12.8; DB 4; Length 47;
Best Local Similarity 77.8%; Pred. No. 9.6e+02;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ACGAGTCAGAGTGTGT 18
DB 37 ACGAGTCAGAGTGTGT 20

RESULT 11
US-09-422-978-218
Sequence 218, Application US/09422978
Patent No. 6537751
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marla
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENEST.020CPI
CURRENT APPLICATION NUMBER: US/09/422,978
EARLIER FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: US 09/298,850
EARLIER FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,732
EARLIER FILING DATE: 1998-11-23
EARLIER APPLICATION NUMBER: US 60/082,614
EARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
SEQ ID NO 218
LENGTH: 47
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: allele
LOCATION: 24
OTHER INFORMATION: 99-13589-362 : polymorphic base A or G
US-09-422-978-218

Query Match 63.0%; Score 12.6; DB 4; Length 47;
Best Local Similarity 78.9%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ACGAGTCAGAGTGTGTG 19
DB 3 ACGAGTCAGAGTGTGTG 21

RESULT 12
US-09-798-096-58
Sequence 58, Application US/09798096
Patent No. 6399378
GENERAL INFORMATION:
APPLICANT: Donna T. Ward
APPLICANT: Andrew T. Walt
TITLE OF INVENTION: ANTISENSE MODULATION OF RECOL2 EXPRESSION
FILE REFERENCE: RTS-0207
CURRENT APPLICATION NUMBER: US/09/798,096
CURRENT FILING DATE: 2001-03-01
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 58
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-798-096-58

Query Match 62.0%; Score 12.4; DB 4; Length 20;
Best Local Similarity 92.9%; Pred. No. 1.4e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGAGTCAGAGTGT 15
DB 6 CTGAGTCAGAGTGT 19

RESULT 13
US-09-198-452A-5700/C
Sequence 5700, Application US/09198452A
Patent No. 6559294
GENERAL INFORMATION:
APPLICANT: Griffiths, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 5700
LENGTH: 20
TYPE: DNA
ORGANISM: Chlamydia pneumoniae
US-09-198-452A-5700

Query Match 62.0%; Score 12.4; DB 4; Length 20;
Best Local Similarity 92.9%; Pred. No. 1.4e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 AGTCAGAGTGTGT 18
DB 17 ACTCAGAGTGTGT 4

RESULT 14
US-08-559-303B-44/C
Sequence 44, Application US/08559303B
Patent No. 5824501
GENERAL INFORMATION:
APPLICANT: NATHAN A. ELLIS, JAMES GERMAN, AND JOANNA
APPLICANT: GRODEN
TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT
TITLE OF INVENTION: OF BLOOM'S SYNDROME
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
ADDRESS: AMSTER, ROTHSTEIN & EBENSTEIN
STREET: 90 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH 1.44 MB STORAGE DISKETTE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/559,303B
FILING DATE: NOVEMBER 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: ELIZABETH A. BOGOSIAN
REGISTRATION NUMBER: 39,911
REFERENCE/DOCKET NUMBER: 63475/65
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-5995
TELEFAX: (212) 286-0854 or 286-0082
TELEX: TWX 710-581-4766
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 21
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR

MOLECULE TYPE:
DESCRIPTION: OTHER NUCLEIC ACID
HYPOTHETICAL: YES
ANTI-SENSE: NO
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
US-08-559-303B-44

Query Match 62.0%; Score 12.4; DB 1; Length 21;
Best Local Similarity 92.9%; Pred. No. 1.4e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CGAGTCAGGATGT 15
DB 15 CTGAGTCAGGATGT 2

RESULT 15

US-09-175-828-44/C
Sequence 44, Application US/09175828
Patent No. 6221643

GENERAL INFORMATION:

APPLICANT: NATHAN A. ELLIS, JAMES GERMAN, AND JOANNA

APPLICANT: GRODEN

TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT

NUMBER OF SEQUENCES: OF BLOOM'S SYNDROME 78

CORRESPONDENCE ADDRESS:

ADDRESSEE: AMSTER, ROTHSTEIN & EBENSTEIN

STREET: 90 PARK AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: U.S.A.

ZIP: 10016

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 INCH 1.44 MB STORAGE DISKETTE

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: MS-DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/175,828

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/559,303

FILING DATE: NOVEMBER 15, 1995

ATTORNEY/AGENT INFORMATION:

NAME: ELIZABETH A. BOGOSIAN

REGISTRATION NUMBER: 39,911

REFERENCE/DOCKET NUMBER: 63475/65

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 697-5995

TELEFAX: (212) 286-0854 or 286-0082

TELEX: TWX 710-581-4766

INFORMATION FOR SEQ. ID NO: 44:

SEQUENCE CHARACTERISTICS:

LENGTH: 21

TYPE: NUCLEIC ACID

STRANDEDNESS: SINGLE

TOPOLOGY: LINEAR

MOLECULE TYPE: OTHER NUCLEIC ACID

DESCRIPTION: YES

HYPOTHETICAL: YES

ANTI-SENSE: NO

FEATURE:

NAME/KEY:

LOCATION:

IDENTIFICATION METHOD:

OTHER INFORMATION:

US-09-175-828-44

Query Match 62.0%; Score 12.4; DB 3; Length 21;
Best Local Similarity 92.9%; Pred. No. 1.4e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CGAGTCAGGATGT 15
DB 15 CTGAGTCAGGATGT 2

Search completed: April 15, 2004, 13:25:40
Job time : 53 secs

Result No.	Score	Query			DB	ID	Description
		Match	Length				
1	26	1.7	26	1	BD097225	ACCESSION: BD097225	
C 2	24	1.6	24	1	BD097226	ACCESSION: BD097226	
C 3	21	1.4	21	1	AX763858	ACCESSION: AX763858	
C 4	20	1.3	20	1	AX763859	ACCESSION: AX763859	
C 5	20	1.3	21	1	AX145918	ACCESSION: AX145918	
C 6	20	1.3	21	1	AX145919	ACCESSION: AX145919	
C 7	19	1.3	20	1	AR030917	ACCESSION: AR030917	
C 8	19	1.3	20	1	I28309	ACCESSION: I28309	
C 9	19	1.3	20	1	I47310	ACCESSION: I47310	
C 10	19	1.3	21	1	AX825109	ACCESSION: AX825109	
C 11	18.4	1.2	21	1	AX825127	ACCESSION: AX825127	
C 12	18	1.2	20	1	AR139961	ACCESSION: AR139961	
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C 14	18	1.2	20	1	AR140558	ACCESSION: AR140558	
C 15	18	1.2	21	1	AX825107	ACCESSION: AX825107	
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C 18	18	1.2	21	1	AX825152	ACCESSION: AX825152	
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C 30	16.4	1.1	18	1	AX085251	ACCESSION: AX085251	
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C 109	16	1.1	18	1	AX105651	ACCESSION:AX105651	C 182	15	1.0	15	1	AX711176	ACCESSION:AX711176
C 110	16	1.1	18	1	AX108642	ACCESSION:AX108642	C 183	15	1.0	15	1	BD074424	ACCESSION:BD074424
C 111	16	1.1	18	1	AX268883	ACCESSION:AX268883	C 184	15	1.0	15	1	BD084687	ACCESSION:BD084687
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C 113	16	1.1	18	1	AX547774	ACCESSION:AX547774	C 186	15	1.0	15	1	BD206432	ACCESSION:BD206432
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C 116	16	1.1	18	1	AX814723	ACCESSION:AX814723	C 189	15	1.0	16	1	AR221694	ACCESSION:AR221694
C 117	16	1.1	18	1	AX814724	ACCESSION:AX814724	C 190	15	1.0	16	1	AR221695	ACCESSION:AR221695
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C 119	16	1.1	18	1	AX814736	ACCESSION:AX814736	C 192	15	1.0	16	1	AR221697	ACCESSION:AR221697
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C 121	16	1.1	18	1	BD190553	ACCESSION:BD190553	C 194	15	1.0	16	1	AR257438	ACCESSION:AR257438
C 122	16	1.1	18	1	BD222596	ACCESSION:BD222596	C 195	15	1.0	16	1	AR257439	ACCESSION:AR257439
C 123	15.6	1.0	17	1	BD233654	ACCESSION:BD233654	C 196	15	1.0	16	1	AR257440	ACCESSION:AR257440
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C 139	15	1.0	15	1	AR029403	ACCESSION:AR029403	C 212	15	1.0	17	1	AR397940	ACCESSION:AR397940
C 140	15	1.0	15	1	AR034895	ACCESSION:AR034895	C 213	15	1.0	17	1	AX692524	ACCESSION:AX692524
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C 160	15	1.0	15	1	AR180723	ACCESSION:AR180723	C 233	15	1.0	17	1	BD168113	ACCESSION:BD168113
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ALIGNMENTS

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VERSION	BD097225.1	GI:22642799				
KEYWORDS	WO 0158459-A/12.					
SOURCE	synthetic construct					
ORGANISM	synthetic construct					
REFERENCE	1 (bases 1 to 26)					
AUTHORS	Itami, S., Shibui, T., Seki, M., Yotsumoto, Y., Matsuura, Y. and Miyamura, T.					
TITLE	A therapeutic agent for hepatitis type C					
JOURNAL	Patent: WO 0158459-A 12 16-AUG-2001;					
	MITSUBISHI TOKYO PHARMACEUTICALS INC, SEIMA ITAMI, TATSURO SHIBUI,					
	MAKOTO SEKI, YOSHIHISA YOTSUMOTO, YOSHIHARU MATSUURA, TATSUO MIYAMURA					
COMMENT	OS Artificial Sequence					
	PN WO 0158459-A/12					
	PD 16-AUG-2001					
	PF 13-FEB-2001					
	PR 14-FEB-2000					
	PI SEIMA ITAMI, TATSURO SHIBUI, MAKOTO SEKI, YOSHIHISA YOTSUMOTO, PI					
	YOSHIHARU MATSUURA, TATSUO MIYAMURA					
	PC A61K31/737, A61K38/17, A61K39/395, A61K45/00, A61P31/20, C07K16/10,					
	PC C12N15/09					
	CC GOIN33/50, GOIN33/53, GOIN33/576					
	CC Primer					
	FT Key					
	FT Location/Qualifiers					
	FT source					
	FT 1.36					

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FEATURES
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    Location/Qualifiers
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        /organism="Artificial Sequence"
        /organism="synthetic construct"
        /mol_type="genomic DNA"
        /db_xref="taxon:32630"

Query Match
  Best Local Similarity 1.7%; Score 26; DB 1; Length 26;
  Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 231 GCGCCGCCATGGAGTGGAGGGCTGC 256
      |||||
      1 GCGCCGCCATGGAGTGGAGGGCTGC 26

Db
  1 GCGCCGCCATGGAGTGGAGGGCTGC 26

RESULT 2
BD097226/c
LOCUS BD097226 24 bp DNA linear PAT 27-AUG-2002
DEFINITION A therapeutic agent for hepatitis type C.
ACCESSION BD097226
VERSION WO 0158459-A/13.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 24)
AUTHORS Itami,S., Shibui,T., Seki,M., Yotsumoto,Y., Matsuura,Y. and Miyamura,T.
TITLE A therapeutic agent for hepatitis type C
JOURNAL Patent: WO 0158459-A/13 16-AUG-2001;
MITSUBISHI TOKYO PHARMACEUTICALS INC,SEIMA ITAMI,TATSURO SHIBUI,
MAKOTO SEKI,YOSHIHISA YOTSUMOTO,YOSHIHARU MATSUURA,TATSUO MIYAMURA
OS Artificial Sequence
PN WO 0158459-A/13
PD 16-AUG-2001
PF 13-FEB-2001 WO 2001JP000967
PR 14-FEB-2000 JP 00P 034906
PI SEIMA ITAMI,TATSURO SHIBUI,MAKOTO SEKI,YOSHIHISA YOTSUMOTO,PI
YOSHIHARU MATSUURA,TATSUO MIYAMURA
PC A61K31/737,A61K38/17,A61K39/395,A61K45/00,A61P31/20,C07K16/10,
PC C12N15/09.
PC G01N33/50,G01N33/53,G01N33/576
CC Primer
FH Key
FT source
FT Location/Qualifiers
  source
    Location/Qualifiers
      1..24
        /organism="Artificial Sequence"

FEATURES
  source
    Location/Qualifiers
      1..24
        /organism="synthetic construct"
        /mol_type="genomic DNA"
        /db_xref="taxon:32630"

Query Match
  Best Local Similarity 1.6%; Score 24; DB 1; Length 24;
  Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

927 TCCGACACGCTCCGTGCTACTGAG 950
      |||||
      24 TCCGACACGCTCCGTGCTACTGAG 1

RESULT 3
AX763858
LOCUS AX763858 21 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 13 from Patent WO03040407.
ACCESSION AX763858
VERSION AX763858.1 GI:32258220
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
  source
    Location/Qualifiers
      1..21
        /organism="Homo sapiens"
        /mol_type="unassigned DNA"

AUTHORS Ruiz,P., Grzeskowiak,R., Drungowski,M., Witt,H., Osterziel,K.,
Perrot,A. and Saleh,A.
TITLE Novel markers for cardiopathies
JOURNAL Patent: WO 03040407-A 13 15-MAY-2003;
MAX-PLANCK-GESELLSCHAFT (DE)
FEATURES
  source
    Location/Qualifiers
      1..21
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Primer CD81_F"

Query Match
  Best Local Similarity 1.4%; Score 21; DB 1; Length 21;
  Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 668 AAGGCTGTGGTGAACCTTC 688
      |||||
      1 AAGGCTGTGGTGAACCTTC 21

Db
  1 AAGGCTGTGGTGAACCTTC 21

RESULT 4
AX763859/c
LOCUS AX763859 20 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 14 from Patent WO03040407.
ACCESSION AX763859
VERSION AX763859.1 GI:32258221
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Ruiz,P., Grzeskowiak,R., Drungowski,M., Witt,H., Osterziel,K.,
Perrot,A. and Saleh,A.
TITLE Novel markers for cardiopathies
JOURNAL Patent: WO 03040407-A 14 15-MAY-2003;
MAX-PLANCK-GESELLSCHAFT (DE)
FEATURES
  source
    Location/Qualifiers
      1..20
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Primer CD81_R"

Query Match
  Best Local Similarity 1.3%; Score 20; DB 1; Length 20;
  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 931 GAACGCTCCGTGCTACTGAG 950
      |||||
      20 GAACGCTCCGTGCTACTGAG 1

Db
  20 GAACGCTCCGTGCTACTGAG 1

RESULT 5
AX145918
LOCUS AX145918 21 bp DNA linear PAT 31-MAY-2001
DEFINITION Sequence 109 from Patent WO0134840.
ACCESSION AX145918
VERSION AX145918.1 GI:14284436
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Au,K.G., Chen,J.G., Patil,N. and Thomas,D.
TITLE Genetic compositions and methods
JOURNAL Patent: WO 0134840-A 109 17-MAY-2001;
GLAXO GROUP LIMITED (GB); Affymetrix, Inc. (US)
FEATURES
  source
    Location/Qualifiers
      1..21
        /organism="Homo sapiens"
        /mol_type="unassigned DNA"

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/db_xref="taxon:9606"
1..21
/notes="n" represents a polymorphic base"

variation
Query Match
  1.3%; Score 20; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 979 TGCAGTGCCTCCCTTAAGTGACC 999
|||||
Db 1 TGCAGTGCCTCCCTTAAGTGACC 21

RESULT 6
AX145919
LOCUS AX145919 21 bp DNA linear PAT 31-MAY-2001
DEFINITION Sequence 110 from Patent WO0134840.
ACCESSION AX145919
VERSION AX145919.1 GI:14284437
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1
AUTHORS Au,K.G., Chen,J.G., Patil,N. and Thomas,D.
TITLE Genetic compositions and methods
JOURNAL Patent: WO 0134840-A 110 17-MAY-2001;
GLAXO GROUP LIMITED (GB) ; Affymetrix, Inc. (US)
FEATURES
  source
    1..21
      /organism="Homo sapiens"
      /mol_type="unassigned DNA"
variation
  1..21
    /notes="n" represents a polymorphic base"

Query Match
  1.3%; Score 20; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1036 ATAACTTTCCGTATTACTC 1056
|||||
Db 1 ATAACTTTCCGTATTACTC 21

RESULT 7
AR030917/c
LOCUS AR030917 20 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 20 from patent US 5861487.
ACCESSION AR030917
VERSION AR030917.1 GI:5944131
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE
  1 (bases 1 to 20)
AUTHORS Holton,T.Albert., Cornish,E.Cecily., Kovacic,F., Tanaka,Y. and
Lester,D.Ruth.
TITLE Genetic sequences encoding flavonoid pathway enzymes and uses
therefor
JOURNAL Patent: US 5861487-A 20 19-JAN-1999;
FEATURES
  source
    1..20
      /organism="unknown"
      /mol_type="unassigned DNA"

Query Match
  1.3%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1478 GCTAAAAA 1496
|||||
Db 1478 GCTAAAAA 1496

RESULT 8
AX825109/c
LOCUS AX825109 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 7 from Patent WO03072818.
ACCESSION AX825109
VERSION AX825109.1 GI:39750838
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
  1
  Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
```

TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 7 04-SEP-2003;
Degussa Bioactives GmbH (DE)

FEATURES
source 1..21
Location/Qualifiers

/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"

misc_binding 1
/bound_moiety="Biotin"

modified_base 3
/notes="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

modified_base 6
/notes="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

modified_base 9
/notes="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

modified_base 12
/notes="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

modified_base 15
/notes="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

modified_base 18
/notes="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

Query Match 1..3%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1478 GCTAAAAA 1496
|||||
Db 21 GCTAAAAA 3

RESULT 11
AX825127/c
LOCUS AX825127 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 25 from Patent WO03072818.
ACCESSION AX825127
VERSION AX825127.1 GI:39750856

KEYWORDS
synthetic construct
synthetic construct
artificial sequences.

REFERENCE 1
Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
AUTHORS Method for sorting single-stranded nucleic acids
TITLE Patent: WO 03072818-A 25 04-SEP-2003;
JOURNAL Degussa Bioactives GmbH (DE)

FEATURES
source 1..21
Location/Qualifiers

/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"

misc_binding 1
/bound_moiety="Biotin"

modified_base 3
/notes="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

modified_base 6
/notes="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

modified_base 9
/notes="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

modified_base 12
/notes="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

modified_base 12
/notes="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

modified_base 15
/notes="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

modified_base 18
/notes="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

Query Match 1.2%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 41;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1477 TGCTAAAA 1496
|||||

Db 21 TGCAAAAA 2

RESULT 12
AR139961/c
LOCUS AR139961 20 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 33 from patent US 6207417.
ACCESSION AR139961
VERSION AR139961.1 GI:14482457

KEYWORDS
Unknown.
SOURCE
ORGANISM
Unclassified.

REFERENCE 1 (bases 1 to 20)
AUTHORS Zsebo,K.M., Bosselman,R.A., Suggs,S.V. and Martin,F.H.
TITLE DNA encoding stem cell factor
JOURNAL Patent: US 6207417-A 33 27-MAR-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.2%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAATAAA 1496
|||||

Db 20 CTAATAAA 3

RESULT 13
AR140280/c
LOCUS AR140280 20 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 33 from patent US 6207454.
ACCESSION AR140280
VERSION AR140280.1 GI:14482776

KEYWORDS
Unknown.
SOURCE
ORGANISM
Unclassified.

REFERENCE 1 (bases 1 to 20)
AUTHORS Zsebo,K.M., Bosselman,R.A., Suggs,S.V. and Martin,F.H.
TITLE Method for enhancing the efficiency of gene transfer with stem cell
factor (SCF) polypeptide
JOURNAL Patent: US 6207454-A 33 27-MAR-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.2%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAATAAA 1496
|||||

Db 20 CTAACAAAAA 1496

RESULT 14
LOCUS ARI40558/c
DEFINITION Sequence 33 from patent US 6207802.
ACCESSION ARI40558
VERSION ARI40558.1 GI:14483054
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Zeebo,K.M., Bosselman,R.A., Suggs,S.V. and Martin,F.H.
TITLE Stem cell factor and compositions
JOURNAL Patent: US 6207802-A 33 27-MAR-2001;
FEATURES
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.2%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAACAAAAA 1496
Db 20 CTAACAAAAA 1496

RESULT 15
LOCUS AX825107/c
DEFINITION Sequence 5 from Patent WO03072818.
ACCESSION AX825107
VERSION AX825107.1 GI:39750836
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 5 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Beschreibung der kuenstlichen Sequenz:Capture-Oligonukleotid"

misc_binding 1
modified_base 3
modified_base 6
modified_base 9
modified_base 12
modified_base 15
modified_base 18

Query Match 1.2%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAACAAAAA 1496
Db 20 CTAACAAAAA 1496

RESULT 16
LOCUS AX825108/c
DEFINITION Sequence 6 from Patent WO03072818.
ACCESSION AX825108
VERSION AX825108.1 GI:39750837
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 6 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Beschreibung der kuenstlichen Sequenz:Capture-Oligonukleotid"

misc_binding 1
modified_base 3
modified_base 6
modified_base 9
modified_base 12
modified_base 15
modified_base 18

Query Match 1.2%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAACAAAAA 1496
Db 20 CTAACAAAAA 1496

RESULT 17
LOCUS AX825110/c
DEFINITION Sequence 8 from Patent WO03072818.
ACCESSION AX825110
VERSION AX825110.1 GI:39750839
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1

Query Match 1.2%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAACAAAAA 1496
Db 20 CTAACAAAAA 1496

RESULT 16
LOCUS AX825108/c
DEFINITION Sequence 6 from Patent WO03072818.
ACCESSION AX825108
VERSION AX825108.1 GI:39750837
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 6 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Beschreibung der kuenstlichen Sequenz:Capture-Oligonukleotid"

misc_binding 1
modified_base 3
modified_base 6
modified_base 9
modified_base 12
modified_base 15
modified_base 18

Query Match 1.2%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAACAAAAA 1496
Db 20 CTAACAAAAA 1496

RESULT 17
LOCUS AX825110/c
DEFINITION Sequence 8 from Patent WO03072818.
ACCESSION AX825110
VERSION AX825110.1 GI:39750839
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1

AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
 TITLE Method for sorting single-stranded nucleic acids
 JOURNAL Patent: WO 03072818-A 8 04-SEP-2003;
 Degussa Bioactives GmbH (DE)

FEATURES

source
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 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /notes="Beschreibung der kuenstlichen
 Sequenz:Capture-Oligonukleotid"
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 /bound_moiety="Biotin"
 3
 /note="LNA-T (Locked Nucleic Acid)"
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 /mod_base=OTHER
 9
 /notes="LNA-T (Locked Nucleic Acid)"
 12
 /mod_base=OTHER
 15
 /notes="LNA-T (Locked Nucleic Acid)"
 18
 /mod_base=OTHER
 20
 /notes="LNA-T (Locked Nucleic Acid)"
 /mod_base=OTHER

Query Match 1.2%; Score 18; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 49;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAAGAAAAA 1496
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 Db 20 CTAAGAAAAA 3

RESULT 18
 AX825152/c
 LOCUS AX825152 21 bp DNA linear PAT 11-DEC-2003
 DEFINITION Sequence 50 from Patent WO03072818.
 ACCESSION AX825152
 VERSION AX825152.1 GI:39750881
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.

REFERENCE 1
 AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
 TITLE Method for sorting single-stranded nucleic acids
 JOURNAL Patent: WO 03072818-A 50 04-SEP-2003;
 Degussa Bioactives GmbH (DE)

FEATURES
 source
 1..21
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /notes="Beschreibung der kuenstlichen
 Sequenz:Capture-Oligonukleotid"
 1
 /bound_moiety="Biotin"
 3
 /note="LNA-T (Locked Nucleic Acid)"
 6
 /mod_base=OTHER
 9
 /notes="LNA-T (Locked Nucleic Acid)"
 12
 /mod_base=OTHER
 15
 /notes="LNA-T (Locked Nucleic Acid)"
 18
 /mod_base=OTHER
 20
 /note="LNA-T (Locked Nucleic Acid)"

modified_base
 12
 /mod_base=OTHER
 15
 /mod_base=OTHER
 18
 /note="LNA-T (Locked Nucleic Acid)"
 21
 /mod_base=OTHER
 24
 /note="LNA-T (Locked Nucleic Acid)"
 27
 /mod_base=OTHER

Query Match 1.2%; Score 18; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 49;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAAGAAAAA 1496
 |||||
 Db 21 CTAAGAAAAA 4

RESULT 19
 E12411/c
 LOCUS E12411 20 bp DNA linear PAT 27-APR-1998
 DEFINITION Oligonucleotide.
 ACCESSION E12411
 VERSION E12411.1 GI:3251244
 KEYWORDS JP 1996332100-A/1.
 SOURCE unidentified
 ORGANISM unclassified.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Okano,K. and Kanbara,H.
 TITLE PRIMER FOR DNA POLYMERASE REACTION AND DETERMINATION OF
 POLYNUCLEOTIDE SEQUENCE USING THE SAME
 JOURNAL Patent: JP 1996332100-A 1 17-DEC-1996;
 HITACHI LTD

COMMENT
 OS None
 OC Artificial sequences.
 FN JP 1996332100-A/1
 PD 17-DEC-1996
 PF 06-JUN-1995 JP 1995139051
 PI OKANO KAZUNOBU, KANBARA HIDEKI
 PC C1201/68,C07H21/04//C12N15/09;
 CC strandedness: Single;
 CC topology: Linear;
 FH Key
 FT Location/Qualifiers

FT source 1..20
 /organism='Artificial sequences'.
 Location/Qualifiers
 1..20
 /organism="unidentified"
 /mol_type="genomic DNA"
 /db_xref="taxon:32644"

Query Match 1.2%; Score 17.4; DB 1; Length 20;
 Best Local Similarity 94.7%; Pred. No. 58;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1475 CATGCTAAAAA 1493
 |||||
 Db 19 CAGCTAAAAA 1

RESULT 20
 AX040984/c
 LOCUS AX040984 20 bp DNA linear PAT 23-NOV-2000
 DEFINITION Sequence 31 from Patent WO0065040.
 ACCESSION AX040984
 VERSION AX040984.1 GI:11340580
 KEYWORDS
 SOURCE Zea mays
 ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE

AUTHORS Helentjaris, T.G., Habben, J.E. and Sun, Y.
TITLE Cell cycle genes and methods of use
JOURNAL Patent: WO 0065040-A 31 02-NOV-2000;
PIONEER HI-BRED INTERNATIONAL, INC. (US)

FEATURES

source
1. .20
/organism="Zea mays"
/mol_type="unassigned DNA"
/db_xref="taxon:4577"

Query Match 1.2%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 58;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 222 CCGCGCGCGCGCGGCAT 240

Db 19 CAGCGCGCGCGCGGCAT 1
|||||

RESULT 21

A67588
LOCUS A67588 18 bp DNA linear PAT 05-MAY-1999
DEFINITION Sequence 8 from Patent WO9744485.
ACCESSION A67588
VERSION A67588.1 GI:4756451

KEYWORDS unclassified
SOURCE unclassified
ORGANISM unclassified

REFERENCE 1 (bases 1 to 18)

AUTHORS Goodfellow, P.N.
TITLE METHODS FOR IDENTIFYING A MUTATION IN A GENE OF INTEREST
JOURNAL Patent: WO 9744485-A 8 27-NOV-1997;
HEXAGEN TECHNOLOGY LIMITED (GB)

FEATURES

source
1. .18
/organism="unclassified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 1.1%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 CCGCGCGCGCGCGGC 41

Db 2 CCGCGCGCGCGCGGC 18
|||||

RESULT 22

AR089726
LOCUS AR089726 18 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 8 from patent US 5994075.
ACCESSION AR089726

VERSION AR089726.1 GI:10016481

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 18)

AUTHORS Goodfellow, P.N.
TITLE Methods for identifying a mutation in a gene of interest without a
phenotypic guide
JOURNAL Patent: US 5994075-A 8 30-NOV-1999;
HEXAGEN TECHNOLOGY LIMITED (GB)

FEATURES

source
1. .18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 CCGCGCGCGCGCGGC 41

Db 2 CCGCGCGCGCGCGGC 18
|||||

RESULT 23

E32450/c
LOCUS E32450 18 bp DNA linear PAT 18-JUN-2001
DEFINITION Mammal-derived tissue specific physiologically active protein.

ACCESSION E32450

VERSION E32450.1 GI:13018686

KEYWORDS JP 2000037190-A/10.

SOURCE synthetic construct

ORGANISM synthetic construct

REFERENCE 1 (bases 1 to 18)

AUTHORS Jun, N., Yusuke, N. and Toshihiro, T.

TITLE Mammal-derived tissue specific physiologically active protein

JOURNAL Patent: JP 2000037190-A 10 08-FEB-2000;

JAPAN TOBACCO INC

COMMENT OS Artificial Sequence

PN JP 2000037190-A/10

PD 08-FEB-2000

PF 23-JUL-1998 JP 1998225228

PR JUN NISHIU, YUSUKE NAKAMURA, TOSHIHIRO TANAKA

PI C12N15/09, C07K14/47, C07K16/18, C12N1/19, C12N1/21, C12N5/10, PC

PC C12N15/02, C12P21/08, C12N5/10, C12R1/91, (C12P21/08, C12R1/91),

PC C12N15/00.

PC C12N5/00, C12N15/00, (C12N5/00, C12R1/91)

CC

FT primer bind (1). .(18).

Key Location/Qualifiers

1. .18

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

Query Match 1.1%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAATAAAAAAAAAAAAA 1495

Db 18 CTAATAAAAAAAAAAAAA 2
|||||

RESULT 24

AX028843/c
LOCUS AX028843 18 bp DNA linear PAT 24-NOV-2000
DEFINITION Sequence 27 from Patent WO9732023.

ACCESSION AX028843

VERSION AX028843.1 GI:10189946

KEYWORDS synthetic construct

SOURCE synthetic construct

ORGANISM artificial sequences.

REFERENCE 1

AUTHORS Brugliera, F., Holton, T.A. and Michael, M.Z.

TITLE Genetic sequences encoding flavonoid pathway enzymes and uses

JOURNAL Patent: WO 9732023-A 27 04-SEP-1997;

FLORIGENE LIMITED (AU); BRUGLIERA FILIPPA (AU); HOLTON TIMOTHY

ALBERT (AU); MICHAEL MICHAEL ZENON (AU)

Location/Qualifiers

1. .18

/organism="synthetic construct"

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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide"

Query Match
Best Local Similarity 1.1%; Score 17; DB 1; Length 18;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAAAAAAA 1496
Db 18 TAAAAAAAAAAAAAAAAA 2

RESULT 25
A79657/c
LOCUS A79657 19 bp DNA linear PAT 20-OCT-1999
DEFINITION Sequence 6 from Patent WO9720069.
ACCESSION A79657
VERSION A79657.1 GI:6092611
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 19)
AUTHORS Emrich,T. and Leying,H.
TITLE METHOD OF DETECTING TELOMERASE ACTIVITY
JOURNAL Patent: WO 9720069-A 6 05-JUN-1997;
BOEHRINGER MANNHEIM GMBH (DE); EMRICH THOMAS (DE)
FEATURES
source
1..19
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match
Best Local Similarity 1.1%; Score 16.6; DB 1; Length 19;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAAAAAAA 1496
Db 18 KAAAAAAAAAAAAAAAAA 2

RESULT 26
AR147331/c
LOCUS AR147331 19 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 6 from patent US 6221584.
ACCESSION AR147331
VERSION AR147331.1 GI:15111134
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Emrich,T., Leying,H., Hinzpeter,M. and Karl,G.
TITLE Method of detecting telomerase activity
JOURNAL Patent: US 6221584-A 6 24-APR-2001;
FEATURES
source
1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.1%; Score 16.6; DB 1; Length 19;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAAAAAAA 1496
Db 18 KAAAAAAAAAAAAAAAAA 2

RESULT 27
A14689
LOCUS A14689 18 bp DNA linear PAT 28-MAR-1994
DEFINITION Nucleotide sequence 9 from patent number WO8303623.
ACCESSION A14689
VERSION A14689.1 GI:513760
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 18)
AUTHORS
TITLE CODING DNA FRAGMENTS FOR POLYPEPTIDES CONTAINING AT LEAST ONE
ANTIGENIC DETERMINANT OF THE PAPILLOMAVIRUS PARTICULARLY OF THE 1a
HPV TYPE AND CORRESPONDING POLYPEPTIDES
JOURNAL Patent: WO 8303623-A 9 27-OCT-1983;
FEATURES
source
1..18
Location/Qualifiers
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match
Best Local Similarity 1.1%; Score 16.4; DB 1; Length 18;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1478 GCTAAAAAAAAAAAAAAAAA 1495
Db 1 GCAAAAAAAAAAAAAAAAAA 18

RESULT 28
AR208425/c
LOCUS AR208425 18 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 5 from patent US 6383754.
ACCESSION AR208425
VERSION AR208425.1 GI:21509576
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kaufman,J.C., Roth,M.E., Lizardi,P.M., Feng,L. and Latimer,D.R.
TITLE Binary encoded sequence tags
JOURNAL Patent: US 6383754-A 5 07-MAY-2002;
FEATURES
source
1..18
Location/Qualifiers
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.1%; Score 16.4; DB 1; Length 18;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1478 GCTAAAAAAAAAAAAAAAAA 1495
Db 18 GCAAAAAAAAAAAAAAAAAA 1

RESULT 29
AX028845/c
LOCUS AX028845 18 bp DNA linear PAT 24-NOV-2000
DEFINITION Sequence 29 from Patent WO9732023.
ACCESSION AX028845
VERSION AX028845.1 GI:10189948
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Brugliera,F., Holton,T.A. and Michael,M.Z.
TITLE Genetic sequences encoding flavonoid pathway enzymes and uses
therefor
JOURNAL Patent: WO 9732023-A 29 04-SEP-1997;
FLORIGENE LIMITED (AU) ; BRUGLIERA FILIPPA (AU) ; HOLTON TIMOTHY
```



```
ALBERT (AU) ; MICHAEL MICHAEL ZENON (AU)
FEATURES
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    1. .18
      /organism="synthetic construct"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"
      /note="Oligonucleotide"

Query Match
  Best Local Similarity 1.1%; Score 16.4; DB 1; Length 18;
  Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1479 CTAAAAA 1496
  18 CGAAAAA 1
  |||||
  |||||

RESULT 30
AX085251/c
LOCUS
  DEFINITION
    Sequence 5 from Patent W00112855.
  ACCESSION
    AX085251
  VERSION
    AX085251.1 GI:13275309
  KEYWORDS
    .
  SOURCE
    synthetic construct
  ORGANISM
    synthetic construct
    artificial sequences.
  REFERENCE
    1
  AUTHORS
    Kaufman,J.C., Roth,M.E., Lizardi,P.M., Peng,L. and Latimer,D.R.
  TITLE
    Binary encoded sequence tags
  JOURNAL
    Patent: WO 0112855-A 5 22-FEB-2001;
    YALE UNIVERSITY (US)
  FEATURES
    source
      1. .18
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Primer"

Query Match
  Best Local Similarity 1.1%; Score 16.4; DB 1; Length 18;
  Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1478 GCTAAAAA 1495
  18 GCAAAAAA 1
  |||||
  |||||

RESULT 31
AX361600/c
LOCUS
  DEFINITION
    Sequence 18 from Patent W0208461.
  ACCESSION
    AX361600
  VERSION
    AX361600.1 GI:18694219
  KEYWORDS
    .
  SOURCE
    synthetic construct
  ORGANISM
    synthetic construct
    artificial sequences.
  REFERENCE
    1
  AUTHORS
    Linnarsson,S.G., Ernfors,P.G. and Bauren,G.G.
  TITLE
    A method and an algorithm for mrna expression analysis
  JOURNAL
    Patent: WO 0208461-A 18 31-JAN-2002;
    Global Genomics AB (SE)
  FEATURES
    source
      1. .18
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Double-stranded product DNA"

Query Match
  Best Local Similarity 1.1%; Score 16.4; DB 1; Length 18;
  Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

ALBERT (AU) ; MICHAEL MICHAEL ZENON (AU)
FEATURES
  source
    1. .18
      /organism="synthetic construct"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"
      /note="Oligonucleotide"

Query Match
  Best Local Similarity 1.1%; Score 16.4; DB 1; Length 18;
  Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1479 CTAAAAA 1496
  18 CGAAAAA 1
  |||||
  |||||

RESULT 32
AX814932/c
LOCUS
  DEFINITION
    Sequence 18 from Patent W003064691.
  ACCESSION
    AX814932
  VERSION
    AX814932.1 GI:39104070
  KEYWORDS
    .
  SOURCE
    synthetic construct
  ORGANISM
    synthetic construct
    artificial sequences.
  REFERENCE
    1
  AUTHORS
    Linnarsson,S., Ernfors,P., Bauren,G., Metsis,A., Pihlak,A. and
    Montellius,A.
  TITLE
    Methods and means for manipulating nucleic acid
  JOURNAL
    Patent: WO 03064691-A 18 07-AUG-2003;
    Global Genomics AB (SE)
  FEATURES
    source
      1. .18
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Description of Artificial Sequence: Double-stranded
        product DNA"

Query Match
  Best Local Similarity 1.1%; Score 16.4; DB 1; Length 18;
  Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1479 CTAAAAA 1496
  18 CGAAAAA 1
  |||||
  |||||

RESULT 33
AR102020/c
LOCUS
  DEFINITION
    Sequence 18 from patent US 6083731.
  ACCESSION
    AR102020
  VERSION
    AR102020.1 GI:12812818
  KEYWORDS
    .
  SOURCE
    Unknown.
  ORGANISM
    Unknown.
  REFERENCE
    1 (bases 1 to 19)
  AUTHORS
    Croteau,R.Bruce., Lupien,S.Lee. and Karp,F.
  TITLE
    Recombinant materials and methods for the production of limonene
    hydroxylases
  JOURNAL
    Patent: US 6083731-A 18 04-JUL-2000;
  FEATURES
    source
      1. .19
        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match
  Best Local Similarity 1.1%; Score 16.2; DB 1; Length 19;
  Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAA 1496
  19 DAAAAA 3
  :|||
  :|||

RESULT 34
AR134802/c
LOCUS
  DEFINITION
    Sequence 18 from patent US 6194185.
  ACCESSION
    AR134802
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```
VERSION AR134802.1 GI:14123707
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Croteau,R.Bruce., Lupien,S.Lee. and Karp,F.
TITLE Recombinant materials and methods for production of limonene
JOURNAL hydroxylases
FEATURES Patent: US 6194185-A 18 27-FEB-2001;
source Location/Qualifiers
1..19
/mol_type="unknown"
/mol_type="unassigned DNA"

Query Match 1..1%; Score 16.2; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 89;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAA 1496
Db 19 DAAAAA 3

RESULT 35
AR163080
LOCUS AR163080 19 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 1 from patent US 6270966.
ACCESSION AR163080
VERSION AR163080.1 GI:16233563
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Weinstein,J.N. and Buolamwini,J.
TITLE Restriction display (RD-PCR) of differentially expressed mRNAs
JOURNAL Patent: US 6270966-A 1 07-AUG-2001;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1..1%; Score 16.2; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 89;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAA 1496
Db 19 DAAAAA 3

RESULT 36
E08331/c
LOCUS E08331 19 bp DNA linear PAT 29-SEP-1997
DEFINITION Reverse transcription primer.
ACCESSION E08331
VERSION E08331.1 GI:2176448
KEYWORDS JP 1994303997-A/2.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Takagi,S. and Kamioka,S.
TITLE DETERMINATION OF CDNA
JOURNAL Patent: JP 1994303997-A 2 01-NOV-1994;
COMMENT NIPPON TELEGR & TELEPH CORP <NTT>
OS None
OC Artificial sequences.
FN JP 1994303997-A/2
PD 01-NOV-1994
PF 16-APR-1993 JP 1993112515
PI TAKAGI SHIGERU, KAMIOKA SUKEYUKI

VERSION AR134802.1 GI:14123707
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Croteau,R.Bruce., Lupien,S.Lee. and Karp,F.
TITLE Recombinant materials and methods for production of limonene
JOURNAL hydroxylases
FEATURES Patent: US 6194185-A 18 27-FEB-2001;
source Location/Qualifiers
1..19
/mol_type="unknown"
/mol_type="unassigned DNA"

Query Match 1..1%; Score 16.2; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 89;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAA 1496
Db 19 DAAAAA 3

RESULT 35
AR163080
LOCUS AR163080 19 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 1 from patent US 6270966.
ACCESSION AR163080
VERSION AR163080.1 GI:16233563
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Weinstein,J.N. and Buolamwini,J.
TITLE Restriction display (RD-PCR) of differentially expressed mRNAs
JOURNAL Patent: US 6270966-A 1 07-AUG-2001;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1..1%; Score 16.2; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 89;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAA 1496
Db 19 DAAAAA 3

RESULT 36
E08331/c
LOCUS E08331 19 bp DNA linear PAT 29-SEP-1997
DEFINITION Reverse transcription primer.
ACCESSION E08331
VERSION E08331.1 GI:2176448
KEYWORDS JP 1994303997-A/2.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Takagi,S. and Kamioka,S.
TITLE DETERMINATION OF CDNA
JOURNAL Patent: JP 1994303997-A 2 01-NOV-1994;
COMMENT NIPPON TELEGR & TELEPH CORP <NTT>
OS None
OC Artificial sequences.
FN JP 1994303997-A/2
PD 01-NOV-1994
PF 16-APR-1993 JP 1993112515
PI TAKAGI SHIGERU, KAMIOKA SUKEYUKI
```

```
PC C12Q1/68,C12N15/10;
CC strandedness: Single;
CC topology: Linear;
CC hypothetical; No;
CC anti-sense: Yes;
FH Key Location/Qualifiers
FH source 1..19
FH /organism='Artificial sequences'.
FT Location/Qualifiers
1..19
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

FEATURES
source Location/Qualifiers
1..19
/organism="unknown"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 1..1%; Score 16.2; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 89;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAA 1496
Db 18 BAAAAA 2

RESULT 37
AR027678/c
LOCUS AR027678 16 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 15 from patent US 5856435.
ACCESSION AR027678
VERSION AR027678.1 GI:5938498
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Bazile,D., Emile,C., Helene,C. and Spenlehauer,G.
TITLE Nucleic acid-containing composition, its preparation and use
JOURNAL Patent: US 5856435-A 15 05-JAN-1999;
FEATURES Location/Qualifiers
source 1..16
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1..1%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAA 1496
Db 16 AAAAAA 1

RESULT 38
AR037355/c
LOCUS AR037355 16 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 2 from patent US 5801155.
ACCESSION AR037355
VERSION AR037355.1 GI:5955211
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL Patent: US 5801155-A 2 01-SEP-1998;
FEATURES Location/Qualifiers
source 1..16
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1..1%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAA 1496
Db 16 AAAAAA 1
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Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
Db 16 AAAAAAAAAAAAAA 1

RESULT 39
LOCUS AR104584 PAT 14-FEB-2001
DEFINITION Sequence 131 from patent US 6093809.
ACCESSION AR104584
VERSION AR104584.1 GI:12817292
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Cech,T.R. and Lingner,J.
TITLE Telomerase
JOURNAL Patent: US 6093809-A 131 25-JUL-2000;
FEATURES Location/Qualifiers
source 1..16
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1..16; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
Db 1 AAAAAAAAAAAAAA 16

RESULT 40
LOCUS AR175845 PAT 17-DEC-2001
DEFINITION Sequence 131 from patent US 6309867.
ACCESSION AR175845
VERSION AR175845.1 GI:17917144
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Cech,T.R. and Nakamura,T.
TITLE Telomerase
JOURNAL Patent: US 6309867-A 131 30-OCT-2001;
FEATURES Location/Qualifiers
source 1..16
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1..16; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
Db 1 AAAAAAAAAAAAAA 16

RESULT 41
LOCUS I38676 PAT 13-MAY-1997
DEFINITION Sequence 36 from patent US 5614617.
ACCESSION I38676
VERSION I38676.1 GI:2084730
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Cook,P.D. and Sanghvi,Y.S.
TITLE Nuclease resistant, pyrimidine modified oligonucleotides that detect and modulate gene expression
JOURNAL Patent: US 5614617-A 60 25-MAR-1997;
FEATURES Location/Qualifiers
source 1..16
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1..16; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
Db 1 AAAAAAAAAAAAAA 16

REFERENCE 1 (bases 1 to 16)
AUTHORS Cook,P.D. and Sanghvi,Y.S.
TITLE Nuclease resistant, pyrimidine modified oligonucleotides that detect and modulate gene expression
JOURNAL Patent: US 5614617-A 36 25-MAR-1997;
FEATURES Location/Qualifiers
source 1..16
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1..16; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
Db 16 AAAAAAAAAAAAAA 1

RESULT 42
LOCUS I38682/c PAT 13-MAY-1997
DEFINITION Sequence 42 from patent US 5614617.
ACCESSION I38682
VERSION I38682.1 GI:2084736
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Cook,P.D. and Sanghvi,Y.S.
TITLE Nuclease resistant, pyrimidine modified oligonucleotides that detect and modulate gene expression
JOURNAL Patent: US 5614617-A 42 25-MAR-1997;
FEATURES Location/Qualifiers
source 1..16
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1..16; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
Db 16 AAAAAAAAAAAAAA 1

RESULT 43
LOCUS I38700/c PAT 13-MAY-1997
DEFINITION Sequence 60 from patent US 5614617.
ACCESSION I38700
VERSION I38700.1 GI:2084754
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Cook,P.D. and Sanghvi,Y.S.
TITLE Nuclease resistant, pyrimidine modified oligonucleotides that detect and modulate gene expression
JOURNAL Patent: US 5614617-A 60 25-MAR-1997;
FEATURES Location/Qualifiers
source 1..16
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1..16; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
Db 16 AAAAAAAAAAAAAA 1

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Db      16 AAAAAAAAAAAAAAAAAA 1
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RESULT 44
AR221692/c
LOCUS      AR221692      16 bp      DNA      linear      PAT 26-SEP-2002
DEFINITION Sequence 2 from patent US 6426408.
ACCESSION  AR221692
VERSION     AR221692.1 GI:23328764
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 16)
AUTHORS     Kutayavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE       Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL     Patent: US 6426408-A 2 30-JUL-2002;
FEATURES
  source
    1. .16
      /organism="unknown"
      /mol_type="genomic DNA"

Query Match      1.1%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAAAAAA 1496
      |||||||
Db      16 AAAAAAAAAAAAAAAAAA 1

RESULT 45
AR222462
LOCUS      AR222462      16 bp      DNA      linear      PAT 26-SEP-2002
DEFINITION Sequence 22 from patent US 6429300.
ACCESSION  AR222462
VERSION     AR222462.1 GI:23329993
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 16)
AUTHORS     Kurz,M., Lohse,P. and Wagner,R.
TITLE       Peptide acceptor ligation methods
JOURNAL     Patent: US 6429300-A 22 06-AUG-2002;
FEATURES
  source
    1. .16
      /organism="unknown"
      /mol_type="genomic DNA"

Query Match      1.1%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAAAAAA 1496
      |||||||
Db      1 AAAAAAAAAAAAAAAAAA 16

RESULT 46
AR257437/c
LOCUS      AR257437      16 bp      DNA      linear      PAT 20-DEC-2002
DEFINITION Sequence 2 from patent US 6486308.
ACCESSION  AR257437
VERSION     AR257437.1 GI:27307448
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 16)
AUTHORS     Kutayavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE       Covalently linked oligonucleotide minor groove binder conjugates

```

```

JOURNAL     Patent: US 6486308-A 2 26-NOV-2002;
FEATURES
  source
    1. .16
      /organism="unknown"
      /mol_type="genomic DNA"

Query Match      1.1%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAAAAAA 1496
      |||||||
Db      16 AAAAAAAAAAAAAAAAAA 1

RESULT 47
AR239049
LOCUS      AX039049      16 bp      DNA      linear      PAT 16-NOV-2000
DEFINITION Sequence 2 from Patent WO0061594.
ACCESSION  AX039049
VERSION     AX039049.1 GI:11228345
KEYWORDS
SOURCE      synthetic construct
ORGANISM    synthetic construct
              artificial sequences.
REFERENCE   1
AUTHORS     Beier,M. and Hoheisel,J.
TITLE       Nucleoside derivatives with photo-unstable protective groups
JOURNAL     Patent: WO 0061594-A 2 19-OCT-2000;
              DEUTSCHES KREBSFORSCH (DE); BEIER MARKUS (DE); HOHEISEL JOERG
              (DE)
FEATURES
  source
    Location/Qualifiers
      1. .16
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Oligonucleotide"

Query Match      1.1%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAAAAAA 1496
      |||||||
Db      1 AAAAAAAAAAAAAAAAAA 16

RESULT 48
AX235176/c
LOCUS      AX235176      16 bp      DNA      linear      PAT 11-SEP-2001
DEFINITION Sequence 9 from Patent WO0163282.
ACCESSION  AX235176
VERSION     AX235176.1 GI:15593767
KEYWORDS
SOURCE      synthetic construct
ORGANISM    synthetic construct
              artificial sequences.
REFERENCE   1
AUTHORS     Cuzin,M., Peltie,P., Fontecave,M., Decout,J.L. and Dueyemes,C.
TITLE       Analysis of biological targets using a biochip comprising a
              fluorescent marker
JOURNAL     Patent: WO 0163282-A 9 30-AUG-2001;
              COMMISSARIAT A L'ENERGIE ATOMIQUE (FR)
FEATURES
  source
    Location/Qualifiers
      1. .16
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="synthetic"

Query Match      1.1%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1481 AAAAAAAAAAAAAAAAAA 1496
Db 16 AAAAAAAAAAAAAAAAAA 1

RESULT 49
BD167413
LOCUS
DEFINITION Surface-roughened slide glass and method of analyzing biological
substance using the same.
ACCESSION BD167413
VERSION BD167413.1 GI:27873225
KEYWORDS JP 2002211954-A/1.
SOURCE unidentified
ORGANISM unclassified
REFERENCE 1 (bases 1 to 16)
AUTHORS Okamura,H., Tanga,M., Oba,M., Yamakawa,K. and Takagi,K.
TITLE Surface-roughened slide glass and method of analyzing biological
substance using the same
JOURNAL Patent: JP 2002211954-A 1 31-JUL-2002;
TOYO KOHAN CO LTD
COMMENT OS Artificial Sequence
PN JP 2002211954-A/1
PD 31-JUL-2002
PF 30-OCT-2001 JP 2001332778
PI HIROSHI OKAMURA,MICHIFUMI TANGA,MITSUYOSHI OBA,KAORU YAMAKAWA,
PC C03C15/00,C03C17/245,C12M1/00,C12N11/14,C12N15/09,C12N15/09,
PC C12Q1/68,
PC GOIN33/53,GOIN33/53,GOIN37/00,C12N15/00,C12N15/00 CC
Surface-roughened slide glass and method of analyzing CC
biological substance
CC using the same
FH Key Location/Qualifiers
FT source 1..16
/organism="Artificial Sequence".

FEATURES
source
1..16
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 1.1%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAAAAAA 1496
Db 1 AAAAAAAAAAAAAAAAAA 16

RESULT 51
A28997/c
LOCUS
DEFINITION primer sequence 4 from patent EP0522880.
ACCESSION A28997
VERSION A28997.1 GI:1248848
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Holton,T.A., Cornish,E.C., Kovacic,F., Tanaka,Y. and Lester,D.R.
TITLE Genetic sequences encoding flavonoid pathway enzymes and uses
therefor
JOURNAL Patent: EP 0522880-A 16 13-JAN-1993;
INTERNATIONAL FLOWER DEVELOPMENTS Pty. Ltd
FEATURES
source
1..17
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAAAAAA 1496
Db 17 AAAAAAAAAAAAAAAAAA 2

RESULT 52
AR104585/c
LOCUS
DEFINITION Sequence 132 from patent US 6093809.
ACCESSION AR104585
VERSION AR104585.1 GI:12817293
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Cech,T.R. and Lingner,J.
TITLE Telomerase
JOURNAL Patent: US 6093809-A 132 25-JUL-2000;
FEATURES
Location/Qualifiers

QY 1481 AAAAAAAAAAAAAAAAAA 1496
Db 1 AAAAAAAAAAAAAAAAAA 16

RESULT 53
BD167414
LOCUS
DEFINITION Surface-roughened slide glass and method of analyzing biological
substance using the same.
ACCESSION BD167414
VERSION BD167414.1 GI:27873226
KEYWORDS JP 2002211954-A/2.
SOURCE unidentified
ORGANISM unclassified
REFERENCE 1 (bases 1 to 16)
AUTHORS Okamura,H., Tanga,M., Oba,M., Yamakawa,K. and Takagi,K.
TITLE Surface-roughened slide glass and method of analyzing biological
substance using the same
JOURNAL Patent: JP 2002211954-A 2 31-JUL-2002;
TOYO KOHAN CO LTD
COMMENT OS Artificial Sequence
PN JP 2002211954-A/2
PD 31-JUL-2002
PF 30-OCT-2001 JP 2001332778
PI HIROSHI OKAMURA,MICHIFUMI TANGA,MITSUYOSHI OBA,KAORU YAMAKAWA,
PC C03C15/00,C03C17/245,C12M1/00,C12N11/14,C12N15/09,C12N15/09,
PC C12Q1/68,
PC GOIN33/53,GOIN33/53,GOIN37/00,C12N15/00,C12N15/00 CC
Surface-roughened slide glass and method of analyzing CC
biological substance
CC using the same
FH Key Location/Qualifiers
FT source 1..16
/organism="Artificial Sequence".

FEATURES
source
1..16
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 1.1%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAAAAAA 1496
Db 1 AAAAAAAAAAAAAAAAAA 16

RESULT 50
BD167414
LOCUS
DEFINITION Surface-roughened slide glass and method of analyzing biological
substance using the same.
ACCESSION BD167414
VERSION BD167414.1 GI:27873226
KEYWORDS JP 2002211954-A/2.
SOURCE unidentified
ORGANISM unclassified
REFERENCE 1 (bases 1 to 16)
AUTHORS Okamura,H., Tanga,M., Oba,M., Yamakawa,K. and Takagi,K.
TITLE Surface-roughened slide glass and method of analyzing biological
substance using the same
JOURNAL Patent: JP 2002211954-A 2 31-JUL-2002;
TOYO KOHAN CO LTD
COMMENT OS Artificial Sequence
PN JP 2002211954-A/2
PD 31-JUL-2002
PF 30-OCT-2001 JP 2001332778
PI HIROSHI OKAMURA,MICHIFUMI TANGA,MITSUYOSHI OBA,KAORU YAMAKAWA,
PC C03C15/00,C03C17/245,C12M1/00,C12N11/14,C12N15/09,C12N15/09,
PC C12Q1/68,
PC GOIN33/53,GOIN33/53,GOIN37/00,C12N15/00,C12N15/00 CC
Surface-roughened slide glass and method of analyzing CC
biological substance
CC using the same
FH Key Location/Qualifiers
FT source 1..16
/organism="Artificial Sequence".

FEATURES
source
1..16
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAAAAAA 1496
Db 17 AAAAAAAAAAAAAAAAAA 2

RESULT 54
AR104585/c
LOCUS
DEFINITION Sequence 132 from patent US 6093809.
ACCESSION AR104585
VERSION AR104585.1 GI:12817293
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Cech,T.R. and Lingner,J.
TITLE Telomerase
JOURNAL Patent: US 6093809-A 132 25-JUL-2000;
FEATURES
Location/Qualifiers

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source
1. .17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.1%; Score 16; DB 1; Length 17;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
Db 17 AAAAAAAAAAAAAA 2

RESULT 53
AR141074/c
LOCUS AR141074 17 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 5 from patent US 6207819.
ACCESSION AR141074
VERSION AR141074.1 GI:14483570
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Manoharan,M. and Maier,M.A.
TITLE Compounds, processes and intermediates for synthesis of mixed
backbone oligomeric compounds
JOURNAL Patent: US 6207819-A 5 27-MAR-2001;
FEATURES Location/Qualifiers
source
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.1%; Score 16; DB 1; Length 17;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
Db 17 AAAAAAAAAAAAAA 2

RESULT 54
AR172076/c
LOCUS AR172076 17 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 30 from patent US 6297425.
ACCESSION AR172076
VERSION AR172076.1 GI:17911026
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Scelonge,C.J. and Bidney,D.L.
TITLE Gene encoding oxalate decarboxylase from aspergillus phoenices
JOURNAL Patent: US 6297425-A 30 02-OCT-2001;
FEATURES Location/Qualifiers
source
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.1%; Score 16; DB 1; Length 17;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
Db 17 AAAAAAAAAAAAAA 2

RESULT 55
AR173367/c
LOCUS AR173367 17 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 30 from patent US 6303846.
ACCESSION AR173367
VERSION AR173367.1 GI:17912858
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Scelonge,C.J. and Bidney,D.L.
TITLE Gene encoding oxalate decarboxylase from aspergillus phoenices
JOURNAL Patent: US 6303846-A 30 16-OCT-2001;
FEATURES Location/Qualifiers
source
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.1%; Score 16; DB 1; Length 17;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
Db 17 AAAAAAAAAAAAAA 2

RESULT 56
AR175846/c
LOCUS AR175846 17 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 132 from patent US 6309867.
ACCESSION AR175846
VERSION AR175846.1 GI:17917145
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Cech,T.R. and Nakamura,T.
TITLE Telomerase
JOURNAL Patent: US 6309867-A 132 30-OCT-2001;
FEATURES Location/Qualifiers
source
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.1%; Score 16; DB 1; Length 17;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
Db 17 AAAAAAAAAAAAAA 2

RESULT 57
E34258/c
LOCUS E34258 17 bp DNA linear PAT 31-JAN-2002
DEFINITION Pollinosis-associated gene.
ACCESSION E34258
VERSION E34258.1 GI:18624263
KEYWORDS JP 2000106879-A/2.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
Gunji,S., Obayashi,I., Imai,Y., No.N. and Ogawa,K.
TITLE Pollinosis-associated gene
JOURNAL Patent: JP 2000106879-A 2 18-APR-2000;
COMMENT GENOX RESEARCH INC
OS Artificial Sequence
PN JP 2000106879-A/2
PD 18-APR-2000
PF 06-OCT-1998 JP 1998284610
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Db          20 CTGACTCCGTCATTAAATAA 1
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RESULT 42
ADC35554/c
ID ADC35554 standard; DNA; 20 BP.
XX
AC ADC35554;
DT 18-DEC-2003 (first entry)
XX
DE Human CD81/TAPA-1 antisense oligonucleotide #14.
XX
KW Antisense; ss; human; CD81; tetraspanin; viral infection;
KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.
XX
OS Homo sapiens.
XX
PH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT -methyl cytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
XX
PN US2003113914-A1.
XX
PD 19-JUN-2003.
XX
PF 10-DEC-2001; 2001US-00006430.
XX
PR 10-DEC-2001; 2001US-00006430.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Graham MJ, Dobie K;
XX
DR WPI; 2003-810907/76.
XX
PT Novel compound hybridizing with nucleic acid molecule encoding CD81 and
PT inhibiting the expression of CD81, useful for treating infections and
PT disease associated with expression of CD81 such as inflammation disorder.
PS Claim 3; SEQ ID NO 26; 55pp; English.
XX
CC The invention relates to a compound (antisense oligonucleotide)
CC hybridizing with the eighth nucleobase portion of an active site on a
CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
CC and inhibiting the expression of CD81. Also included is a composition
CC comprising the antisense oligonucleotide and a carrier or a diluent. The
CC antisense oligonucleotide is useful for inhibiting the expression of CD81
CC in cells or tissues. The antisense oligonucleotide is also useful for
CC treating infections preferably viral, bacterial and parasitic and
CC diseases such as inflammatory disorders and autoimmune disorders. The
CC disease or condition is characterised by chemical dependency (e.g.
CC cocaine addiction). The present sequence is a CD81 antisense
CC oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 4 A; 8 C; 6 G; 2 T; 0 U; 0 Other;
Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 471 TGGGCTGCTACGGGGCCATC 490
|||||
Db 20 TGGGCTGCTACGGGGCCATC 1
|||||
RESULT 43
ADC35566/c
ID ADC35566 standard; DNA; 20 BP.
XX
AC ADC35566;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human CD81/TAPA-1 antisense oligonucleotide #26.
XX
KW Antisense; ss; human; CD81; tetraspanin; viral infection;
KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.
XX
OS Homo sapiens.
XX
PH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT -methyl cytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
XX
PN US2003113914-A1.
XX
PD 19-JUN-2003.
XX
PF 10-DEC-2001; 2001US-00006430.
XX
PR 10-DEC-2001; 2001US-00006430.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Graham MJ, Dobie K;
XX
DR WPI; 2003-810907/76.
XX
PT Novel compound hybridizing with nucleic acid molecule encoding CD81 and
PT inhibiting the expression of CD81, useful for treating infections and
PT disease associated with expression of CD81 such as inflammation disorder.
PS Claim 3; SEQ ID NO 38; 55pp; English.
XX
CC The invention relates to a compound (antisense oligonucleotide)
CC hybridizing with the eighth nucleobase portion of an active site on a
CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
CC and inhibiting the expression of CD81. Also included is a composition
CC comprising the antisense oligonucleotide and a carrier or a diluent. The
CC antisense oligonucleotide is useful for inhibiting the expression of CD81
CC in cells or tissues. The antisense oligonucleotide is also useful for
CC treating infections preferably viral, bacterial and parasitic and
CC diseases such as inflammatory disorders and autoimmune disorders. The
CC disease or condition is characterised by chemical dependency (e.g.
CC cocaine addiction). The present sequence is a CD81 antisense
CC oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 6 A; 5 C; 6 G; 3 T; 0 U; 0 Other;
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Query Match      1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 753 ACAATTGTGCTCCCTCGGC 772
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Db 20 ACAATTGTGCTCCCTCGGC 1

RESULT 44
ADC35579/c
XX ID ADC35579 standard; DNA; 20 BP.
XX AC ADC35579;
XX DT 18-DEC-2003 (first entry)
XX DE Human CD81/TAPA-1 antisense oligonucleotide #39.
XX KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
XX KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
XX KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
XX KW bacterial infection.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT -methyl cytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT modified_base 15..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
XX US2003113914-A1.
XX PN 19-JUN-2003.
XX PD 10-DEC-2001; 2001US-00006430.
XX PF 10-DEC-2001; 2001US-00006430.
XX PR 10-DEC-2001; 2001US-00006430.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Graham MJ, Dobie K;
XX DR WPI; 2003-810907/76.
XX DR Novel compound hybridizing with nucleic acid molecule encoding CD81 and
PT inhibiting the expression of CD81, useful for treating infections and
PT disease associated with expression of CD81 such as inflammation disorder.
XX Claim 3; SEQ ID NO 51; 55pp; English.
XX PS The invention relates to a compound (antisense oligonucleotide)
CC hybridising with the eighth nucleobase portion of an active site on a
CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
CC and inhibiting the expression of CD81. Also included is a composition
CC comprising the antisense oligonucleotide and a carrier or a diluent. The
CC antisense oligonucleotide is useful for inhibiting the expression of CD81
CC in cells or tissues. The antisense oligonucleotide is also useful for
CC treating infections preferably viral, bacterial and parasitic and
CC diseases such as inflammatory disorders and autoimmune disorders. The
CC disease or condition is characterised by chemical dependency (e.g.
CC cocaine addiction). The present sequence is a CD81 antisense

CC oligonucleotide of the invention.
XX Sequence 20 BP; 6 A; 8 C; 5 G; 1 T; 0 U; 0 Other;
SQ Query Match      1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 912 TGCTGTGCTGTGCATCCGG 931
   |||||
Db 20 TGCTGTGCTGTGCATCCGG 1

RESULT 45
ADC35587/c
XX ID ADC35587 standard; DNA; 20 BP.
XX AC ADC35587;
XX DT 18-DEC-2003 (first entry)
XX DE Human CD81/TAPA-1 antisense oligonucleotide #47.
XX KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
XX KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
XX KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
XX KW bacterial infection.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT -methyl cytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT modified_base 15..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
XX US2003113914-A1.
XX PN 19-JUN-2003.
XX PD 10-DEC-2001; 2001US-00006430.
XX PF 10-DEC-2001; 2001US-00006430.
XX PR 10-DEC-2001; 2001US-00006430.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Graham MJ, Dobie K;
XX DR WPI; 2003-810907/76.
XX DR Novel compound hybridizing with nucleic acid molecule encoding CD81 and
PT inhibiting the expression of CD81, useful for treating infections and
PT disease associated with expression of CD81 such as inflammation disorder.
XX Claim 3; SEQ ID NO 59; 55pp; English.
XX PS The invention relates to a compound (antisense oligonucleotide)
CC hybridising with the eighth nucleobase portion of an active site on a
CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
CC and inhibiting the expression of CD81. Also included is a composition
CC comprising the antisense oligonucleotide and a carrier or a diluent. The
CC antisense oligonucleotide is useful for inhibiting the expression of CD81
CC in cells or tissues. The antisense oligonucleotide is also useful for
CC treating infections preferably viral, bacterial and parasitic and
```


CC diseases such as inflammatory disorders and autoimmune disorders. The
 CC disease or condition is characterised by chemical dependency (e.g.
 CC cocaine addiction). The present sequence is a CD81 antisense
 CC oligonucleotide of the invention.
 XX
 SQ Sequence 20 BP; 9 A; 2 C; 5 G; 4 T; 0 U; 0 Other;
 Query Match 1.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1060 TACACGTAGCCTTTTACTT 1079
 Db 20 TACACGTAGCCTTTTACTT 1
 RESULT 46
 ADC35589/c
 ID ADC35589 standard; DNA; 20 BP.
 XX
 AC ADC35589;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human CD81/TAPA-1 antisense oligonucleotide #49.
 XX
 KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
 KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
 KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
 KW bacterial infection.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /*tag= b
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate backbone and all cytidines are 5
 FT modified_base 1..5
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl nucleotide"
 FT modified_base 16..20
 FT /*tag= c
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl nucleotide"
 XX
 PN US2003113914-A1.
 XX
 PD 19-JUN-2003.
 XX
 PF 10-DEC-2001; 2001US-00006430.
 XX
 PR 10-DEC-2001; 2001US-00006430.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Graham MJ, Dobie K;
 XX
 DR WPI; 2003-810907/76.
 XX
 PT Novel compound hybridizing with nucleic acid molecule encoding CD81 and
 PT inhibiting the expression of CD81, useful for treating infections and
 PT disease associated with expression of CD81 such as inflammation disorder.
 XX
 PS Claim 3; SEQ ID NO 61; 55pp; English.
 XX
 CC The invention relates to a compound (antisense oligonucleotide)
 CC hybridising with the eighth nucleobase portion of an active site on a
 CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
 CC and inhibiting the expression of CD81. Also included is a composition
 CC comprising the antisense oligonucleotide and a carrier or a diluent. The

CC antisense oligonucleotide is useful for inhibiting the expression of CD81
 CC in cells or tissues. The antisense oligonucleotide is also useful for
 CC treating infections preferably viral, bacterial and parasitic and
 CC diseases such as inflammatory disorders and autoimmune disorders. The
 CC disease or condition is characterised by chemical dependency (e.g.
 CC cocaine addiction). The present sequence is a CD81 antisense
 CC oligonucleotide of the invention.
 XX
 SQ Sequence 20 BP; 8 A; 5 C; 4 G; 3 T; 0 U; 0 Other;
 Query Match 1.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1112 TTACCTTTTCAGGGCTGATG 1131
 Db 20 TTACCTTTTCAGGGCTGATG 1
 RESULT 47
 ADC35581/c
 ID ADC35581 standard; DNA; 20 BP.
 XX
 AC ADC35581;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human CD81/TAPA-1 antisense oligonucleotide #41.
 XX
 KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
 KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
 KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
 KW bacterial infection.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /*tag= b
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate backbone and all cytidines are 5
 FT modified_base 1..5
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl nucleotide"
 FT modified_base 16..20
 FT /*tag= c
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl nucleotide"
 XX
 PN US2003113914-A1.
 XX
 PD 19-JUN-2003.
 XX
 PF 10-DEC-2001; 2001US-00006430.
 XX
 PR 10-DEC-2001; 2001US-00006430.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Graham MJ, Dobie K;
 XX
 DR WPI; 2003-810907/76.
 XX
 PT Novel compound hybridizing with nucleic acid molecule encoding CD81 and
 PT inhibiting the expression of CD81, useful for treating infections and
 PT disease associated with expression of CD81 such as inflammation disorder.
 XX
 PS Claim 3; SEQ ID NO 53; 55pp; English.
 XX
 CC The invention relates to a compound (antisense oligonucleotide)
 CC hybridising with the eighth nucleobase portion of an active site on a

CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
 CC and inhibiting the expression of CD81. Also included is a composition
 CC comprising the antisense oligonucleotide and a carrier or a diluent. The
 CC antisense oligonucleotide is useful for inhibiting the expression of CD81
 CC in cells or tissues. The antisense oligonucleotide is also useful for
 CC treating infections preferably viral, bacterial and parasitic and
 CC diseases such as inflammatory disorders and autoimmune disorders. The
 CC disease or condition is characterised by chemical dependency (e.g.
 CC cocaine addiction). The present sequence is a CD81 antisense
 CC oligonucleotide of the invention.

XX
 SQ Sequence 20 BP; 3 A; 6 C; 7 G; 4 T; 0 U; 0 Other;
 Query Match 1.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 922 TGGCATCCGGACAGCTCCG 941
 |||||
 Db 20 TGGCATCCGGACAGCTCCG 1

RESULT 48
 ADC35582/c
 ID ADC35582 standard; DNA; 20 BP.
 AC ADC35582;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human CD81/TAPA-1 antisense oligonucleotide #42.
 XX
 KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
 KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
 KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
 KW bacterial infection.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /*tag= b
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate backbone and all cytidines are 5
 FT -methyl cytidines"
 FT modified_base 1..5
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl nucleotide"
 FT modified_base 16..20
 FT /*tag= c
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl nucleotide"
 XX
 PN US2003113914-A1.
 XX
 PD 19-JUN-2003.
 XX
 PF 10-DEC-2001; 2001US-00006430.
 XX
 PR 10-DEC-2001; 2001US-00006430.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Graham MJ, Dobie K;
 XX WPI; 2003-810907/76.
 DR
 XX Novel compound hybridizing with nucleic acid molecule encoding CD81 and
 PT inhibiting the expression of CD81, useful for treating infections and
 PT disease associated with expression of CD81 such as inflammation disorder.
 XX
 PS Claim 3; SEQ ID NO 54; 55pp; English.

XX The invention relates to a compound (antisense oligonucleotide)
 CC hybridising with the eighth nucleobase portion of an active site on a
 CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
 CC and inhibiting the expression of CD81. Also included is a composition
 CC comprising the antisense oligonucleotide and a carrier or a diluent. The
 CC antisense oligonucleotide is useful for inhibiting the expression of CD81
 CC in cells or tissues. The antisense oligonucleotide is also useful for
 CC treating infections preferably viral, bacterial and parasitic and
 CC diseases such as inflammatory disorders and autoimmune disorders. The
 CC disease or condition is characterised by chemical dependency (e.g.
 CC cocaine addiction). The present sequence is a CD81 antisense
 CC oligonucleotide of the invention.

XX
 SQ Sequence 20 BP; 4 A; 5 C; 7 G; 4 T; 0 U; 0 Other;
 Query Match 1.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 927 TCCGGACAGCTCCGTGTAC 946
 |||||
 Db 20 TCCGGACAGCTCCGTGTAC 1

RESULT 49
 ADC35598/c
 ID ADC35598 standard; DNA; 20 BP.
 AC ADC35598;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human CD81/TAPA-1 antisense oligonucleotide #58.
 XX
 KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
 KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
 KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
 KW bacterial infection.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /*tag= b
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate backbone and all cytidines are 5
 FT -methyl cytidines"
 FT modified_base 1..5
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl nucleotide"
 FT modified_base 16..20
 FT /*tag= c
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl nucleotide"
 XX
 PN US2003113914-A1.
 XX
 PD 19-JUN-2003.
 XX
 PF 10-DEC-2001; 2001US-00006430.
 XX
 PR 10-DEC-2001; 2001US-00006430.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Graham MJ, Dobie K;
 XX WPI; 2003-810907/76.
 DR
 XX Novel compound hybridizing with nucleic acid molecule encoding CD81 and
 PT inhibiting the expression of CD81, useful for treating infections and

PT disease associated with expression of CD81 such as inflammation disorder.
 PS Example 15; SEQ ID NO 70; 55pp; English.
 XX
 CC The invention relates to a compound (antisense oligonucleotide)
 CC hybridizing with the eighth nucleobase portion of an active site on a
 CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
 CC and inhibiting the expression of CD81. Also included is a composition
 CC comprising the antisense oligonucleotide and a carrier or a diluent. The
 CC antisense oligonucleotide is useful for inhibiting the expression of CD81
 CC in cells or tissues. The antisense oligonucleotide is also useful for
 CC treating infections preferably viral, bacterial and parasitic and
 CC diseases such as inflammatory disorders and autoimmune disorders. The
 CC disease or condition is characterised by chemical dependency (e.g.
 CC cocaine addiction). The present sequence is a CD81 antisense
 CC oligonucleotide of the invention.
 XX
 SQ Sequence 20 BP; 5 A; 8 C; 4 G; 3 T; 0 U; 0 Other;
 Query Match 1.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1355 GTTCGAGACCGAGTCTGTG 1374
 Db 20 GTTCGAGACCGAGTCTGTG 1
 RESULT 50
 ADC35550/c
 ID ADC35550 standard; DNA; 20 BP.
 XX
 AC ADC35550;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human CD81/TAPA-1 antisense oligonucleotide #10.
 XX
 KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
 KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
 KW viricide; antiparasitic; inflammatory disorder; parasitic infection;
 KW bacterial infection.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /tag= b
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate backbone and all cytidines are 5
 FT modified_base 1..5
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl nucleotide"
 FT modified_base 16..20
 FT /tag= c
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl nucleotide"
 XX
 PN US2003113914-A1.
 XX
 PD 19-JUN-2003.
 XX
 PP 10-DEC-2001; 2001US-00006430.
 XX
 PR 10-DEC-2001; 2001US-00006430.
 XX
 XX (ISIS-) ISIS PHARM INC.
 XX
 PI Graham MJ, Dobie K;
 XX
 DR WPI; 2003-810907/76.

XX
 PT Novel compound hybridizing with nucleic acid molecule encoding CD81 and
 PT inhibiting the expression of CD81, useful for treating infections and
 PT disease associated with expression of CD81 such as inflammation disorder.
 XX
 PS Claim 3; SEQ ID NO 22; 55pp; English.
 XX
 CC The invention relates to a compound (antisense oligonucleotide)
 CC hybridizing with the eighth nucleobase portion of an active site on a
 CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
 CC and inhibiting the expression of CD81. Also included is a composition
 CC comprising the antisense oligonucleotide and a carrier or a diluent. The
 CC antisense oligonucleotide is useful for inhibiting the expression of CD81
 CC in cells or tissues. The antisense oligonucleotide is also useful for
 CC treating infections preferably viral, bacterial and parasitic and
 CC diseases such as inflammatory disorders and autoimmune disorders. The
 CC disease or condition is characterised by chemical dependency (e.g.
 CC cocaine addiction). The present sequence is a CD81 antisense
 CC oligonucleotide of the invention.
 XX
 SQ Sequence 20 BP; 6 A; 8 C; 5 G; 1 T; 0 U; 0 Other;
 Query Match 1.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 320 ATCCTGGGTGTGGCCCTGTG 339
 Db 20 ATCCTGGGTGTGGCCCTGTG 1
 RESULT 51
 ADC35552/c
 ID ADC35552 standard; DNA; 20 BP.
 XX
 AC ADC35552;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human CD81/TAPA-1 antisense oligonucleotide #12.
 XX
 KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
 KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
 KW viricide; antiparasitic; inflammatory disorder; parasitic infection;
 KW bacterial infection.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /tag= b
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate backbone and all cytidines are 5
 FT modified_base 1..5
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl nucleotide"
 FT modified_base 16..20
 FT /tag= c
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl nucleotide"
 XX
 PN US2003113914-A1.
 XX
 PD 19-JUN-2003.
 XX
 PP 10-DEC-2001; 2001US-00006430.
 XX
 PR 10-DEC-2001; 2001US-00006430.
 XX
 XX (ISIS-) ISIS PHARM INC.
 XX
 PI (ISIS-) ISIS PHARM INC.
 XX
 PA

PI Graham MJ, Dobie K;
XX WPI; 2003-810907/76.
XX Novel compound hybridizing with nucleic acid molecule encoding CD81 and
PT inhibiting the expression of CD81, useful for treating infections and
PT disease associated with expression of CD81 such as inflammation disorder.
XX Claim 3; SEQ ID NO 24; 55pp; English.
XX The invention relates to a compound (antisense oligonucleotide)
CC hybridising with the eighth nucleobase portion of an active site on a
CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
CC and inhibiting the expression of CD81. Also included is a composition
CC comprising the antisense oligonucleotide and a carrier or a diluent. The
CC antisense oligonucleotide is useful for inhibiting the expression of CD81
CC in cells or tissues. The antisense oligonucleotide is also useful for
CC treating infections preferably viral, bacterial and parasitic and
CC diseases such as inflammatory disorders and autoimmune disorders. The
CC disease or condition is characterised by chemical dependency (e.g.
CC cocaine addiction). The present sequence is a CD81 antisense
CC oligonucleotide of the invention.
XX Sequence 20 BP; 5 A; 3 C; 7 G; 5 T; 0 U; 0 Other;
SQ Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 402 CCAACACCTTCTATGTAGGC 421
DB 20 CCAACACCTTCTATGTAGGC 1
RESULT 52
ADC35555/c
ID ADC35555 standard; DNA; 20 BP.
XX ADC35555;
XX 18-DEC-2003 (first entry)
XX Human CD81/TAPA-1 antisense oligonucleotide #15.
DE Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
XX cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.
OS Homo sapiens.
XX Key Location/Qualifiers
FH modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT -methyl cytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
PN US2003113914-A1.
XX 19-JUN-2003.
PD 10-DEC-2001; 2001US-00006430.
XX 10-DEC-2001; 2001US-00006430.
PR

XX (ISIS-) ISIS PHARM INC.
PA Graham MJ, Dobie K;
PI WPI; 2003-810907/76.
XX Novel compound hybridizing with nucleic acid molecule encoding CD81 and
PT inhibiting the expression of CD81, useful for treating infections and
PT disease associated with expression of CD81 such as inflammation disorder.
XX Claim 3; SEQ ID NO 27; 55pp; English.
XX The invention relates to a compound (antisense oligonucleotide)
CC hybridising with the eighth nucleobase portion of an active site on a
CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
CC and inhibiting the expression of CD81. Also included is a composition
CC comprising the antisense oligonucleotide and a carrier or a diluent. The
CC antisense oligonucleotide is useful for inhibiting the expression of CD81
CC in cells or tissues. The antisense oligonucleotide is also useful for
CC treating infections preferably viral, bacterial and parasitic and
CC diseases such as inflammatory disorders and autoimmune disorders. The
CC disease or condition is characterised by chemical dependency (e.g.
CC cocaine addiction). The present sequence is a CD81 antisense
CC oligonucleotide of the invention.
XX Sequence 20 BP; 4 A; 7 C; 7 G; 2 T; 0 U; 0 Other;
SQ Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 497 TCCAGTGCCTCTCGGGAC 516
DB 20 TCCAGTGCCTCTCGGGAC 1
RESULT 53
ADC35569/c
ID ADC35569 standard; DNA; 20 BP.
XX ADC35569;
XX 18-DEC-2003 (first entry)
XX Human CD81/TAPA-1 antisense oligonucleotide #29.
DE Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.
OS Homo sapiens.
XX Key Location/Qualifiers
FH modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT -methyl cytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
PN US2003113914-A1.
XX 19-JUN-2003.
PD

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PF 10-DEC-2001; 2001US-00006430.
XX
PR 10-DEC-2001; 2001US-00006430.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Graham MJ, Dobie K;
XX
XX WPI; 2003-810907/76.
XX
DR Novel compound hybridizing with nucleic acid molecule encoding CD81 and
PT inhibiting the expression of CD81, useful for treating infections and
PT disease associated with expression of CD81 such as inflammation disorder.
XX
XX Claim 3; SEQ ID NO 41; 55pp; English.
XX
XX The invention relates to a compound (antisense oligonucleotide)
CC hybridising with the eighth nucleobase portion of an active site on a
CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
CC and inhibiting the expression of CD81. Also included is a composition
CC comprising the antisense oligonucleotide and a carrier or a diluent. The
CC antisense oligonucleotide is useful for inhibiting the expression of CD81
CC in cells or tissues. The antisense oligonucleotide is also useful for
CC treating infections preferably viral, bacterial and parasitic and
CC diseases such as inflammatory disorders and autoimmune disorders. The
CC disease or condition is characterised by chemical dependency (e.g.
CC cocaine addiction). The present sequence is a CD81 antisense
CC oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 6 A; 5 C; 6 G; 3 T; 0 U; 0 Other;
Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 830 TTCTCCGGGAGCTGTACCT 849
Db 20 TTCTCCGGGAGCTGTACCT 1
RESULT 54
ADC35593/c
ID ADC35593 standard; DNA; 20 BP.
XX
AC ADC35593;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human CD81/TAPA-1 antisense oligonucleotide #53.
XX
KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH modified_base 1..20
FT /tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT modified_base 1..5
FT /tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
XX
PN US2003113914-A1.

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XX 19-JUN-2003.
XX
PD 10-DEC-2001; 2001US-00006430.
XX
PF 10-DEC-2001; 2001US-00006430.
XX
PR 10-DEC-2001; 2001US-00006430.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Graham MJ, Dobie K;
XX
XX WPI; 2003-810907/76.
XX
DR Novel compound hybridizing with nucleic acid molecule encoding CD81 and
PT inhibiting the expression of CD81, useful for treating infections and
PT disease associated with expression of CD81 such as inflammation disorder.
XX
XX Claim 3; SEQ ID NO 65; 55pp; English.
XX
XX The invention relates to a compound (antisense oligonucleotide)
CC hybridising with the eighth nucleobase portion of an active site on a
CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
CC and inhibiting the expression of CD81. Also included is a composition
CC comprising the antisense oligonucleotide and a carrier or a diluent. The
CC antisense oligonucleotide is useful for inhibiting the expression of CD81
CC in cells or tissues. The antisense oligonucleotide is also useful for
CC treating infections preferably viral, bacterial and parasitic and
CC diseases such as inflammatory disorders and autoimmune disorders. The
CC disease or condition is characterised by chemical dependency (e.g.
CC cocaine addiction). The present sequence is a CD81 antisense
CC oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 5 A; 7 C; 7 G; 1 T; 0 U; 0 Other;
Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1210 GGTCCAGGGTGTCTGCCT 1229
Db 20 GGTCCAGGGTGTCTGCCT 1
RESULT 55
ADC35560/c
ID ADC35560 standard; DNA; 20 BP.
XX
AC ADC35560;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human CD81/TAPA-1 antisense oligonucleotide #20.
XX
KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH modified_base 1..20
FT /tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT modified_base 1..5
FT /tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER

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FT      /note= "2'-methoxyethyl nucleotide"
XX
PN      US2003113914-A1.
XX
XX      19-JUN-2003.
XX
PF      10-DEC-2001; 2001US-00006430.
XX
PR      10-DEC-2001; 2001US-00006430.
XX
PA      (ISIS-) ISIS PHARM INC.
XX
PI      Graham MJ, Dobie K;
XX
DR      WPI; 2003-810907/76.
XX
XX      Novel compound hybridizing with nucleic acid molecule encoding CD81 and
PT      inhibiting the expression of CD81, useful for treating infections and
PT      disease associated with expression of CD81 such as inflammation disorder.
XX
PS      Claim 3; SEQ ID NO 32; 55pp; English.
XX
CC      The invention relates to a compound (antisense oligonucleotide)
CC      hybridising with the eighth nucleobase portion of an active site on a
CC      nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
CC      and inhibiting the expression of CD81. Also included is a composition
CC      comprising the antisense oligonucleotide and a carrier or a diluent. The
CC      antisense oligonucleotide is useful for inhibiting the expression of CD81
CC      in cells or tissues. The antisense oligonucleotide is also useful for
CC      treating infections preferably viral, bacterial and parasitic and
CC      diseases such as inflammatory disorders and autoimmune disorders. The
CC      disease or condition is characterised by chemical dependency (e.g.
CC      cocaine addiction). The present sequence is a CD81 antisense
CC      oligonucleotide of the invention.
XX
SQ      Sequence 20 BP; 4 A; 6 C; 4 G; 6 T; 0 U; 0 Other;

Query Match      1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      597 CCAAGGATGTGAAGCAGTTC 616
Db      20 CCAAGGATGTGAAGCAGTTC 1

RESULT 56
ADC35588/c
ID      ADC35588 standard; DNA; 20 BP.
XX
AC      ADC35588;
XX
XX      18-DEC-2003 (first entry)
XX
DE      Human CD81/TAPA-1 antisense oligonucleotide #48.
XX
KW      Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
KW      cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
KW      virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW      bacterial infection.
XX
OS      Homo sapiens.
XX
XX      Key      Location/Qualifiers
FH      modified_base 1..20
FT      /*tag= b
FT      /mod_base= OTHER
FT      /note= "Phosphorothioate backbone and all cytidines are 5
FT      -methyl cytidines"
FT      modified_base 1..5
FT      /*tag= a
FT      /mod_base= OTHER
FT      /note= "2'-methoxyethyl nucleotide"
FT

```

```

FT      modified_base 16..20
FT      /*tag= c
FT      /mod_base= OTHER
FT      /note= "2'-methoxyethyl nucleotide"
XX
PN      US2003113914-A1.
XX
XX      19-JUN-2003.
XX
PF      10-DEC-2001; 2001US-00006430.
XX
PR      10-DEC-2001; 2001US-00006430.
XX
PA      (ISIS-) ISIS PHARM INC.
XX
PI      Graham MJ, Dobie K;
XX
DR      WPI; 2003-810907/76.
XX
XX      Novel compound hybridizing with nucleic acid molecule encoding CD81 and
PT      inhibiting the expression of CD81, useful for treating infections and
PT      disease associated with expression of CD81 such as inflammation disorder.
XX
PS      Claim 3; SEQ ID NO 60; 55pp; English.
XX
CC      The invention relates to a compound (antisense oligonucleotide)
CC      hybridising with the eighth nucleobase portion of an active site on a
CC      nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
CC      and inhibiting the expression of CD81. Also included is a composition
CC      comprising the antisense oligonucleotide and a carrier or a diluent. The
CC      antisense oligonucleotide is useful for inhibiting the expression of CD81
CC      in cells or tissues. The antisense oligonucleotide is also useful for
CC      treating infections preferably viral, bacterial and parasitic and
CC      diseases such as inflammatory disorders and autoimmune disorders. The
CC      disease or condition is characterised by chemical dependency (e.g.
CC      cocaine addiction). The present sequence is a CD81 antisense
CC      oligonucleotide of the invention.
XX
SQ      Sequence 20 BP; 9 A; 2 C; 6 G; 3 T; 0 U; 0 Other;

Query Match      1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1098 TCTGAACCTTCCTGTACCT 1117
Db      20 TCTGAACCTTCCTGTACCT 1

RESULT 57
ADC35594/c
ID      ADC35594 standard; DNA; 20 BP.
XX
AC      ADC35594;
XX
XX      18-DEC-2003 (first entry)
XX
DE      Human CD81/TAPA-1 antisense oligonucleotide #54.
XX
KW      Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
KW      cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
KW      virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW      bacterial infection.
XX
OS      Homo sapiens.
XX
XX      Key      Location/Qualifiers
FH      modified_base 1..20
FT      /*tag= b
FT      /mod_base= OTHER
FT      /note= "Phosphorothioate backbone and all cytidines are 5
FT      -methyl cytidines"
FT      modified_base 1..5
FT

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```

FT modified_base 1..20
FT /tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT -methyl cytidines"
FT modified_base 1..5
FT /tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
XX US2003113914-A1.
XX PN 19-JUN-2003.
XX PD 10-DEC-2001; 2001US-00006430.
XX PF 10-DEC-2001; 2001US-00006430.
XX PR (ISIS-) ISIS PHARM INC.
XX PA Graham MJ, Dobie K;
XX PI WPI; 2003-810907/76.
XX DR Novel compound hybridizing with nucleic acid molecule encoding CD81 and
XX PT inhibiting the expression of CD81, useful for treating infections and
XX PT disease associated with expression of CD81 such as inflammation disorder.
XX PS Claim 3; SEQ ID NO 14; 55pp; English.
XX CC The invention relates to a compound (antisense oligonucleotide)
XX CC hybridising with the eighth nucleobase portion of an active site on a
XX CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
XX CC and inhibiting the expression of CD81. Also included is a composition
XX CC comprising the antisense oligonucleotide and a carrier or a diluent. The
XX CC antisense oligonucleotide is useful for inhibiting the expression of CD81
XX CC in cells or tissues. The antisense oligonucleotide is also useful for
XX CC treating infections preferably viral, bacterial and parasitic and
XX CC diseases such as inflammatory disorders and autoimmune disorders. The
XX CC disease or condition is characterised by chemical dependency (e.g.
XX CC cocaine addiction). The present sequence is a CD81 antisense
XX CC oligonucleotide of the invention.
XX SQ Sequence 20 BP; 9 A; 5 C; 5 G; 1 T; 0 U; 0 Other;
Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 291 ATTTCGTCCTTCGCTGGCT 310
Db |||||
20 ATTTCGTCCTTCGCTGGCT 1
RESULT 60
ADC35553/c
ID ADC35553 standard; DNA; 20 BP.
XX AC ADC35553;
XX 18-DEC-2003 (first entry)
XX DT Human CD81/TAPA-1 antisense oligonucleotide #13.
XX DE
XX Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
XX cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
XX virucide; antiparasitic; inflammatory disorder; parasitic infection;
XX bacterial infection.
XX KW
XX

```

```

OS Homo sapiens.
XX Key Location/Qualifiers
XX modified_base 1..20
XX /tag= b
XX /mod_base= OTHER
XX /note= "Phosphorothioate backbone and all cytidines are 5
XX -methyl cytidines"
XX modified_base 1..5
XX /tag= a
XX /mod_base= OTHER
XX /note= "2'-methoxyethyl nucleotide"
XX modified_base 16..20
XX /tag= c
XX /mod_base= OTHER
XX /note= "2'-methoxyethyl nucleotide"
XX PN US2003113914-A1.
XX PD 19-JUN-2003.
XX PF 10-DEC-2001; 2001US-00006430.
XX PR 10-DEC-2001; 2001US-00006430.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Graham MJ, Dobie K;
XX DR WPI; 2003-810907/76.
XX PT Novel compound hybridizing with nucleic acid molecule encoding CD81 and
XX PT inhibiting the expression of CD81, useful for treating infections and
XX PT disease associated with expression of CD81 such as inflammation disorder.
XX PS Example 15; SEQ ID NO 25; 55pp; English.
XX CC The invention relates to a compound (antisense oligonucleotide)
XX CC hybridising with the eighth nucleobase portion of an active site on a
XX CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
XX CC and inhibiting the expression of CD81. Also included is a composition
XX CC comprising the antisense oligonucleotide and a carrier or a diluent. The
XX CC antisense oligonucleotide is useful for inhibiting the expression of CD81
XX CC in cells or tissues. The antisense oligonucleotide is also useful for
XX CC treating infections preferably viral, bacterial and parasitic and
XX CC diseases such as inflammatory disorders and autoimmune disorders. The
XX CC disease or condition is characterised by chemical dependency (e.g.
XX CC cocaine addiction). The present sequence is a CD81 antisense
XX CC oligonucleotide of the invention.
XX SQ Sequence 20 BP; 8 A; 3 C; 4 G; 5 T; 0 U; 0 Other;
Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 410 TTCTATGTAGGCATCTACAT 429
Db |||||
20 TTCTATGTAGGCATCTACAT 1
RESULT 61
ADC35576/c
ID ADC35576 standard; DNA; 20 BP.
XX AC ADC35576;
XX 18-DEC-2003 (first entry)
XX DT Human CD81/TAPA-1 antisense oligonucleotide #36.
XX DE Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
XX cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
XX KW
XX

```


KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
 KW bacterial infection.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /tag= b
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate backbone and all cytidines are 5
 FT modified_base 1..5
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl nucleotide"
 FT modified_base 16..20
 FT /tag= c
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl nucleotide"
 XX US2003113914-A1.
 PN 19-JUN-2003.
 XX 10-DEC-2001; 2001US-00006430.
 XX 10-DEC-2001; 2001US-00006430.
 XX (ISIS-) ISIS PHARM INC.
 PA Graham MJ, Dobie K;
 PI WPI; 2003-810907/76.
 XX Novel compound hybridizing with nucleic acid molecule encoding CD81 and
 PT inhibiting the expression of CD81, useful for treating infections and
 PT disease associated with expression of CD81 such as inflammation disorder.
 XX Claim 3; SEQ ID NO 48; 55pp; English.
 XX The invention relates to a compound (antisense oligonucleotide)
 CC hybridizing with the eighth nucleobase portion of an active site on a
 CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
 CC and inhibiting the expression of CD81. Also included is a composition
 CC comprising the antisense oligonucleotide and a carrier or a diluent. The
 CC antisense oligonucleotide is useful for inhibiting the expression of CD81
 CC in cells or tissues. The antisense oligonucleotide is also useful for
 CC treating infections, preferably viral, bacterial and parasitic and
 CC diseases such as inflammatory disorders and autoimmune disorders. The
 CC disease or condition is characterised by chemical dependency (e.g.
 CC cocaine addiction). The present sequence is a CD81 antisense
 CC oligonucleotide of the invention.
 XX Sequence 20 BP; 6 A; 6 C; 4 G; 4 T; 0 U; 0 Other;
 SQ
 Query Match 1.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 896 ATGATCCTGAGCATGTGCT 915
 DB 20 ATGATCCTGAGCATGTGCT 1
 RESULT 62
 ADC35596/c
 ID ADC35596 standard; DNA; 20 BP.
 XX
 AC ADC35596;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human CD81/TAPA-1 antisense oligonucleotide #56.

XX Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
 KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
 KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
 KW bacterial infection.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /tag= b
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate backbone and all cytidines are 5
 FT modified_base 1..5
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl nucleotide"
 FT modified_base 16..20
 FT /tag= c
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl nucleotide"
 XX US2003113914-A1.
 PN 19-JUN-2003.
 XX 10-DEC-2001; 2001US-00006430.
 XX 10-DEC-2001; 2001US-00006430.
 XX (ISIS-) ISIS PHARM INC.
 PA Graham MJ, Dobie K;
 PI WPI; 2003-810907/76.
 XX Novel compound hybridizing with nucleic acid molecule encoding CD81 and
 PT inhibiting the expression of CD81, useful for treating infections and
 PT disease associated with expression of CD81 such as inflammation disorder.
 XX Claim 3; SEQ ID NO 68; 55pp; English.
 XX The invention relates to a compound (antisense oligonucleotide)
 CC hybridizing with the eighth nucleobase portion of an active site on a
 CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
 CC and inhibiting the expression of CD81. Also included is a composition
 CC comprising the antisense oligonucleotide and a carrier or a diluent. The
 CC antisense oligonucleotide is useful for inhibiting the expression of CD81
 CC in cells or tissues. The antisense oligonucleotide is also useful for
 CC treating infections, preferably viral, bacterial and parasitic and
 CC diseases such as inflammatory disorders and autoimmune disorders. The
 CC disease or condition is characterised by chemical dependency (e.g.
 CC cocaine addiction). The present sequence is a CD81 antisense
 CC oligonucleotide of the invention.
 XX Sequence 20 BP; 4 A; 7 C; 8 G; 1 T; 0 U; 0 Other;
 SQ
 Query Match 1.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1309 GCCCGTCCTGTGGCTGCAC 1328
 DB 20 GCCCGTCCTGTGGCTGCAC 1
 RESULT 63
 ADC35541/c
 ID ADC35541 standard; DNA; 20 BP.
 XX
 AC ADC35541;
 XX

```
DT 18-DEC-2003 (first entry)
XX
DE Human CD81/TAPA-1 antisense oligonucleotide #1.
XX
KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
XX
PN US2003113914-A1.
XX
PD 19-JUN-2003.
XX
PF 10-DEC-2001; 2001US-00006430.
XX
PR 10-DEC-2001; 2001US-00006430.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Graham MJ, Dobie K;
XX
DR WPI; 2003-810907/76.
XX
PT Novel compound hybridizing with nucleic acid molecule encoding CD81 and
PT inhibiting the expression of CD81, useful for treating infections and
PT disease associated with expression of CD81 such as inflammation disorder.
XX
PS Example 15; SEQ ID NO 13; 55pp; English.
XX
CC The invention relates to a compound (antisense oligonucleotide)
CC hybridising with the eighth nucleobase portion of an active site on a
CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
CC and inhibiting the expression of CD81. Also included is a composition
CC comprising the antisense oligonucleotide and a carrier or a diluent. The
CC antisense oligonucleotide is useful for inhibiting the expression of CD81
CC in cells or tissues. The antisense oligonucleotide is also useful for
CC treating infections preferably viral, bacterial and parasitic and
CC diseases such as inflammatory disorders and autoimmune disorders. The
CC disease or condition is characterised by chemical dependency (e.g.
CC cocaine addiction). The present sequence is a CD81 antisense
CC oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;
Query Match 1..3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCATTGTGCTGGAAGCGC 20
Db 20 CCATTGTGCTGGAAGCGC 1
RESULT 64
ADC35546/c
ID ADC35546 standard; DNA; 20 BP.
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```
XX ADC35546;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human CD81/TAPA-1 antisense oligonucleotide #6.
XX
KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
XX
PN US2003113914-A1.
XX
PD 19-JUN-2003.
XX
PF 10-DEC-2001; 2001US-00006430.
XX
PR 10-DEC-2001; 2001US-00006430.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Graham MJ, Dobie K;
XX
DR WPI; 2003-810907/76.
XX
PT Novel compound hybridizing with nucleic acid molecule encoding CD81 and
PT inhibiting the expression of CD81, useful for treating infections and
PT disease associated with expression of CD81 such as inflammation disorder.
XX
PS Example 15; SEQ ID NO 18; 55pp; English.
XX
CC The invention relates to a compound (antisense oligonucleotide)
CC hybridising with the eighth nucleobase portion of an active site on a
CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
CC and inhibiting the expression of CD81. Also included is a composition
CC comprising the antisense oligonucleotide and a carrier or a diluent. The
CC antisense oligonucleotide is useful for inhibiting the expression of CD81
CC in cells or tissues. The antisense oligonucleotide is also useful for
CC treating infections preferably viral, bacterial and parasitic and
CC diseases such as inflammatory disorders and autoimmune disorders. The
CC disease or condition is characterised by chemical dependency (e.g.
CC cocaine addiction). The present sequence is a CD81 antisense
CC oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 9 A; 3 C; 6 G; 2 T; 0 U; 0 Other;
Query Match 1..3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 277 GCTCTTCGTCCTCAATTTCG 296
Db 20 GCTCTTCGTCCTCAATTTCG 1
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```
RESULT 65
ADC35559/c
ID ADC35559 standard; DNA; 20 BP.
XX
AC ADC35559;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human CD81/TAPA-1 antisense oligonucleotide #19.
XX
KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
XX
PN US2003113914-A1.
XX
PD 19-JUN-2003.
XX
PF 10-DEC-2001; 2001US-00006430.
XX
PR 10-DEC-2001; 2001US-00006430.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Graham MJ, Dobie K;
XX
DR WPI; 2003-810907/76.
XX
PS Novel compound hybridizing with nucleic acid molecule encoding CD81 and
PT inhibiting the expression of CD81, useful for treating infections and
PT disease associated with expression of CD81 such as inflammation disorder.
XX
PP Claim 3; SEQ ID NO 31; 55pp; English.
XX
CC The invention relates to a compound (antisense oligonucleotide)
CC hybridizing with the eighth nucleobase portion of an active site on a
CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
CC and inhibiting the expression of CD81. Also included is a composition
CC comprising the antisense oligonucleotide and a carrier or a diluent. The
CC antisense oligonucleotide is useful for inhibiting the expression of CD81
CC in cells or tissues. The antisense oligonucleotide is also useful for
CC treating infections preferably viral, bacterial and parasitic and
CC diseases such as inflammatory disorders and autoimmune disorders. The
CC disease or condition is characterised by chemical dependency (e.g.
CC cocaine addiction). The present sequence is a CD81 antisense
CC oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 3 A; 7 C; 4 G; 6 T; 0 U; 0 Other;
XX
Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 592 GATCGCCAGGATGTGAAGC 611
|||||
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Db 20 GATCGCCAGGATGTGAAGC 1
RESULT 66
ADC35601/c
ID ADC35601 standard; DNA; 20 BP.
XX
AC ADC35601;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human CD81/TAPA-1 antisense oligonucleotide #61.
XX
KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
XX
PN US2003113914-A1.
XX
PD 19-JUN-2003.
XX
PF 10-DEC-2001; 2001US-00006430.
XX
PR 10-DEC-2001; 2001US-00006430.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Graham MJ, Dobie K;
XX
DR WPI; 2003-810907/76.
XX
PS Novel compound hybridizing with nucleic acid molecule encoding CD81 and
PT inhibiting the expression of CD81, useful for treating infections and
PT disease associated with expression of CD81 such as inflammation disorder.
XX
PP Example 15; SEQ ID NO 73; 55pp; English.
XX
CC The invention relates to a compound (antisense oligonucleotide)
CC hybridizing with the eighth nucleobase portion of an active site on a
CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
CC and inhibiting the expression of CD81. Also included is a composition
CC comprising the antisense oligonucleotide and a carrier or a diluent. The
CC antisense oligonucleotide is useful for inhibiting the expression of CD81
CC in cells or tissues. The antisense oligonucleotide is also useful for
CC treating infections preferably viral, bacterial and parasitic and
CC diseases such as inflammatory disorders and autoimmune disorders. The
CC disease or condition is characterised by chemical dependency (e.g.
CC cocaine addiction). The present sequence is a CD81 antisense
CC oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 6 A; 2 C; 8 G; 4 T; 0 U; 0 Other;
XX
Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY
```

QY 1393 GCACCTGCTCTTCTAACAC 1412
|||||
Db 20 GCACCTGCTCTTCTAACAC 1

RESULT 67
ADC35604/c
ID ADC35604 standard; DNA; 20 BP.
XX
AC ADC35604;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human CD81/TAPA-1 antisense oligonucleotide #64.
XX
KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT -methyl cytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
XX
PN US2003113914-A1.
XX
PD 19-JUN-2003.
XX
PF 10-DEC-2001; 2001US-00006430.
XX
PR 10-DEC-2001; 2001US-00006430.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Graham MJ, Dobie K;
XX
DR WPI; 2003-810907/76.
XX
PS Novel compound hybridizing with nucleic acid molecule encoding CD81 and
PT inhibiting the expression of CD81, useful for treating infections and
PT disease associated with expression of CD81 such as inflammation disorder.
XX
PS Claim 3; SEQ ID NO 76; 55pp; English.
XX
CC The invention relates to a compound (antisense oligonucleotide)
CC hybridizing with the eighth nucleobase portion of an active site on a
CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
CC and inhibiting the expression of CD81. Also included is a composition
CC comprising the antisense oligonucleotide and a carrier or a diluent. The
CC antisense oligonucleotide is useful for inhibiting the expression of CD81
CC in cells or tissues. The antisense oligonucleotide is also useful for
CC treating infections preferably viral, bacterial and parasitic and
CC diseases such as inflammatory disorders and autoimmune disorders. The
CC disease or condition is characterised by chemical dependency (e.g.
CC cocaine addiction). The present sequence is a CD81 antisense
CC oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 5 A; 2 C; 8 G; 5 T; 0 U; 0 Other;

Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1430 TCACAACATCTCTGACTCCGT 1449
|||||
Db 20 TCACAACATCTCTGACTCCGT 1

RESULT 68
ADC35532
ID ADC35532 standard; DNA; 20 BP.
XX
AC ADC35532;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human CD81/TAPA-1 RT-PCR primer #1.
XX
KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection; PCR; primer; RT-PCR; reverse transcriptase PCR;
KW GAPDH; glyceraldehyde-3-phosphate dehydrogenase.
XX
OS Homo sapiens.
XX
PN US2003113914-A1.
XX
PD 19-JUN-2003.
XX
PF 10-DEC-2001; 2001US-00006430.
XX
PR 10-DEC-2001; 2001US-00006430.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Graham MJ, Dobie K;
XX
DR WPI; 2003-810907/76.
XX
PS Novel compound hybridizing with nucleic acid molecule encoding CD81 and
PT inhibiting the expression of CD81, useful for treating infections and
PT disease associated with expression of CD81 such as inflammation disorder.
XX
PS Example 13; SEQ ID NO 4; 55pp; English.
XX
CC The invention relates to a compound (antisense oligonucleotide)
CC hybridizing with the eighth nucleobase portion of an active site on a
CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
CC and inhibiting the expression of CD81. Also included is a composition
CC comprising the antisense oligonucleotide and a carrier or a diluent. The
CC antisense oligonucleotide is useful for inhibiting the expression of CD81
CC in cells or tissues. The antisense oligonucleotide is also useful for
CC treating infections preferably viral, bacterial and parasitic and
CC diseases such as inflammatory disorders and autoimmune disorders. The
CC disease or condition is characterised by chemical dependency (e.g.
CC cocaine addiction). The present sequence is a reverse transcriptase (RT)-
CC PCR primer (either for CD81 or glyceraldehyde-3-phosphate dehydrogenase,
CC GAPDH) used to assay the level of mRNA pre and post treatment with the
CC antisense oligonucleotides.
XX
SQ Sequence 20 BP; 7 A; 4 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 590 CAGATCGCCCAAGGATGTGAA 609
|||||
Db 1 CAGATCGCCCAAGGATGTGAA 20

```
RESULT 69
ADC35573/c
ID ADC35573 standard; DNA; 20 BP.
AC ADC35573;
XX
XX
DT 18-DEC-2003 (first entry)
XX
DE Human CD81/TAPA-1 antisense oligonucleotide #33.
XX
XX Antisense; ss; human; CD81; tetraspanin; viral infection;
KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
XX
XX US2003113914-A1.
XX
XX 19-JUN-2003.
XX
XX 10-DEC-2001; 2001US-00006430.
XX
XX 10-DEC-2001; 2001US-00006430.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Graham MJ, Dobie K;
XX WPI; 2003-810907/76.
XX
XX Novel compound hybridizing with nucleic acid molecule encoding CD81 and
XX inhibiting the expression of CD81, useful for treating infections and
XX disease associated with expression of CD81 such as inflammation disorder.
XX
XX Claim 3; SEQ ID NO 45; 55pp; English.
XX
XX The invention relates to a compound (antisense oligonucleotide)
XX hybridizing with the eighth nucleobase portion of an active site on a
XX nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
XX and inhibiting the expression of CD81. Also included is a composition
XX comprising the antisense oligonucleotide and a carrier or a diluent. The
XX antisense oligonucleotide is useful for inhibiting the expression of CD81
XX in cells or tissues. The antisense oligonucleotide is also useful for
XX treating infections preferably viral, bacterial and parasitic and
XX diseases such as inflammatory disorders and autoimmune disorders. The
XX disease or condition is characterised by chemical dependency (e.g.
XX cocaine addiction). The present sequence is a CD81 antisense
XX oligonucleotide of the invention.
XX
XX Sequence 20 BP; 6 A; 6 C; 6 G; 2 T; 0 U; 0 Other;
XX
Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 857 ATTGCTGCCATCGTGTGCG 876
|||||||
```

```
Db 20 ATTGCTGCCATCGTGTGCG 1
RESULT 70
ADC35562/c
ID ADC35562 standard; DNA; 20 BP.
XX
XX
AC ADC35562;
XX
XX 18-DEC-2003 (first entry)
XX
XX Human CD81/TAPA-1 antisense oligonucleotide #22.
XX
XX Antisense; ss; human; CD81; tetraspanin; viral infection;
KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
XX
XX US2003113914-A1.
XX
XX 19-JUN-2003.
XX
XX 10-DEC-2001; 2001US-00006430.
XX
XX 10-DEC-2001; 2001US-00006430.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Graham MJ, Dobie K;
XX WPI; 2003-810907/76.
XX
XX Novel compound hybridizing with nucleic acid molecule encoding CD81 and
XX inhibiting the expression of CD81, useful for treating infections and
XX disease associated with expression of CD81 such as inflammation disorder.
XX
XX Claim 3; SEQ ID NO 34; 55pp; English.
XX
XX The invention relates to a compound (antisense oligonucleotide)
XX hybridizing with the eighth nucleobase portion of an active site on a
XX nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
XX and inhibiting the expression of CD81. Also included is a composition
XX comprising the antisense oligonucleotide and a carrier or a diluent. The
XX antisense oligonucleotide is useful for inhibiting the expression of CD81
XX in cells or tissues. The antisense oligonucleotide is also useful for
XX treating infections preferably viral, bacterial and parasitic and
XX diseases such as inflammatory disorders and autoimmune disorders. The
XX disease or condition is characterised by chemical dependency (e.g.
XX cocaine addiction). The present sequence is a CD81 antisense
XX oligonucleotide of the invention.
XX
XX Sequence 20 BP; 4 A; 6 C; 4 G; 6 T; 0 U; 0 Other;
XX
Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY
```

QY 607 GAAGCAGTCTATGACCAGG 626
|||||
Db 20 GAAGCAGTCTATGACCAGG 1

RESULT 71
ADC35565/c
ID ADC35565 standard; DNA; 20 BP.
AC ADC35565;
DT 18-DEC-2003 (first entry)
XX
DE Human CD81/TAPA-1 antisense oligonucleotide #25.
XX
KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
XX
PN US2003113914-A1.
XX
PD 19-JUN-2003.
XX
PF 10-DEC-2001; 2001US-00006430.
XX
PR 10-DEC-2001; 2001US-00006430.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Graham MJ, Dobie K;
XX
DR WPI; 2003-810907/76.
XX
PT Novel compound hybridizing with nucleic acid molecule encoding CD81 and
PT inhibiting the expression of CD81, useful for treating infections and
PT disease associated with expression of CD81 such as inflammation disorder.
XX
PS Claim 3; SEQ ID NO 37; 55pp; English.
XX
CC The invention relates to a compound (antisense oligonucleotide)
CC hybridizing with the eighth nucleobase portion of an active site on a
CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
CC and inhibiting the expression of CD81. Also included is a composition
CC comprising the antisense oligonucleotide and a carrier or a diluent. The
CC antisense oligonucleotide is useful for inhibiting the expression of CD81
CC in cells or tissues. The antisense oligonucleotide is also useful for
CC treating infections preferably viral, bacterial and parasitic and
CC diseases such as inflammatory disorders and autoimmune disorders. The
CC disease or condition is characterised by chemical dependency (e.g.
CC cocaine addiction). The present sequence is a CD81 antisense
XX oligonucleotide of the invention.
SQ Sequence 20 BP; 6 A; 3 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 747 TCAAGACAAATTTGTGTCCC 766
|||||
Db 20 TCAAGACAAATTTGTGTCCC 1

RESULT 72
ADC35578/c
ID ADC35578 standard; DNA; 20 BP.
XX
AC ADC35578;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human CD81/TAPA-1 antisense oligonucleotide #38.
XX
KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
XX
PN US2003113914-A1.
XX
PD 19-JUN-2003.
XX
PF 10-DEC-2001; 2001US-00006430.
XX
PR 10-DEC-2001; 2001US-00006430.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Graham MJ, Dobie K;
XX
DR WPI; 2003-810907/76.
XX
PT Novel compound hybridizing with nucleic acid molecule encoding CD81 and
PT inhibiting the expression of CD81, useful for treating infections and
PT disease associated with expression of CD81 such as inflammation disorder.
XX
PS Example 15; SEQ ID NO 50; 55pp; English.
XX
CC The invention relates to a compound (antisense oligonucleotide)
CC hybridizing with the eighth nucleobase portion of an active site on a
CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
CC and inhibiting the expression of CD81. Also included is a composition
CC comprising the antisense oligonucleotide and a carrier or a diluent. The
CC antisense oligonucleotide is useful for inhibiting the expression of CD81
CC in cells or tissues. The antisense oligonucleotide is also useful for
CC treating infections preferably viral, bacterial and parasitic and
CC diseases such as inflammatory disorders and autoimmune disorders. The
CC disease or condition is characterised by chemical dependency (e.g.
CC cocaine addiction). The present sequence is a CD81 antisense
XX oligonucleotide of the invention.

```
XX SQ Sequence 20 BP; 6 A; 8 C; 4 G; 2 T; 0 U; 0 Other;
Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 907 CATGGTCTGTCTGTGGCA 926
Db 20 CATGGTCTGTCTGTGGCA 1
RESULT 73
ADC35580/c
ID ADC35580-standard; DNA; 20 BP.
XX AC ADC35580;
XX DT 18-DEC-2003 (first entry)
XX DE Human CD81/TAPA-1 antisense oligonucleotide #40.
XX KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
XX KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
XX KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
XX KW bacterial infection.
XX OS Homo sapiens.
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
XX US2003113914-A1.
XX PN 19-JUN-2003.
XX PD 10-DEC-2001; 2001US-00006430.
XX PF 10-DEC-2001; 2001US-00006430.
XX PR 10-DEC-2001; 2001US-00006430.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Graham MJ, Dobie K;
XX DR WPI; 2003-810907/76.
XX PT Novel compound hybridizing with nucleic acid molecule encoding CD81 and
XX PT inhibiting the expression of CD81, useful for treating infections and
XX PT disease associated with expression of CD81 such as inflammation disorder.
XX PS Claim 3; SEQ ID NO 52; 55pp; English.
XX CC The invention relates to a compound (antisense oligonucleotide)
XX CC hybridizing with the eighth nucleobase portion of an active site on a
XX CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
XX CC and inhibiting the expression of CD81. Also included is a composition
XX CC comprising the antisense oligonucleotide and a carrier or a diluent. The
XX CC antisense oligonucleotide is useful for inhibiting the expression of CD81
XX CC in cells or tissues. The antisense oligonucleotide is also useful for
XX CC treating infections preferably viral, bacterial and parasitic and
XX CC diseases such as inflammatory disorders and autoimmune disorders. The
XX SQ Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;
Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 917 TGCTGGCATCGGAACAG 936
Db 20 TGCTGGCATCGGAACAG 1
RESULT 74
ADC35603/c
ID ADC35603 standard; DNA; 20 BP.
XX AC ADC35603;
XX DT 18-DEC-2003 (first entry)
XX DE Human CD81/TAPA-1 antisense oligonucleotide #63.
XX KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
XX KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
XX KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
XX KW bacterial infection.
XX OS Homo sapiens.
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
XX US2003113914-A1.
XX PN 19-JUN-2003.
XX PD 10-DEC-2001; 2001US-00006430.
XX PF 10-DEC-2001; 2001US-00006430.
XX PR 10-DEC-2001; 2001US-00006430.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Graham MJ, Dobie K;
XX DR WPI; 2003-810907/76.
XX PT Novel compound hybridizing with nucleic acid molecule encoding CD81 and
XX PT inhibiting the expression of CD81, useful for treating infections and
XX PT disease associated with expression of CD81 such as inflammation disorder.
XX PS Claim 3; SEQ ID NO 75; 55pp; English.
XX CC The invention relates to a compound (antisense oligonucleotide)
XX CC hybridizing with the eighth nucleobase portion of an active site on a
XX CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
XX CC and inhibiting the expression of CD81. Also included is a composition
XX CC comprising the antisense oligonucleotide and a carrier or a diluent. The
XX CC antisense oligonucleotide is useful for inhibiting the expression of CD81
XX CC in cells or tissues. The antisense oligonucleotide is also useful for
XX CC treating infections preferably viral, bacterial and parasitic and
XX CC diseases such as inflammatory disorders and autoimmune disorders. The
```

CC in cells or tissues. The antisense oligonucleotide is also useful for
 CC treating infections preferably viral, bacterial and parasitic and
 CC diseases such as inflammatory disorders and autoimmune disorders. The
 CC disease or condition is characterised by chemical dependency (e.g.
 CC cocaine addiction). The present sequence is a CD81 antisense
 CC oligonucleotide of the invention.

XX Sequence 20 BP; 5 A; 2 C; 7 G; 6 T; 0 U; 0 Other;
 SQ Query Match 1.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1415 CGCCTTCAACTGTAATCACA 1434
 |||||
 DB 20 CGCCTTCAACTGTAATCACA 1

RESULT 75
 ADC35606/c
 ID ADC35606 standard; DNA; 20 BP.
 XX AC ADC35606;
 XX DT 18-DEC-2003 (first entry)
 XX DE Human CD81/TAPA-1 antisense oligonucleotide #66.
 XX KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
 KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
 KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
 KW bacterial infection.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /*tag= b
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate backbone and all cytidines are 5
 FT -methyl cytidines"
 FT modified_base 1..5
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl nucleotide"
 FT modified_base 16..20
 FT /*tag= c
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl nucleotide"
 XX PN US2003113914-A1.
 XX PD 19-JUN-2003.
 XX PF 10-DEC-2001; 2001US-00006430.
 XX PR 10-DEC-2001; 2001US-00006430.
 XX PA (ISIS-) ISIS PHARM INC.
 XX PI Graham MJ, Dobie K;
 XX DR WPI; 2003-810907/76.
 XX PT Novel compound hybridizing with nucleic acid molecule encoding CD81 and
 PT inhibiting the expression of CD81, useful for treating infections and
 PT disease associated with expression of CD81 such as inflammation disorder.
 XX Claim 3; SEQ ID NO 78; 55pp; English.
 PS The invention relates to a compound (antisense oligonucleotide)
 CC hybridising with the eighth nucleobase portion of an active site on a
 CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)

CC and inhibiting the expression of CD81. Also included is a composition
 CC comprising the antisense oligonucleotide and a carrier or a diluent. The
 CC antisense oligonucleotide is useful for inhibiting the expression of CD81
 CC in cells or tissues. The antisense oligonucleotide is also useful for
 CC treating infections preferably viral, bacterial and parasitic and
 CC diseases such as inflammatory disorders and autoimmune disorders. The
 CC disease or condition is characterised by chemical dependency (e.g.
 CC cocaine addiction). The present sequence is a CD81 antisense
 CC oligonucleotide of the invention.

XX Sequence 20 BP; 5 A; 4 C; 2 G; 9 T; 0 U; 0 Other;
 SQ Query Match 1.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1447 CGTCATTTAATAAAGAAGA 1466
 |||||
 DB 20 CGTCATTTAATAAAGAAGA 1

RESULT 76
 ADC35547/c
 ID ADC35547 standard; DNA; 20 BP.
 XX AC ADC35547;
 XX DT 18-DEC-2003 (first entry)
 XX DE Human CD81/TAPA-1 antisense oligonucleotide #7.
 XX KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
 KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
 KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
 KW bacterial infection.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /*tag= b
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate backbone and all cytidines are 5
 FT -methyl cytidines"
 FT modified_base 1..5
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl nucleotide"
 FT modified_base 16..20
 FT /*tag= c
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl nucleotide"
 XX PN US2003113914-A1.
 XX PD 19-JUN-2003.
 XX PF 10-DEC-2001; 2001US-00006430.
 XX PR 10-DEC-2001; 2001US-00006430.
 XX PA (ISIS-) ISIS PHARM INC.
 XX PI Graham MJ, Dobie K;
 XX DR WPI; 2003-810907/76.
 XX PT Novel compound hybridizing with nucleic acid molecule encoding CD81 and
 PT inhibiting the expression of CD81, useful for treating infections and
 PT disease associated with expression of CD81 such as inflammation disorder.
 XX Example 15; SEQ ID NO 19; 55pp; English.

CC The invention relates to a compound (antisense oligonucleotide)
 CC hybridizing with the eighth nucleobase portion of an active site on a
 CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
 CC and inhibiting the expression of CD81. Also included is a composition
 CC comprising the antisense oligonucleotide and a carrier or a diluent. The
 CC antisense oligonucleotide is useful for inhibiting the expression of CD81
 CC in cells or tissues. The antisense oligonucleotide is also useful for
 CC treating infections preferably viral, bacterial and parasitic and
 CC diseases such as inflammatory disorders and autoimmune disorders. The
 CC disease or condition is characterised by chemical dependency (e.g.
 CC cocaine addiction). The present sequence is a CD81 antisense
 CC oligonucleotide of the invention.

XX Sequence 20 BP; 9 A; 3 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 1.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 286 CTTCAATTGCTGCTTCGGC 305
 |||||
 DB 20 CTTCAATTGCTGCTTCGGC 1

RESULT 77
 ADC35549/C
 ID ADC35549 standard; DNA; 20 BP.

XX ADC35549;

XX 18-DEC-2003 (first entry)

XX Human CD81/TAPA-1 antisense oligonucleotide #9.

XX Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
 KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
 KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
 KW bacterial infection.

XX Homo sapiens.

Key	Location/Qualifiers
modified_base	1..20
	/tag= b
	/mod_base= OTHER
	/note= "Phosphorothioate backbone and all cytidines are 5
modified_base	1..5
	/tag= a
	/mod_base= OTHER
	/note= "2'-methoxyethyl nucleotide"
modified_base	15..20
	/tag= c
	/mod_base= OTHER
	/note= "2'-methoxyethyl nucleotide"

US2003113914-A1.

19-JUN-2003.

10-DEC-2001; 2001US-00006430.

10-DEC-2001; 2001US-00006430.

(ISIS-) ISIS PHARM INC.

Graham MJ, Dobie K;

WPI; 2003-810907/76.

Novel compound hybridizing with nucleic acid molecule encoding CD81 and
 inhibiting the expression of CD81, useful for treating infections and
 disease associated with expression of CD81 such as inflammation disorder.

Claim 3; SEQ ID NO 21; 55pp; English.

The invention relates to a compound (antisense oligonucleotide)
 hybridizing with the eighth nucleobase portion of an active site on a
 nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
 and inhibiting the expression of CD81. Also included is a composition
 comprising the antisense oligonucleotide and a carrier or a diluent. The
 antisense oligonucleotide is useful for inhibiting the expression of CD81
 in cells or tissues. The antisense oligonucleotide is also useful for
 treating infections preferably viral, bacterial and parasitic and
 diseases such as inflammatory disorders and autoimmune disorders. The
 disease or condition is characterised by chemical dependency (e.g.
 cocaine addiction). The present sequence is a CD81 antisense
 oligonucleotide of the invention.

XX Sequence 20 BP; 4 A; 9 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 1.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 304 GCTGGCTGGAGCGGTGATCC 323
 |||||
 DB 20 GCTGGCTGGAGCGGTGATCC 1

RESULT 78

ADC35561/C
 ID ADC35561 standard; DNA; 20 BP.

XX ADC35561;

XX 18-DEC-2003 (first entry)

XX Human CD81/TAPA-1 antisense oligonucleotide #21.

XX Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
 KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
 KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
 KW bacterial infection.

XX Homo sapiens.

Key	Location/Qualifiers
modified_base	1..20
	/tag= b
	/mod_base= OTHER
	/note= "Phosphorothioate backbone and all cytidines are 5
modified_base	1..5
	/tag= a
	/mod_base= OTHER
	/note= "2'-methoxyethyl nucleotide"
modified_base	15..20
	/tag= c
	/mod_base= OTHER
	/note= "2'-methoxyethyl nucleotide"

US2003113914-A1.

19-JUN-2003.

10-DEC-2001; 2001US-00006430.

10-DEC-2001; 2001US-00006430.

(ISIS-) ISIS PHARM INC.

Graham MJ, Dobie K;

WPI; 2003-810907/76.

PT Novel compound hybridizing with nucleic acid molecule encoding CD81 and
PT inhibiting the expression of CD81, useful for treating infections and
PS disease associated with expression of CD81 such as inflammation disorder.
XX Example 15; SEQ ID NO 33; 55pp; English.

CC The invention relates to a compound (antisense oligonucleotide)
CC hybridising with the eighth nucleobase portion of an active site on a
CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
CC and inhibiting the expression of CD81. Also included is a composition
CC comprising the antisense oligonucleotide and a carrier or a diluent. The
CC antisense oligonucleotide is useful for inhibiting the expression of CD81
CC in cells or tissues. The antisense oligonucleotide is also useful for
CC treating infections preferably viral, bacterial and parasitic and
CC diseases such as inflammatory disorders and autoimmune disorders. The
CC disease or condition is characterised by chemical dependency (e.g.
CC cocaine addiction). The present sequence is a CD81 antisense
CC oligonucleotide of the invention.

XX Sequence 20 BP; 6 A; 6 C; 2 G; 6 T; 0 U; 0 Other;
SQ Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 602 GATGTGAGCAGTCTTATCA 621
Db |||||
20 GATGTGAGCAGTCTTATCA 1

RESULT 79
ADC35563/c
ID ADC35563 standard; DNA; 20 BP.
XX AC ADC35563;
XX 18-DEC-2003 (first entry)
XX Human CD81/TAPA-1 antisense oligonucleotide #23.
DE Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.
XX Homo sapiens.
XX Key Location/Qualifiers
FH modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
XX US2003113914-A1.
XX 19-JUN-2003.
XX 10-DEC-2001; 2001US-00006430.
XX 10-DEC-2001; 2001US-00006430.
XX (ISIS-) ISIS PHARM INC.
XX Graham MJ, Dobie K;

XX WPI; 2003-810907/76.
DR Novel compound hybridizing with nucleic acid molecule encoding CD81 and
XX inhibiting the expression of CD81, useful for treating infections and
PT disease associated with expression of CD81 such as inflammation disorder.
PS Claim 3; SEQ ID NO 35; 55pp; English.

XX The invention relates to a compound (antisense oligonucleotide)
CC hybridising with the eighth nucleobase portion of an active site on a
CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
CC and inhibiting the expression of CD81. Also included is a composition
CC comprising the antisense oligonucleotide and a carrier or a diluent. The
CC antisense oligonucleotide is useful for inhibiting the expression of CD81
CC in cells or tissues. The antisense oligonucleotide is also useful for
CC treating infections preferably viral, bacterial and parasitic and
CC diseases such as inflammatory disorders and autoimmune disorders. The
CC disease or condition is characterised by chemical dependency (e.g.
CC cocaine addiction). The present sequence is a CD81 antisense
CC oligonucleotide of the invention.

XX Sequence 20 BP; 3 A; 8 C; 4 G; 5 T; 0 U; 0 Other;
SQ Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 665 GCCAAGGCTGTGTTGAAGAC 684
Db |||||
20 GCCAAGGCTGTGTTGAAGAC 1

RESULT 80
ADC35570/c
ID ADC35570 standard; DNA; 20 BP.
XX AC ADC35570;
XX 18-DEC-2003 (first entry)
XX Human CD81/TAPA-1 antisense oligonucleotide #30.
DE Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.
XX Homo sapiens.
XX Key Location/Qualifiers
FH modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
XX US2003113914-A1.
XX 19-JUN-2003.
XX 10-DEC-2001; 2001US-00006430.
XX 10-DEC-2001; 2001US-00006430.

```
PA (ISIS-) ISIS PHARM INC.
XX Graham MJ, Dobie K;
XX WPI; 2003-810907/76.
XX
XX Novel compound hybridizing with nucleic acid molecule encoding CD81 and
XX inhibiting the expression of CD81, useful for treating infections and
XX disease associated with expression of CD81 such as inflammation disorder.
XX
XX Claim 3; SEQ ID NO 42; 55pp; English.
XX
XX The invention relates to a compound (antisense oligonucleotide)
XX hybridizing with the eighth nucleobase portion of an active site on a
XX nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
XX and inhibiting the expression of CD81. Also included is a composition
XX comprising the antisense oligonucleotide and a carrier or a diluent. The
XX antisense oligonucleotide is useful for inhibiting the expression of CD81
XX in cells or tissues. The antisense oligonucleotide is also useful for
XX treating infections preferably viral, bacterial and parasitic and
XX diseases such as inflammatory disorders and autoimmune disorders. The
XX disease or condition is characterised by chemical dependency (e.g.
XX cocaine addiction). The present sequence is a CD81 antisense
XX oligonucleotide of the invention.
XX
XX Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;
XX
Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 836 GGGAGCTGTACTCTACGG 855
DB 20 GGGAGCTGTACTCTACGG 1
RESULT 81
ADC35575/c
ID ADC35575 standard; DNA; 20 BP.
AC ADC35575;
XX
XX 18-DEC-2003 (first entry)
XX
XX Human CD81/TAPA-1 antisense oligonucleotide #35.
XX
XX Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
XX cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
XX virucide; antiparasitic; inflammatory disorder; parasitic infection;
XX bacterial infection.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX modified_base 1..20
XX /tag= b
XX /mod_base= OTHER
XX /note= "Phosphorothioate backbone and all cytidines are 5
XX -methyl cytidines"
XX modified_base 1..5
XX /tag= a
XX /mod_base= OTHER
XX /note= "2'-methoxyethyl nucleotide"
XX modified_base 16..20
XX /tag= c
XX /mod_base= OTHER
XX /note= "2'-methoxyethyl nucleotide"
XX
XX US2003113914-A1.
XX
XX 19-JUN-2003.
XX
XX 10-DEC-2001; 2001US-00006430.
XX
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XX
XX 10-DEC-2001; 2001US-00006430.
XX (ISIS-) ISIS PHARM INC.
XX Graham MJ, Dobie K;
XX WPI; 2003-810907/76.
XX
XX Novel compound hybridizing with nucleic acid molecule encoding CD81 and
XX inhibiting the expression of CD81, useful for treating infections and
XX disease associated with expression of CD81 such as inflammation disorder.
XX
XX Example 15; SEQ ID NO 47; 55pp; English.
XX
XX The invention relates to a compound (antisense oligonucleotide)
XX hybridizing with the eighth nucleobase portion of an active site on a
XX nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
XX and inhibiting the expression of CD81. Also included is a composition
XX comprising the antisense oligonucleotide and a carrier or a diluent. The
XX antisense oligonucleotide is useful for inhibiting the expression of CD81
XX in cells or tissues. The antisense oligonucleotide is also useful for
XX treating infections preferably viral, bacterial and parasitic and
XX diseases such as inflammatory disorders and autoimmune disorders. The
XX disease or condition is characterised by chemical dependency (e.g.
XX cocaine addiction). The present sequence is a CD81 antisense
XX oligonucleotide of the invention.
XX
XX Sequence 20 BP; 7 A; 4 C; 4 G; 5 T; 0 U; 0 Other;
XX
Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 884 ATGATCTTCGAGATGATCCT 903
DB 20 ATGATCTTCGAGATGATCCT 1
RESULT 82
ADC35583/c
ID ADC35583 standard; DNA; 20 BP.
AC ADC35583;
XX
XX 18-DEC-2003 (first entry)
XX
XX Human CD81/TAPA-1 antisense oligonucleotide #43.
XX
XX Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
XX cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
XX virucide; antiparasitic; inflammatory disorder; parasitic infection;
XX bacterial infection.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX modified_base 1..20
XX /tag= b
XX /mod_base= OTHER
XX /note= "Phosphorothioate backbone and all cytidines are 5
XX -methyl cytidines"
XX modified_base 1..5
XX /tag= a
XX /mod_base= OTHER
XX /note= "2'-methoxyethyl nucleotide"
XX modified_base 16..20
XX /tag= c
XX /mod_base= OTHER
XX /note= "2'-methoxyethyl nucleotide"
XX
XX US2003113914-A1.
XX
```

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PD 19-JUN-2003.
XX
XX 10-DEC-2001; 2001US-00006430.
XX
XX 10-DEC-2001; 2001US-00006430.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Graham MJ, Dobie K;
XX
XX WPI; 2003-810907/76.
XX
XX Novel compound hybridizing with nucleic acid molecule encoding CD81 and
XX inhibiting the expression of CD81, useful for treating infections and
XX disease associated with expression of CD81 such as inflammation disorder.
XX
XX Claim 3; SEQ ID NO 55; 55pp; English.
XX
XX The invention relates to a compound (antisense oligonucleotide)
XX hybridising with the eighth nucleobase portion of an active site on a
XX nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
XX and inhibiting the expression of CD81. Also included is a composition
XX comprising the antisense oligonucleotide and a carrier or a diluent. The
XX antisense oligonucleotide is useful for inhibiting the expression of CD81
XX in cells or tissues. The antisense oligonucleotide is also useful for
XX treating infections preferably viral, bacterial and parasitic and
XX diseases such as inflammatory disorders and autoimmune disorders. The
XX disease or condition is characterised by chemical dependency (e.g.
XX cocaine addiction). The present sequence is a CD81 antisense
XX oligonucleotide of the invention.
XX
XX Sequence 20 BP; 4 A; 6 C; 7 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 1.3%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 33;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 935 AGCTCGGTACTGAGGCC 954
Db 20 AGCTCGGTACTGAGGCC 1
|||||
|||||

RESULT 83
ADC35592/c
ID ADC35592 standard; DNA; 20 BP.
XX
XX ADC35592;
XX
XX 18-DEC-2003 (first entry)
XX
XX Human CD81/TAPA-1 antisense oligonucleotide #52.
XX
XX Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
XX cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
XX virucide; antiparasitic; inflammatory disorder; parasitic infection;
XX bacterial infection.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX modified_base 1..20
XX /tag= b
XX /mod_base= OTHER
XX /note= "Phosphorothioate backbone and all cytidines are 5
FT modified_base 1..5
FT -methyl cytidines"
FT
FT /tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT

```

```

XX US2003113914-A1.
XX
XX 19-JUN-2003.
XX
XX 10-DEC-2001; 2001US-00006430.
XX
XX 10-DEC-2001; 2001US-00006430.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Graham MJ, Dobie K;
XX
XX WPI; 2003-810907/76.
XX
XX Novel compound hybridizing with nucleic acid molecule encoding CD81 and
XX inhibiting the expression of CD81, useful for treating infections and
XX disease associated with expression of CD81 such as inflammation disorder.
XX
XX Claim 3; SEQ ID NO 64; 55pp; English.
XX
XX The invention relates to a compound (antisense oligonucleotide)
XX hybridising with the eighth nucleobase portion of an active site on a
XX nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
XX and inhibiting the expression of CD81. Also included is a composition
XX comprising the antisense oligonucleotide and a carrier or a diluent. The
XX antisense oligonucleotide is useful for inhibiting the expression of CD81
XX in cells or tissues. The antisense oligonucleotide is also useful for
XX treating infections preferably viral, bacterial and parasitic and
XX diseases such as inflammatory disorders and autoimmune disorders. The
XX disease or condition is characterised by chemical dependency (e.g.
XX cocaine addiction). The present sequence is a CD81 antisense
XX oligonucleotide of the invention.
XX
XX Sequence 20 BP; 4 A; 8 C; 7 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 1.3%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 33;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1205 CCTGGGGTCCCAGGTGCTC 1224
Db 20 CCTGGGGTCCCAGGTGCTC 1
|||||
|||||

RESULT 84
ADC35600/c
ID ADC35600 standard; DNA; 20 BP.
XX
XX ADC35600;
XX
XX 18-DEC-2003 (first entry)
XX
XX Human CD81/TAPA-1 antisense oligonucleotide #60.
XX
XX Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
XX cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
XX virucide; antiparasitic; inflammatory disorder; parasitic infection;
XX bacterial infection.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX modified_base 1..20
XX /tag= b
XX /mod_base= OTHER
XX /note= "Phosphorothioate backbone and all cytidines are 5
FT modified_base 1..5
FT -methyl cytidines"
FT
FT /tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT

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FT FT      /*tag= c
FT FT      /mod_base= OTHER
XX XX      /note= "2'-methoxyethyl nucleotide"
PN PN      US2003113914-A1.
XX XX      19-JUN-2003.
XX XX
XX XX      10-DEC-2001; 2001US-00006430.
XX XX
XX XX      10-DEC-2001; 2001US-00006430.
XX XX
XX XX      (ISIS-) ISIS PHARM INC.
XX XX
XX XX      Graham MJ, Dobie K;
XX XX
XX XX      WPI; 2003-810907/76.
XX XX
XX XX      Novel compound hybridizing with nucleic acid molecule encoding CD81 and
XX XX      inhibiting the expression of CD81, useful for treating infections and
XX XX      disease associated with expression of CD81 such as inflammation disorder.
XX XX
XX XX      Claim 3; SEQ ID NO 72; 55pp; English.
XX XX
XX XX      The invention relates to a compound (antisense oligonucleotide)
XX XX      hybridizing with the eighth nucleobase portion of an active site on a
XX XX      nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
XX XX      and inhibiting the expression of CD81. Also included is a composition
XX XX      comprising the antisense oligonucleotide and a carrier or a diluent. The
XX XX      antisense oligonucleotide is useful for inhibiting the expression of CD81
XX XX      in cells or tissues. The antisense oligonucleotide is also useful for
XX XX      treating infections preferably viral, bacterial and parasitic and
XX XX      diseases such as inflammatory disorders and autoimmune disorders. The
XX XX      disease or condition is characterised by chemical dependency (e.g.
XX XX      cocaine addiction). The present sequence is a CD81 antisense
XX XX      oligonucleotide of the invention.
XX XX
XX XX      Sequence 20 BP; 6 A; 4 C; 8 G; 2 T; 0 U; 0 Other;
XX XX
XX XX      Query Match      1.3%; Score 20; DB 1; Length 20;
XX XX      Best Local Similarity 100.0%; Pred. No. 33;
XX XX      Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX XX
XX XX      QY      1375 GGCACCTCTGCTTCATGC 1394
XX XX      |||||
XX XX      20 GGCACCTCTGCTTCATGC 1
XX XX
XX XX      RESULT 85
XX XX      AAQ75716/C
XX XX      ID AAQ75716 standard; DNA; 21 BP.
XX XX
XX XX      AC AAQ75716;
XX XX
XX XX      DT 04-AUG-1995 (first entry)
XX XX
XX XX      DE Reverse transcription primer used in cDNA analysis technique.
XX XX
XX XX      KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX XX      aggregate; restriction enzyme; ss.
XX XX
XX XX      OS Synthetic.
XX XX
XX XX      PN JP06303997-A.
XX XX
XX XX      PD 01-NOV-1994.
XX XX
XX XX      PF 16-APR-1993; 93JP-00112515.
XX XX
XX XX      PR 16-APR-1993; 93JP-00112515.
XX XX
XX XX      PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX XX
XX XX      DR WPI; 1995-018287/03.
XX XX
XX XX      PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX XX      by digestion with restriction enzymes.
XX XX
XX XX      PS Disclosure; Page 6; 11pp; Japanese.
XX XX
XX XX      CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX XX      double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX XX      labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX XX      and using the aggregate of mRNAs as the template for each reverse
XX XX      transcription primer; (b) digesting each of the prepared aggregates of
XX XX      the double-stranded cDNAs with restriction enzyme and; (c)
XX XX      electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX XX      method can be used to analyse gene expression rapidly and easily
XX XX
XX XX      Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;
XX XX
XX XX      Query Match      1.3%; Score 20; DB 1; Length 21;
XX XX      Best Local Similarity 100.0%; Pred. No. 37;
XX XX      Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX XX
XX XX      QY      1477 TGCTAAAAA 1496
XX XX      |||||
XX XX      21 TGCTAAAAA 2
XX XX
XX XX      RESULT 86
XX XX      AAQ75661/C
XX XX      ID AAQ75661 standard; DNA; 21 BP.
XX XX
XX XX      AC AAQ75661;
XX XX
XX XX      DT 04-AUG-1995 (first entry)
XX XX
XX XX      DE Reverse transcription primer used in cDNA analysis technique.
XX XX
XX XX      KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX XX      aggregate; restriction enzyme; ss.
XX XX
XX XX      OS Synthetic.
XX XX
XX XX      PN JP06303997-A.
XX XX
XX XX      PD 01-NOV-1994.
XX XX
XX XX      PF 16-APR-1993; 93JP-00112515.
XX XX
XX XX      PR 16-APR-1993; 93JP-00112515.
XX XX
XX XX      PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX XX
XX XX      DR WPI; 1995-018287/03.
XX XX
XX XX      PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX XX      by digestion with restriction enzymes.
XX XX
XX XX      PS Disclosure; Page 6; 11pp; Japanese.
XX XX
XX XX      CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX XX      double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX XX      labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX XX      and using the aggregate of mRNAs as the template for each reverse
XX XX      transcription primer; (b) digesting each of the prepared aggregates of
XX XX      the double-stranded cDNAs with restriction enzyme and; (c)
XX XX      electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX XX      method can be used to analyse gene expression rapidly and easily
XX XX
XX XX      Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
XX XX
XX XX      Query Match      1.3%; Score 19.4; DB 1; Length 21;
XX XX      Best Local Similarity 95.2%; Pred. No. 48;
XX XX      Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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FT FT /*tag= c
 FT FT /mod_base= OTHER
 XX XX /note= "2'-methoxyethyl nucleotide"

US2003113914-A1.

19-JUN-2003.

10-DEC-2001; 2001US-00006430.

10-DEC-2001; 2001US-00006430.

(ISIS-) ISIS PHARM INC.

Graham MJ, Dobie K;

WPI; 2003-810907/76.

Novel compound hybridizing with nucleic acid molecule encoding CD81 and inhibiting the expression of CD81, useful for treating infections and disease associated with expression of CD81 such as inflammation disorder.

Claim 3; SEQ ID NO 72; 55pp; English.

The invention relates to a compound (antisense oligonucleotide) hybridizing with the eighth nucleobase portion of an active site on a nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin) and inhibiting the expression of CD81. Also included is a composition comprising the antisense oligonucleotide and a carrier or a diluent. The antisense oligonucleotide is useful for inhibiting the expression of CD81 in cells or tissues. The antisense oligonucleotide is also useful for treating infections preferably viral, bacterial and parasitic and diseases such as inflammatory disorders and autoimmune disorders. The disease or condition is characterised by chemical dependency (e.g. cocaine addiction). The present sequence is a CD81 antisense oligonucleotide of the invention.

Sequence 20 BP; 6 A; 4 C; 8 G; 2 T; 0 U; 0 Other;

Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1375 GGCACCTCTGCTTCATGC 1394

|||||
20 GGCACCTCTGCTTCATGC 1

RESULT 85

AAQ75716/C

ID AAQ75716 standard; DNA; 21 BP.

AC AAQ75716;

DT 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

KW Analysis; gene expression; reverse transcription; primer; cDNA; aggregate; restriction enzyme; ss.

OS Synthetic.

PN JP06303997-A.

PD 01-NOV-1994.

PF 16-APR-1993; 93JP-00112515.

PR 16-APR-1993; 93JP-00112515.

PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

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QY 1476 ATGCTAAAAA 1496
DB 21 ATGCAAAAAA 1

RESULT 87
AAQ49436/c
ID AAQ49436 standard; cDNA; 20 BP.
AC AAQ49436;
XX
DT 25-MAR-2003 (revised)
DT 27-APR-1994 (first entry)
XX
DE Cytochrome P450 sequence amplification PCR primer polyT.
KW Transgenic plants; altered petal colour; polymerase chain reaction; ss.
XX
OS Synthetic.
XX
PN WO9320206-A1.
XX
PD 14-OCT-1993.
XX
PF 25-MAR-1993; 93WO-AU000127.
XX
PR 27-MAR-1992; 92AU-00001538.
PR 07-JAN-1993; 93AU-00006698.
XX
PA (ITFL-) INT FLOWER DEV PTY LTD.
XX
PI Holton TA, Cornish EC, Tanaka Y;
XX
DR WPI; 1993-336914/42.
XX
PT Nucleic acid isolate encoding flavonoid-3'-hydroxylase - is used to
PT create transgenic plants with altered petal colour.
XX
PS Disclosure; Page 25; 86pp; English.
XX
CC The sequence is that of a PCR primer which was used in polymerase chain
CC reactions for the amplification of cloned cytochrome P450 sequences.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 1.3%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1478 GCTAAAAA 1496
DB 20 GCTAAAAA 2

RESULT 89
ABZ88266
ID ABZ88266 standard; DNA; 20 BP.
XX
AC ABZ88266;
XX
DT 17-OCT-2003 (first entry)
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandraseagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.

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XX Disclosure; SEQ ID NO 3508; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a

XX first active agent comprising an oligonucleotide antisense to the

XX initiation codon, coding region, 5' or 3' end genomic flanking regions,

XX 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of

XX junctions of genes encoding a polypeptide associated with lung and/or

XX nasal airway dysfunction and a second active agent comprising an

XX antiinflammatory steroid and ubiquinone. A composition of the invention

XX has antiinflammatory, antiasthmatic, hypotensive, immunosuppressive,

XX and cytostatic activity. The composition may have a use in antisense gene

XX therapy. The composition is useful for treating or preventing a

XX respiratory, lung or malignant disease or condition, also for enhancing the

XX prophylactic or therapeutic respiratory effect of an antiinflammatory

XX steroid in a subject, for reducing or depleting levels of, or reducing

XX sensitivity to adenosine, reducing levels of adenosine receptor,

XX producing bronchodilation, increasing levels of ubiquinone or lung

XX surfactant in a subject's tissue, or treating bronchoconstriction, lung

XX inflammation, lung allergies, or a respiratory disease or condition.

XX Note: The sequence data for this patent is not represented in the printed

XX specification, but was obtained in electronic format directly from WIPO

XX at ftp.wipo.int/pub/published_pct_sequences

XX

XX Sequence 20 BP; 17 A; 1 C; 1 G; 1 T; 0 U; 0 Other;

XX

XX Query Match 1.3%; Score 19; DB 1; Length 20;

XX Best Local Similarity 100.0%; Pred. No. 52;

XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX

QY 1478 GCTAAAAA 1496

DB 1 GCTAAAAA 19

RESULT 90

AAQ75718/c

ID AAQ75718 standard; DNA; 21 BP.

AC AAQ75718;

XX

XX 04-AUG-1995 (first entry)

XX

XX Reverse transcription primer used in cDNA analysis technique.

XX

XX Analysis; gene expression; reverse transcription; primer; cDNA;

XX aggregate; restriction enzyme; ss.

XX Synthetic.

XX JP06303997-A.

XX

XX 01-NOV-1994.

XX

XX 16-APR-1993; 93JP-00112515.

XX

XX 16-APR-1993; 93JP-00112515.

XX

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX

XX WPI; 1995-018287/03.

XX

XX Analysis of cDNA and gene expression - by amplification of mRNA followed

XX by digestion with restriction enzymes.

XX

XX Disclosure; Page 8; 11pp; Japanese.

XX

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of

XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of

XX labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)

XX and using the aggregate of mRNAs as the template for each reverse

XX transcription primer; (b) digesting each of the prepared aggregates of

XX the double-stranded cDNAs with restriction enzyme and; (c)

XX electrophoresing the digested aggregate of cDNAs in separate lanes. The

XX method can be used to analyse gene expression rapidly and easily

XX

XX Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

XX

XX Query Match 1.3%; Score 19; DB 1; Length 21;

XX Best Local Similarity 100.0%; Pred. No. 57;

XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX

QY 1478 GCTAAAAA 1496

DB 20 GCTAAAAA 2

RESULT 92

AAQ75717/c

ID AAQ75717 standard; DNA; 21 BP.

XX

XX AAQ75717;

XX

XX 04-AUG-1995 (first entry)

XX

XX	Reverse transcription primer used in cDNA analysis technique.
DE	Analysis; gene expression; reverse transcription; primer; cDNA;
XX	aggregate; restriction enzyme; ss.
KW	Synthetic.
XX	
OS	JP06303997-A.
XX	
PN	01-NOV-1994.
XX	
PD	
XX	16-APR-1993; 93JP-00112515.
PF	
XX	16-APR-1993; 93JP-00112515.
XX	
PR	(NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX	
PA	WPI, 1995-018287/03.
XX	
DR	Analysis of cDNA and gene expression - by amplification of mRNA followed
XX	by digestion with restriction enzymes.
PT	
XX	Disclosure; Page 6; lipp; Japanese.
XX	
PS	A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX	double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC	labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC	and using the aggregate of mRNAs as the template for each reverse
CC	transcription primer; (b) digesting each of the prepared aggregates of
CC	the double-stranded cDNAs with restriction enzyme and; (c)
CC	electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC	method can be used to analyse gene expression rapidly and easily
XX	
XX	Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;
SQ	
	Query Match 1.2%; Score 18.4; DB 1; Length 21;
	Best Local Similarity 95.0%; Pred. No. 75;
	Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy	1477 TGCTAAAAAAAAAAAAAAAAAAAA 1496
Db	21 TGCCAAAAAAAAAAAAAAAAAAAA 2
RESULT 97	
AAQ75732/c	
ID	AAQ75732 standard; DNA; 21 BP.
XX	
AC	AAQ75732;
XX	
AC	
XX	04-AUG-1995 (first entry)
DT	
XX	
XX	Reverse transcription primer used in cDNA analysis technique.
DE	
XX	Analysis; gene expression; reverse transcription; primer; cDNA;
KW	aggregate; restriction enzyme; ss.
XX	
XX	Synthetic.
OS	
XX	
XX	JP06303997-A.
PN	
XX	01-NOV-1994.
PD	
XX	
XX	16-APR-1993; 93JP-00112515.
PF	
XX	16-APR-1993; 93JP-00112515.
XX	
PR	(NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX	
PA	WPI, 1995-018287/03.
XX	
DR	Analysis of cDNA and gene expression - by amplification of mRNA followed
XX	
PT	

```
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 8; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 3 A; 1 C; 0 G; 17 T; 0 U; 0 Other;

Query Match      1.2%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 75;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1477 TGCTAAAAA 1496
DB 21 TGTAAAAA 2

RESULT 98
AAQ75660/c
ID AAQ75660 standard; DNA; 21 BP.
XX
XX AC AAQ75660;
XX
XX DT 04-AUG-1995 (first entry)
XX
XX DE Reverse transcription primer used in cDNA analysis technique.
XX
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX OS Synthetic.
XX
XX PN JP06303997-A.
XX
XX PD 01-NOV-1994.
XX
XX PF 16-APR-1993; 93JP-00112515.
XX
XX PR 16-APR-1993; 93JP-00112515.
XX
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX DR WPI; 1995-018287/03.
XX
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

Query Match      1.2%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 75;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1477 TGCTAAAAA 1496
DB 21 TGTAAAAA 2

RESULT 99
AAQ75684/c
ID AAQ75684 standard; DNA; 21 BP.
XX
XX AC AAQ75684;
XX
XX DT 04-AUG-1995 (first entry)
XX
XX DE Reverse transcription primer used in cDNA analysis technique.
XX
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX OS Synthetic.
XX
XX PN JP06303997-A.
XX
XX PD 01-NOV-1994.
XX
XX PF 16-APR-1993; 93JP-00112515.
XX
XX PR 16-APR-1993; 93JP-00112515.
XX
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX DR WPI; 1995-018287/03.
XX
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

Query Match      1.2%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 75;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1477 TGCTAAAAA 1496
DB 21 TGTAAAAA 2

RESULT 100
AAQ75700/c
ID AAQ75700 standard; DNA; 21 BP.
XX
XX AC AAQ75700;
XX
XX DT 04-AUG-1995 (first entry)
XX
XX DE Reverse transcription primer used in cDNA analysis technique.
XX
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX OS Synthetic.
XX
XX PN JP06303997-A.
XX
XX PD 01-NOV-1994.
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XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX PS WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 7; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 21 BP; 2 A; 2 C; 0 G; 17 T; 0 U; 0 Other;
      Query Match 1.2%; Score 18.4; DB 1; Length 21;
      Best Local Similarity 95.0%; Pred. No. 75;
      Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1477 TCGTAAAAAATAAAAAAAAAA 1496
DB 21 TCGTAAAAAATAAAAAAAAAA 2
      RESULT 101
      AAQ75659/c
      ID AAQ75659 standard; DNA; 21 BP.
      AC AAQ75659;
      DT 04-AUG-1995 (first entry)
      DE Reverse transcription primer used in cDNA analysis technique.
      KW Analysis; gene expression; reverse transcription; primer; cDNA;
      KW aggregate; restriction enzyme; ss.
      OS Synthetic.
      PN JP06303997-A.
      PD 01-NOV-1994.
      PF 16-APR-1993; 93JP-00112515.
      PR 16-APR-1993; 93JP-00112515.
      PS (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
      PS WPI; 1995-018287/03.
      PT Analysis of cDNA and gene expression - by amplification of mRNA followed
      PT by digestion with restriction enzymes.
      PS Disclosure; Page 6; 11pp; Japanese.
      CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
      CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
      CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
      CC and using the aggregate of mRNAs as the template for each reverse
      CC transcription primer; (b) digesting each of the prepared aggregates of
      CC the double-stranded cDNAs with restriction enzyme and; (c)
      CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
      CC method can be used to analyse gene expression rapidly and easily

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CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;
      Query Match 1.2%; Score 18.4; DB 1; Length 21;
      Best Local Similarity 95.0%; Pred. No. 75;
      Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1477 TCGTAAAAAATAAAAAAAAAA 1496
DB 20 TCGTAAAAAATAAAAAAAAAA 1
      RESULT 102
      AAQ75712/c
      ID AAQ75712 standard; DNA; 21 BP.
      AC AAQ75712;
      DT 04-AUG-1995 (first entry)
      DE Reverse transcription primer used in cDNA analysis technique.
      KW Analysis; gene expression; reverse transcription; primer; cDNA;
      KW aggregate; restriction enzyme; ss.
      OS Synthetic.
      PN JP06303997-A.
      PD 01-NOV-1994.
      PF 16-APR-1993; 93JP-00112515.
      PR 16-APR-1993; 93JP-00112515.
      PS (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
      PS WPI; 1995-018287/03.
      PT Analysis of cDNA and gene expression - by amplification of mRNA followed
      PT by digestion with restriction enzymes.
      PS Disclosure; Page 7; 11pp; Japanese.
      CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
      CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
      CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
      CC and using the aggregate of mRNAs as the template for each reverse
      CC transcription primer; (b) digesting each of the prepared aggregates of
      CC the double-stranded cDNAs with restriction enzyme and; (c)
      CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
      CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
      Query Match 1.2%; Score 18.4; DB 1; Length 21;
      Best Local Similarity 95.0%; Pred. No. 75;
      Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1477 TCGTAAAAAATAAAAAAAAAA 1496
DB 21 TACTAAAAAATAAAAAAAAAA 2
      RESULT 103
      AAQ75704/c
      ID AAQ75704 standard; DNA; 21 BP.
      AC AAQ75704;
      DT 04-AUG-1995 (first entry)
      PS WPI; 1995-018287/03.
      PT Analysis of cDNA and gene expression - by amplification of mRNA followed
      PT by digestion with restriction enzymes.
      PS Disclosure; Page 6; 11pp; Japanese.
      CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
      CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
      CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
      CC and using the aggregate of mRNAs as the template for each reverse
      CC transcription primer; (b) digesting each of the prepared aggregates of
      CC the double-stranded cDNAs with restriction enzyme and; (c)
      CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
      CC method can be used to analyse gene expression rapidly and easily

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DE Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
XX Synthetic.
OS
XX JP06303997-A.
PN
PD 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
PF
XX
XX 16-APR-1993; 93JP-00112515.
PR
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
PA
XX WPI; 1995-018287/03.
DR
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
PT
XX
XX Disclosure; Page 7; 1lpp; Japanese.
PS
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 21 BP; 2 A; 0 C; 2 G; 17 T; 0 U; 0 Other;
SQ
XX
XX Query Match 1.2%; Score 18.4; DB 1; Length 21;
XX Best Local Similarity 95.0%; Pred. No. 75;
XX Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1477 TCGTAAAAAATAAAAAAAAAA 1496
QY
XX
XX 21 TCGTAAAAAATAAAAAAAAAA 2
DB
XX
XX RESULT 104
XX AAQ75708/c
XX ID AAQ75708 standard; DNA; 21 BP.
XX
XX AC AAQ75708;
XX
XX 04-AUG-1995 (first entry)
DT
XX
XX Reverse transcription primer used in cDNA analysis technique.
DE
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
XX Synthetic.
OS
XX JP06303997-A.
PN
PD 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
PF
XX
XX 16-APR-1993; 93JP-00112515.
PR
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
PA
XX WPI; 1995-018287/03.
DR
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
PT
XX
XX Disclosure; Page 6; 1lpp; Japanese.
PS
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;
SQ
XX
XX Query Match 1.2%; Score 18.4; DB 1; Length 21;
XX Best Local Similarity 95.0%; Pred. No. 75;
XX Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1477 TCGTAAAAAATAAAAAAAAAA 1496
QY
XX
XX 20 TCGAAAAAATAAAAAAAAAA 1
DB
XX
XX RESULT 105
XX AAQ75662/c
XX ID AAQ75662 standard; DNA; 21 BP.
XX
XX AC AAQ75662;
XX
XX 04-AUG-1995 (first entry)
DT
XX
XX Reverse transcription primer used in cDNA analysis technique.
DE
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
XX Synthetic.
OS
XX JP06303997-A.
PN
PD 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
PF
XX
XX 16-APR-1993; 93JP-00112515.
PR
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
PA
XX WPI; 1995-018287/03.
DR
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
PT
XX
XX Disclosure; Page 7; 1lpp; Japanese.
PS
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;
SQ
XX
XX Query Match 1.2%; Score 18.4; DB 1; Length 21;
XX Best Local Similarity 95.0%; Pred. No. 75;
XX Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1477 TCGTAAAAAATAAAAAAAAAA 1496
QY
XX
XX 20 TCGAAAAAATAAAAAAAAAA 1
DB
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
PT
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XX DE
XX XX
XX XX
KW KW Reverse transcription primer used in cDNA analysis technique.
KW KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW KW aggregate; restriction enzyme; ss.
XX XX
XX OS Synthetic.
XX XX
XX XX JF06303997-A.
XX XX
XX PD 01-NOV-1994.
XX XX
XX PF 16-APR-1993; 93JP-00112515.
XX XX
XX PR 16-APR-1993; 93JP-00112515.
XX XX
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX XX
XX DR WPI; 1995-018287/03.
XX XX
XX XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX XX PT by digestion with restriction enzymes.
XX XX PS Disclosure; Page 5; 11pp; Japanese.
XX XX
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 19 BP; 1 A; 0 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 1.2%; Score 18; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAATAAAAAAAAAAAAAA 1496
Db 19 CTAATAAAAAAAAAAAAAA 2

RESULT 108
AAQ75575/C
ID AAQ75575 standard; DNA; 20 BP.
XX AC AAQ75575;
XX AC AAQ75575;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX XX
XX PN JF06303997-A.
XX XX
XX PD 01-NOV-1994.
XX XX
XX PF 16-APR-1993; 93JP-00112515.
XX XX
XX PR 16-APR-1993; 93JP-00112515.
XX XX
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX XX
XX DR WPI; 1995-018287/03.
XX XX
XX XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX XX PT by digestion with restriction enzymes.

RESULT 106
ADC35533/C
ID ADC35533 standard; DNA; 18 BP.
XX AC ADC35533;
XX AC ADC35533;
XX DT 18-DEC-2003 (first entry)
XX DE Human CD81/TAPA-1 RT-PCR primer #2.
XX DE
XX KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
XX KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
XX KW viricide; antiparasitic; inflammatory disorder; parasitic infection;
XX KW bacterial infection; PCR; primer; RT-PCR; reverse transcriptase PCR;
XX KW GAPDH; glyceraldehyde-3-phosphate dehydrogenase.
XX OS
XX OS Homo sapiens.
XX XX
XX XX US2003113914-A1.
XX PN
XX XX
XX PD 19-JUN-2003.
XX XX
XX PF 10-DEC-2001; 2001US-00006430.
XX XX
XX PR 10-DEC-2001; 2001US-00006430.
XX XX
XX PA (ISIS-) ISIS PHARM INC.
XX PI
XX PI Graham MJ, Dobie K;
XX XX
XX DR WPI; 2003-810907/76.
XX XX
XX XX Novel compound hybridizing with nucleic acid molecule encoding CD81 and
XX XX PT inhibiting the expression of CD81, useful for treating infections and
XX XX PT disease associated with expression of CD81 such as inflammation disorder.
XX PS Example 13; SEQ ID NO 5; 55pp; English.
XX XX
XX CC The invention relates to a compound (antisense oligonucleotide)
XX CC hybridizing with the eighth nucleobase portion of an active site on a
XX CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
XX CC and inhibiting the expression of CD81. Also included is a composition
XX CC comprising the antisense oligonucleotide and a carrier or a diluent. The
XX CC antisense oligonucleotide is useful for inhibiting the expression of CD81
XX CC in cells or tissues. The antisense oligonucleotide is also useful for
XX CC treating infections preferably viral, bacterial and parasitic and
XX CC diseases such as inflammatory disorders and autoimmune disorders. The
XX CC disease or condition is characterised by chemical dependency (e.g.
XX CC cocaine addiction). The present sequence is a reverse transcriptase (RT)-
XX CC PCR primer (either for CD81 or glyceraldehyde-3-phosphate dehydrogenase,
XX CC GAPDH) used to assay the level of mRNA pre and post treatment with the
XX CC antisense oligonucleotides.
XX SQ Sequence 18 BP; 2 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 1.2%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 649 TGATGACGCCAACACGC 666
Db 18 TGATGACGCCAACACGC 1

RESULT 107
AAQ75551/C
ID AAQ75551 standard; DNA; 19 BP.
XX AC AAQ75551;
XX AC AAQ75551;
XX DT 04-AUG-1995 (first entry)
XX XX
XX XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX XX PT by digestion with restriction enzymes.

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PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 1 A; 0 C; 2 G; 17 T; 0 U; 0 Other;
    Query Match          1.2%; Score 18; DB 1; Length 20;
    Best Local Similarity 100.0%; Pred. No. 81;
    Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAAGAAAAA 1496
    |||||
DB 19 CTAAGAAAAA 2

RESULT 109
AAQ75577/c
ID AAQ75577 standard; DNA; 20 BP.
XX
XX AAQ75577;
AC
XX
XX 04-AUG-1995 (first entry)
DT
XX Reverse transcription primer used in cDNA analysis technique.
DE
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
XX Synthetic.
OS
XX
XX JP06303997-A.
PN
XX
XX 01-NOV-1994.
PD
XX
XX 16-APR-1993; 93JP-00112515.
PF
XX
XX 16-APR-1993; 93JP-00112515.
PR
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
PA
XX
XX WPI; 1995-018287/03.
DR
XX
XX
XX
XX 04-AUG-1995 (first entry)
DT
XX Reverse transcription primer used in cDNA analysis technique.
DE
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
XX Synthetic.
OS
XX
XX JP06303997-A.
PN
XX
XX 01-NOV-1994.
PD
XX
XX 16-APR-1993; 93JP-00112515.
PF
XX
XX 16-APR-1993; 93JP-00112515.
PR
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
PA
XX
XX WPI; 1995-018287/03.
DR
XX
XX
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
    Query Match          1.2%; Score 18; DB 1; Length 20;
    Best Local Similarity 100.0%; Pred. No. 81;
    Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAAGAAAAA 1496
    |||||
DB 19 CTAAGAAAAA 2

RESULT 111
AAQ75577/c
ID AAQ75577 standard; DNA; 20 BP.
XX
XX AAQ75577;
AC
XX
XX 25-MAR-2003 (revised)
DT
XX 15-MAY-1996 (first entry)
DT
XX Mammalian stem cell factor (SCF) cDNA oligonucleotide primer 220-7.
DE
XX Stem cell factor; progenitor; haematopoiesis; SCF; anaemia;
KW thrombocytopenia; leucopenia; AIDS; immunodeficiency; bone graft;
KW transplant; neoplasia; myelosuppression; bone marrow; ss.
XX
XX Synthetic.
OS
XX
XX EP676470-A1.
PN

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XX PD 11-OCT-1995.
XX PF
XX PR 04-OCT-1990; 95EP-00105391.
XX PR 16-OCT-1989; 89US-00422383.
XX PR 11-JUN-1990; 90US-00537198.
XX PR 24-AUG-1990; 90US-00573616.
XX PR 28-SEP-1990; 90US-005548.
XX PR 01-OCT-1990; 90US-00589701.
XX PR 28-SEP-1990; 90WO-US005548.
XX PR 01-OCT-1990; 90US-00589701.
XX PA (AMGE-) AMGEN INC.
XX PI Zsebo KM, Suggs SV, Bosselman RA, Martin FH;
XX PI WPI; 1995-346090/45.
XX DR
XX PT New stem cell factor polypeptide(s) - for stimulating the growth of
XX PT primitive progenitor cells, esp. for treating disorders involving blood
XX PT cells.
XX PS
XX PS Example 3; Fig 12C; 127pp; English.
XX CC
XX CC AAT04915-T04922 are oligonucleotide primers and probes used for the
XX CC amplification and sequencing of mammalian stem cell factor (SCF). Non-
XX CC naturally occurring SCF and C-terminally truncated polypeptides, having
XX CC amino acid sequences sufficiently duplicative of naturally occurring SCF,
XX CC stimulate growth of primitive progenitors such as haematopoietic
XX CC progenitor cells, neural stem cells and primordial germ stem cells. The
XX CC peptides can be used in a composition for treating leucopenia, anaemia or
XX CC thrombocytopenia, for enhancing engraftment of bone marrow during
XX CC transplantation or for bone marrow recovery after chemotherapy or
XX CC radiation-induced bone marrow aplasia or myelosuppression. They can also
XX CC be used for treating neoplasia, nerve damage, infertility, intestinal
XX CC damage or myeloproliferative disorders. Antibodies may be raised against
XX CC the peptides for use in detection or neutralisation of SCF in serum. SCF
XX CC may be useful for the treatment of AIDS and severe combined
XX CC immunodeficiency (SCID) states alone or in combination with other factors
XX CC such as IL-7. (Updated on 25-MAR-2003 to correct PF field.)
XX CC
XX CC Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
XX
XX Query Match 1.2%; Score 18; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 81;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1479 CTAATAAAAAAAAAAAAAA 1496
XX DB 20 CTAATAAAAAAAAAAAAAA 3
XX
XX RESULT 112
XX AA13753/C
XX ID AA13753 standard; DNA; 20 BP.
XX AC AA13753;
XX AC
XX DT 27-JUL-2000 (first entry)
XX DT
XX DE Stem cell factor universal oligonucleotide 220-7.
XX
XX KW Stem cell factor; SCF; haematopoietic progenitor cell; blood forming;
XX KW primitive progenitor cell; haematopoietic disorder; syngeneic;
XX KW allogeneic; autologous bone marrow transplant; gene therapy;
XX KW transfection; haematopoietic stem cell; acute blood loss; neoplasia;
XX KW cancer; ss.
XX OS Synthetic.
XX OS
XX PN EP92579-A1.
XX PN
XX XX 12-APR-2000.
XX PD
XX PD 31-DEC-1998; 98US-00224681.
XX PF

11-OCT-1995.
04-OCT-1990; 95EP-00105391.
16-OCT-1989; 89US-00422383.
11-JUN-1990; 90US-00537198.
24-AUG-1990; 90US-00573616.
28-SEP-1990; 90US-005548.
01-OCT-1990; 90US-00589701.
28-SEP-1990; 90WO-US005548.
01-OCT-1990; 90US-00589701.
(PAGE-) AMGEN INC.
Zsebo KM, Suggs SV, Bosselmann RA, Martin FH;
WPI; 2000-259135/23.
Production of hematopoietic cells suitable for administration to a
subject using progenitor cells and expanding the cells using stem cell
factor.
Example 3; Fig 12C; 123pp; English.
A method has been developed of making haematopoietic cells suitable for
administration to a subject. The method comprises: (a) obtaining the cells
haematopoietic progenitor cells from a donor; and (b) expanding the cells
by adding to the cells a haematopoietically effective dose of a
polypeptide product having at least part of the primary structural
confirmation and one or more of the biological properties of naturally
occurring stem cell factor (SCF). The method is useful for stimulating
primitive progenitor cells including early haematopoietic progenitor
cells which are capable of maturing to erythroid, megakaryocyte,
granulocyte, lymphocyte and macrophage cells. SCF results in absolute
increases in haematopoietic cells of both myeloid and lymphoid lineages.
SCF is useful for treating haematopoietic disorders. The method is useful
for expanding early haematopoietic progenitors in syngeneic, allogeneic
or autologous bone marrow transplant. SCF is useful for enhancing the
efficiency of gene therapy based on transfecting haematopoietic stem
cells. SCF is also useful for combating the myelosuppressive effects of
anti-HIV drugs such as AZT and for enhancing haematopoietic recovery
after acute blood loss and as a boost to the immune system for fighting
neoplasia (cancer). The present sequence represents a universal
oligonucleotide which is used in an example from the present invention
Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
Query Match 1.2%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1479 CTAATAAAAAAAAAAAAAA 1496
DB 20 CTAATAAAAAAAAAAAAAA 3
RESULT 113
AAH41332/C
ID AAH41332 standard; DNA; 20 BP.
XX AC AAH41332;
XX AC
XX DT 21-AUG-2001 (first entry)
XX DT
XX DE Universal stem cell factor (SCF) related oligonucleotide SEQ ID NO:33.
XX KW Stem cell factor; SCF; stem cell factor receptor; blood cell disorder;
XX KW gene therapy; PCR primer; mutagenesis; probe; ss.
XX OS Synthetic.
XX OS
XX PN US6207454-B1.
XX PN
XX PD 27-MAR-2001.
XX PD
XX PD 31-DEC-1998; 98US-00224681.
XX PF

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XX PR 16-OCT-1989; 89US-00422383.
XX PR 11-JUN-1990; 90US-00537198.
XX PR 24-AUG-1990; 90US-00573616.
XX PR 01-OCT-1990; 90US-00589701.
XX PR 25-NOV-1992; 92US-00982255.
XX PR 21-DEC-1993; 93US-00172329.
XX PR 24-MAY-1995; 95US-00449653.
XX PR 12-JAN-1998; 98US-00005893.
XX PA (AMGE-) AMGEN INC.
XX PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX XX WPI; 2001-366062/38.
XX PT Enhancing efficiency of transfer of polynucleotide into a target
XX PT mammalian cell in vitro, involves exposing cell that expresses a stem
XX PT cell factor receptor to stem cell factor, and introducing polynucleotide
XX PT into cell in vitro.
XX PS Example 3; Fig 12C; 210pp; English.
XX CC The present invention describes a method for enhancing (E) the efficiency
XX CC of transfer of a polynucleotide (I) into a target mammalian cell (II) in
XX CC vitro, comprising exposing (II) that expresses a stem cell factor (SCF)
XX CC receptor to a biologically active SCF, its analogue or fragment, which
XX CC induces cell proliferation, and introducing (I) to (II) in vitro.
XX CC Exposure of SCF to (II) results in increased uptake of (I) into the cell.
XX CC The method is useful for enhancing the efficiency of the transfer of a
XX CC polynucleotide into a target mammalian cell in vitro. The method is
XX CC useful in gene therapy techniques. AAH41301 to AAH41364 and AAB98351 to
XX CC AAB98390 represent sequences used in the exemplification of the present
XX CC invention
XX SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 1.2%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAAAAAATAAAAAAAAAA 1496
DB 20 CTAAAAAATAAAAAAAAAA 3

RESULT 114
AA504112/c
ID AA504112 standard; DNA; 20 BP.
XX AA504112;
XX 29-AUG-2001 (first entry)
XX Human SCF (stem cell factor) cDNA universal PCR primer 220-7.
XX Human; stem cell factor; SCF; early haematopoietic progenitor cell;
XX blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
XX anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;
XX PCR primer; ss.
XX Homo sapiens.
XX US6207417-B1.
XX 27-MAR-2001.
XX 07-JUN-1995; 95US-00482918.
XX 16-OCT-1989; 89US-00422383.
XX 11-JUN-1990; 90US-00537198.
XX 24-AUG-1990; 90US-00573616.
XX 01-OCT-1990; 90US-00589701.

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PR 21-DEC-1993; 93US-00172329.
XX (ZSEB/) ZSEBO K M.
PA (BOSS/) BOSSELMAN R A.
PA (SUGG/) SUGGS S V.
XX (MART/) MARTIN F H.
PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX WPI; 2001-298941/31.
XX Novel nucleic acids encoding stem cell factor useful for treating
XX PT disorders involving blood cells, e.g. leukemia, splenomegaly, Hodgkin's
XX PT disease, Kala azar, anemia and septicemia.
XX PS Example 3; Fig 12C; 209pp; English.
XX CC The present sequence for universal PCR primer 220-7 is 1 of 8 universal
XX CC oligonucleotides (AA504110-AA504117) used in the isolation of the human
XX CC SCF (stem cell factor) cDNA sequence. The present invention relates to
XX CC novel stem cell factors (AAU02453-AAU02458, AAU02460, AAU02461) and the
XX CC polynucleotides encoding them. SCF stimulate primitive progenitor cells
XX CC including early haematopoietic progenitor cells. The invention also
XX CC describes SCF peptides (AAU02462-AAU02481) and the oligonucleotides
XX CC (AA504081-AA504117) used in the isolation of human and rat SCF sequences.
XX CC The polynucleotide encoding SCF is useful for producing SCF and useful in
XX CC gene therapy. It is useful for treating disorders involving blood cells
XX CC such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple
XX CC myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,
XX CC congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis,
XX CC disseminated fungus disease, Fulminating septicemia, malaria, vitamin B12
XX CC and folic acid deficiency, pyridoxine deficiency, and hypopigmentation
XX CC disorders such as piebaldism and vitiligo
XX SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 1.2%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAAAAAATAAAAAAAAAA 1496
DB 20 CTAAAAAATAAAAAAAAAA 3

RESULT 115
AAF89092/c
ID AAF89092 standard; DNA; 20 BP.
XX AAF89092;
XX 13-JUL-2001 (first entry)
XX Mammalian stem cell factor PCR primer SEQ ID NO: 33.
XX Human; rat; mammal; stem cell factor; SCF; cell growth stimulation;
XX gene therapy; haematopoietic disorder; aplastic anaemia; leukaemia;
XX neurological damage; intestinal damage; infertility; AIDS; SCID;
XX severe combined immunodeficiency; PCR primer; ss.
XX Mammalia.
XX US6207802-B1.
XX 27-MAR-2001.
XX 09-NOV-1994; 94US-00336728.
XX 16-OCT-1989; 89US-00422383.
XX 11-JUN-1990; 90US-00537198.
XX 24-AUG-1990; 90US-00573616.
XX 01-OCT-1990; 90US-00589701.
XX 25-NOV-1992; 92US-00982255.

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XX PA (AMGE-) AMGEN INC.
XX PI Zeebo KM, Bosselman RA, Suggs SV, Martin FH;
XX DR WPI; 2001-353108/37.
XX PT Novel isolated non-human mammalian stem cell factor polypeptide
XX PT stimulating growth of early hematopoietic progenitor cells, useful for
XX PT treating aplastic anemia, lymphoma, Letterer-Siwe disease, Kala azar,
XX PT sarcoidosis.
XX PS Example 3; Fig 12C; 209pp; English.
XX CC The present invention provides the protein and coding sequences of
XX CC mammalian stem cell factors (SCFs). These are capable of stimulating the
XX CC growth of early hematopoietic progenitor cells, neural stem cells and
XX CC primordial germ stem cells. The sequences are useful in the treatment of
XX CC leukemias, hematopoietic disorders, aplastic anaemia, paroxysmal
XX CC nocturnal haemoglobinuria, malaria, pigmentation disorders, neurological
XX CC and intestinal damage, infertility, AIDS and severe combined
XX CC immunodeficiency (SCID). The present sequence is primer used to amplify
XX CC an SCF in the exemplification of the invention
XX SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 1.2%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAAAAAATAAAAAAAAAA 1496
DB 20 CTAAAAAATAAAAAAAAAA 3

RESULT 116
AAH23890/c
ID AAH23890 standard; DNA; 20 BP.
AC AAH23890;
XX 07-AUG-2001 (first entry)
XX Human SCF (stem cell factor) cDNA universal PCR primer 220-7.
XX Human; stem cell factor; SCF; early haematopoietic progenitor cell;
XX blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
XX anaemia; Kala azar; septicaemia; malaria; hypopigmentation disorder;
XX PCR primer; ss.
XX Homo sapiens.
XX US6204363-B1.
XX 20-MAR-2001.
XX 25-NOV-1992; 92US-00982255.
XX 16-OCT-1989; 89US-00422383.
XX 11-JUN-1990; 90US-00537198.
XX 24-AUG-1990; 90US-00573616.
XX 01-OCT-1990; 90US-00589701.
XX 10-APR-1991; 91US-00684535.
XX (AMGE-) AMGEN INC.
XX Zeebo KM, Bosselman RA, Suggs SV, Martin FH;
XX WPI; 2001-256683/26.
XX New stem cell factor polypeptides and their analogs which stimulate
XX growth of early hematopoietic progenitors, useful for treating aplastic
XX anemia, carcinoma, multiple myeloma, vitiligo, Kala azar, Hodgkin's

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PT disease.
XX Example 3; Fig 12C; 166pp; English.
XX The present sequence for universal PCR primer 220-7 is 1 of 8 universal
XX oligonucleotides (AAH23888-AAH23895) used in the isolation of the human
XX SCF (stem cell factor) cDNA sequence. The present invention relates to
XX novel stem cell factors (AAH73561-AAH73568, AAB73571-AAH73576) and the
XX polynucleotides encoding them. SCF stimulate primitive progenitor cells
XX including early hematopoietic progenitor cells. The invention also
XX describes SCF peptides (AAB73578-AAH73597) and the oligonucleotides
XX (AAH23859-AAH23887) used in the isolation of human and rat SCF sequences.
XX The polynucleotide encoding SCF is useful for producing SCF and useful in
XX gene therapy. It is useful for treating disorders involving blood cells
XX such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple
XX myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,
XX congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis,
XX disseminated fungus disease, Fulminating septicaemia, malaria, vitamin
XX B12 and folic acid deficiency, pyridoxine deficiency, and
XX hypopigmentation disorders such as piebaldism and vitiligo
XX SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 1.2%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAAAAAATAAAAAAAAAA 1496
DB 20 CTAAAAAATAAAAAAAAAA 3

RESULT 117
AAS04213/c
ID AAS04213 standard; DNA; 20 BP.
AC AAS04213;
XX 29-AUG-2001 (first entry)
XX Human SCF (stem cell factor) cDNA universal PCR primer 220-7.
XX Human; stem cell factor; SCF; early haematopoietic progenitor cell;
XX blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
XX anaemia; Kala azar; septicaemia; malaria; hypopigmentation disorder;
XX PCR primer; ss.
XX Homo sapiens.
XX US6218148-B1.
XX 17-APR-2001.
XX 21-DEC-1993; 93US-00172329.
XX 16-OCT-1989; 89US-00422383.
XX 11-JUN-1990; 90US-00537198.
XX 24-AUG-1990; 90US-00573616.
XX 01-OCT-1990; 90US-00589701.
XX 25-NOV-1992; 92US-00982255.
XX (AMGE-) AMGEN INC.
XX Zeebo KM, Bosselman RA, Suggs SV, Martin FH;
XX WPI; 2001-281051/29.
XX Isolated DNA sequence, encoding polypeptide product useful for
XX stimulating growth of early hematopoietic progenitor cells.
XX Example 3; Fig 12C; 167pp; English.
XX The present sequence for universal PCR primer 220-7 is 1 of 8 universal

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CC oligonucleotides (AAS04211-AAS04218) used in the isolation of the human
 CC SCF (stem cell factor) cDNA sequence. The present invention relates to
 CC novel stem cell factors (AAU02761-AAU02767, AAU02770-AAU02775, AAU02797)
 CC and the polynucleotides encoding them. SCF stimulate primitive progenitor
 CC cells including early haematopoietic progenitor cells. The invention also
 CC describes SCF peptides (AAU02777-AAU02794) and the oligonucleotides
 CC (AAS04182-AAS04210) used in the isolation of human and rat SCF sequences.
 CC The polynucleotide encoding SCF is useful for producing SCF and useful in
 CC gene therapy. It is useful for treating disorders involving blood cells
 CC such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple
 CC myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,
 CC congestive splenomegaly, kala azar, sarcoidosis, military tuberculosis,
 CC disseminated fungus disease, Fulminating septicemia, malaria, vitamin B12
 CC and folic acid deficiency, pyridoxine deficiency, and hypopigmentation
 CC disorders such as piebaldism and vitiligo
 XX
 SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 1.2%; Score 18; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 81;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAAAAAATAAAAAAAAAA 1496
 |||||
 DB 20 CTAAAAAATAAAAAAAAAA 3

RESULT 118
 AAS10448/c
 ID AAS10448 standard; DNA; 20 BP.
 XX
 AC AAS10448;
 DT 24-OCT-2001 (first entry)

DE Human stem cell factor (SCF) cDNA universal PCR primer 220-7.

XX Human; stem cell factor; SCF; haematopoietic progenitor cell;
 KW blood disorder; Hodgkin's disease; vitamin B12; folic acid deficiency;
 KW hypopigmentation disorder; viral disorder; AIDS; PCR primer; ss.

OS Homo sapiens.

XX US6248319-B1.

PN 19-JUN-2001.

XX 24-MAY-1995; 95US-00449653.

PR 16-OCT-1989; 89US-00422383.

PR 11-JUN-1990; 90US-00537198.

PR 24-AUG-1990; 90US-00573616.

PR 01-OCT-1990; 90US-00589701.

PR 10-APR-1991; 91US-00684535.

PR 25-NOV-1992; 92US-00982255.

PR 21-DEC-1993; 93US-00172329.

XX (ZSEB/) ZSEBO K M.

PA (BOSS/) BOSSELMAN R A.

PA (SUGG/) SUGGS S V.

PA (MART/) MARTIN F H.

XX Zsebo KM, Bosselman RA, Suggs SV, Martin FH;

XX WPI; 2001-407312/43.

XX Increasing the number of early hematopoietic progenitor cells in the

PT peripheral blood useful for the treatment of blood disorders including

PT Hodgkin's disease comprises the administration of human stem cell factor.

XX Example 3; Fig 12C; 210pp; English.

XX The present sequence for universal PCR primer 220-7 is 1 of 19 PCR

CC primers (AAS10435-AAS10453) used to amplify various portions of the human
 CC SCF cDNA sequence. The sequence is described in an invention relating to
 CC novel stem cell factors, the polynucleotides encoding them and methods
 CC for producing the stem cell factors. The methods involve increasing the
 CC number of early haematopoietic progenitor cells in human peripheral blood
 CC by administering a haematopoietically effective human stem cell factor
 CC polypeptide. The methods are useful for the treatment of blood disorders,
 CC including myelofibrosis, myelocytosis, osteopetrosis, metastatic
 CC carcinoma, acute leukaemia, multiple myeloma, Hodgkin's disease,
 CC lymphoma, Gaucher's disease, Niemann-pick disease, refractory anaemia,
 CC malaria, vitamin B12 and folic acid deficiency, hypopigmentation
 CC disorders i.e. piebaldism and viral induced disorders, including AIDS
 XX
 SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 1.2%; Score 18; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 81;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAAAAAATAAAAAAAAAA 1496
 |||||
 DB 20 CTAAAAAATAAAAAAAAAA 3

RESULT 119

AAD35465/c

ID AAD35465 standard; DNA; 20 BP.

XX

AC AAD35465;

XX

DT 25-JUL-2002 (first entry)

XX

DE Rat SCF 5' cDNA amplifying PCR primer, 220-7.

XX

KW Rat; stem cell factor; SCF protein; leucopaenia; thrombocytopaenia;
 KW anaemia; myelosuppression; nerve damage; myeloproliferative disorder;
 KW infertility; neoplasia; myelofibrosis; myelocytosis; osteopetrosis;
 KW metastatic carcinoma; acute leukaemia; multiple myeloma; sarcoidosis;
 KW Hodgkin's disease; lymphoma; Gaucher's disease; Niemann-pick disease;
 KW Letterer-Siwe disease; refractory erythroblastic anaemia; Kala azar;
 KW Di Guglielmo syndrome; congestive splenomegaly; splenic pancytopenia;
 KW disseminated fungus disease; Fulminating septicaemia; piebaldism; AIDS;
 KW acquired immune deficiency syndrome; malaria; military tuberculosis;
 KW pyridoxine deficiency; vitamin B12 deficiency; folic acid deficiency;
 KW Diamond Blackfan anaemia; hypopigmentation disorder; vitiligo; PCR;
 KW primer; ss.

XX Rattus sp.

OS

XX US2002018763-A1.

XX 14-FEB-2002.

PD

XX 12-JAN-1998; 98US-00005243.

PF

XX 24-MAY-1995; 95US-00449653.

PR

XX (ZSEB/) ZSEBO K M.

PA (BOSS/) BOSSELMAN R A.

PA (SUGG/) SUGGS S V.

PA (MART/) MARTIN F H.

XX Zsebo KM, Bosselman RA, Suggs SV, Martin FH;

XX WPI; 2002-350789/38.

XX Novel non-naturally-occurring stem cell factor polypeptide, useful for

PT treating leucopenia, thrombocytopenia, anemia and for enhancing

PT engraftment of bone marrow during transplantation in a mammal.

XX Example 3; Fig 12C; 217pp; English.

XX The present invention relates to novel non-naturally-occurring stem cell

CC factor (SCF) polypeptides having an amino acid sequence sufficiently
 CC duplicative of that of naturally-occurring SCF to allow possession of
 CC haematopoietic biological activity of naturally occurring SCF. Sequences
 CC of the invention are useful for treating leucopenia, thrombocytopaenia,
 CC anaemia and for enhancing bone marrow recovery in treatment of radiation,
 CC engraftment of bone marrow during transplantation in mammals and chemical
 CC or chemotherapeutic induced bone marrow aplasia or myelosuppression. They
 CC are also useful for treating acquired immune deficiency in a human, nerve
 CC damage, neoplasia, infertility, myeloproliferative disorder, intestinal
 CC damage in a mammal. SCF sequences are useful for preparing biologically
 CC active polymer polypeptide adduct, for enhancing transfection of early
 CC haematopoietic progenitor cells with a gene, and transfer of a gene into
 CC a mammal. They are useful for treating myelofibrosis, myelosclerosis,
 CC osteopetrosis, metastatic carcinoma, acute leukaemia, multiple myeloma,
 CC Hodgkin's disease, lymphoma, Gaucher's disease, Niemann-Pick disease,
 CC Letterer-Siwe disease, refractory erythroid leukaemia, Di Guglielmo
 CC syndrome, congestive splenomegaly, Kala azar, sarcoidosis, primary
 CC splenic pancytopenia, disseminated fungus disease, malaria, military
 CC tuberculosis, fulminating septicaemia, pyridoxine deficiency, vitamin B12
 CC and folic acid deficiency, Diamond Blackfan anaemia, hypopigmentation
 CC disorders such as piebaldism, AIDS (acquired immune deficiency syndrome)
 CC and vitiligo. The present sequence is a PCR primer which is used for
 CC amplifying the 5' end of rat SCF cDNA. This sequence is used in the
 CC exemplification of the invention

XX SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 1.2%; Score 18; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 81;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAAGAAAAA 1496
 DB 20 CTAAGAAAAA 3

RESULT 120
 ABS73849/C
 ID ABS73849 standard; DNA; 20 BP.

AC ABS73849;

DT 05-DEC-2002 (first entry)

DE SCF universal oligonucleotide 220-7.

XX Stem cell factor; SCF; blood-forming system; blood cell disorder;
 KW haematopoietic system; metastatic carcinoma; acute leukaemia;
 KW multiple myeloma; Hodgkin's disease; lymphoma; malaria; vitiligo;
 KW refractory erythroid leukaemia; military tuberculosis; cytostatic;
 KW disseminated fungus disease; haematopoietic; tuberculous;
 KW antianaemic; antifungal; antimarial; dermatological; ss.

OS Synthetic.

XX EP1241258-A2.

PN 18-SEP-2002.

XX 04-OCT-1990; 2002EP-00008587.

PR 16-OCT-1989; 89US-00422383.

PR 11-JUN-1990; 90US-00537198.

PR 24-AUG-1990; 90US-00573616.

PR 28-SEP-1990; 90NO-US005548.

PR 01-OCT-1990; 90US-00589701.

PR 04-OCT-1990; 90EP-00310899.

PR 04-OCT-1990; 95EP-00105391.

XX (AMGE-) AMGEN INC.

XX Zeebo KM, Suggs SV, Bosselman RA, Martin FH;

XX

DR WPI; 2002-684093/74.

XX Production of a human stem cell factor (SCF) polypeptide for treating
 PT disorders involving blood cells, such as leukemia, comprises culturing
 PT mammalian cells comprising non-human SCF promoter DNA linked to DNA
 PT encoding the human SCF.

XX Example 3; Fig 12C; 120pp; English.

XX The present invention relates to novel stem cell factors (SCFs),
 CC polynucleotide sequences encoding the SCFs, and methods of producing
 CC them. SCFs are involved in the blood-forming (haematopoietic) system in
 CC mammals, particularly humans. The method of the invention is useful for
 CC the production of human SCF. The stem cell factors are useful to treat
 CC disorders involving blood cells e.g. metastatic carcinoma, acute
 CC leukaemia, multiple myeloma, Hodgkin's disease, lymphoma, refractory
 CC erythroid leukaemia, myeloid leukemia, disseminated fungus
 CC disease, malaria, and vitiligo. The present sequence representing a
 CC universal oligonucleotide for SCF DNA is used in the examples of the
 CC present invention

XX Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 1.2%; Score 18; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 81;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAAGAAAAA 1496
 DB 20 CTAAGAAAAA 3

RESULT 121

ABA05917/C
 ID ABA05917 standard; DNA; 20 BP.

AC ABA05917;

DT 05-MAR-2002 (first entry)

XX Hepatitis B virus diagnostic PCR primer SEQ ID NO 7.

XX Hepatitis B virus; HBV; infection; hepatocellular carcinoma; diagnosis;
 KW PCR primer; ss.

XX Hepatitis B virus.

XX EP1152063-A1.

XX 07-NOV-2001.

XX 03-MAY-2000; 2000EP-00109436.

XX 03-MAY-2000; 2000EP-00109436.

XX (DEKF-) DEUT KREBSFORSCHUNGSZENTRUM.

XX Schroeder KH, Koike K;

XX WPI; 2002-068256/10.

XX Diagnosing hepatitis B virus (HBV) infection stages and determining the
 PT risk for hepatocellular carcinoma, comprises identifying full length HBV
 PT transcripts and truncated HBV transcripts in a serum sample.

XX Example 1; Page 6; 25pp; English.

XX The invention relates to diagnosis of hepatitis B virus (HBV) infection
 CC stages comprising identification of full length HBV transcripts (I) and
 CC truncated HBV transcripts (II) in a serum sample, where the ratio of I:II
 CC is indicative of a particular infection stage. The method is useful for
 CC diagnosing HBV infection stages and determining the risk for developing
 CC hepatocellular carcinoma. The present sequence is that of a HBV

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CC diagnostic PCR primer, useful for the invention
XX
SQ Sequence 20 BP; 1 A; 2 C; 1 G; 16 T; 0 U; 0 Other;

Query Match      1.2%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1478 GCTAATAAAAAAAAAAAAAA 1495
DB 18 GCTAATAAAAAAAAAAAAAA 1

RESULT 122
ABZ89240
ID ABZ89240 standard; DNA; 20 BP.
XX
AC ABZ89240;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiqunone; antiinflammatory; antiasthmatic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
FN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
WPI; 2003-229219/22.
XX
Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiqunone.
XX
PS Disclosure; SEQ ID NO 4482; 872pp; English.
XX
The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiqunone. A composition of the invention
CC has antiinflammatory, antiasthmatic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiqunone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
```

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CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 18 A; 1 C; 0 G; 1 T; 0 U; 0 Other;

Query Match      1.2%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAAAAAATAAAAAAAAAAAAA 1496
DB 1 CTAAAAAATAAAAAAAAAAAAA 18

RESULT 123
ADE52461/C
ID ADE52461 standard; DNA; 20 BP.
XX
AC ADE52461;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stem cell factor (SCF) related DNA #32.
XX
KW Stem cell factor; SCF; haematopoietic activity; infertility;
KW intestinal damage; myeloproliferative disorder; leucopenia;
KW thrombocytopenia; anaemia; bone marrow transplant; immune deficiency;
KW neoplasia; nerve damage; osteoporosis; metastatic carcinoma; leukaemia;
KW milary tuberculosis; haematopoietic progenitor cell; ss.
XX
OS Synthetic.
XX
FN US2002031491-A1.
XX
PD 14-MAR-2002.
XX
PF 31-DEC-1998; 98US-00224683.
XX
PR 16-OCT-1989; 89US-00422383.
XX
PR 11-JUN-1990; 90US-00537198.
XX
PR 24-AUG-1990; 90US-00573616.
XX
PR 01-OCT-1990; 90US-00589701.
XX
PR 10-APR-1991; 91US-00684535.
XX
PR 25-NOV-1992; 92US-00982255.
XX
PR 21-DEC-1993; 93US-00172329.
XX
PR 24-MAY-1995; 95US-00449653.
XX
PR 12-JAN-1998; 98US-00005893.
XX
(ZSBB/) ZSEBO K M.
PA (BOSS/) BOSSELMAN R A.
PA (SUGG/) SUGGS S V.
PA (MART/) MARTIN F H.
XX
Zsebo KM, Bosseelman RA, Suggs SV, Martin FH;
XX
WPI; 2003-851459/79.
XX
New non-natural stem cell factor, useful for treating e.g. leucopenia or
PT immune deficiency, also related nucleic acid and antibodies.
XX
Disclosure; SEQ ID NO 33; 217pp; English.
XX
The invention relates to stem cell factor (SCF) polypeptides with
CC haematopoietic activity and the polynucleotides encoding them. The
CC polypeptides are used for treating infertility, intestinal damage,
CC myeloproliferative disorders, leucopenia, thrombocytopenia or anaemia,
CC for improving engraftment of bone marrow transplants, for enhancing bone
CC marrow recovery after radiotherapy or chemotherapy and in treatment of
CC immune deficiency, neoplasia, nerve damage, osteoporosis, metastatic
CC carcinoma, leukaemia and milary tuberculosis. The SCF polypeptides are
CC also used to expand haematopoietic progenitor cells for transplantation
CC and to prepare such cells for transfection with a gene. The SCF
CC polynucleotides can be used for recombinant expression of the
CC polypeptides and also as probes for mapping of the SCF gene, for
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CC identifying SCF-related diseases and as a marker for neighbouring genes.
 CC Antibodies raised against the polypeptides are useful in diagnosis and to
 CC remove SCF from blood. This sequence represents SCF related DNA of the
 CC invention.

XX SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
 Query Match 1.2%; Score 18; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 81;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAAAAAATAAAAAAAAA 1496
 DB 20 CTAAAAAATAAAAAAAAA 3

RESULT 124
 AAQ75713/C
 ID AAQ75713 standard; DNA; 21 BP.
 XX AC AAQ75713;
 XX DT 04-AUG-1995 (first entry)
 DE Reverse transcription primer used in cDNA analysis technique.
 XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 OS Synthetic.
 XX PN JP06303997-A.
 PD 01-NOV-1994.
 PF 16-APR-1993; 93JP-00112515.
 XX PR 16-APR-1993; 93JP-00112515.
 XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX DR WPI; 1995-018287/03.
 XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.
 XX PS Disclosure; Page 7; 11pp; Japanese.
 XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily

XX SQ Sequence 21 BP; 1 A; 0 C; 1 G; 19 T; 0 U; 0 Other;
 Query Match 1.2%; Score 18; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 89;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAAAAAATAAAAAAAAA 1496
 DB 19 CTAAAAAATAAAAAAAAA 2

RESULT 125
 AAQ75703/C
 ID AAQ75703 standard; DNA; 21 BP.
 XX AC AAQ75703;
 XX DT 04-AUG-1995 (first entry)
 DE Reverse transcription primer used in cDNA analysis technique.
 XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 OS Synthetic.
 XX PN JP06303997-A.
 PD 01-NOV-1994.
 PF 16-APR-1993; 93JP-00112515.
 XX PR 16-APR-1993; 93JP-00112515.
 XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX DR WPI; 1995-018287/03.

XX DT 04-AUG-1995 (first entry)
 XX DE Reverse transcription primer used in cDNA analysis technique.
 XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 OS Synthetic.
 XX PN JP06303997-A.
 PD 01-NOV-1994.
 PF 16-APR-1993; 93JP-00112515.
 XX PR 16-APR-1993; 93JP-00112515.
 XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX DR WPI; 1995-018287/03.
 XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.
 XX PS Disclosure; Page 7; 11pp; Japanese.
 XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily

XX SQ Sequence 21 BP; 1 A; 0 C; 3 G; 17 T; 0 U; 0 Other;
 Query Match 1.2%; Score 18; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 89;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAAAAAATAAAAAAAAA 1496
 DB 19 CTAAAAAATAAAAAAAAA 2

RESULT 126
 AAQ75714/C
 ID AAQ75714 standard; DNA; 21 BP.
 XX AC AAQ75714;
 XX DT 04-AUG-1995 (first entry)
 DE Reverse transcription primer used in cDNA analysis technique.
 XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 OS Synthetic.
 XX PN JP06303997-A.
 PD 01-NOV-1994.
 PF 16-APR-1993; 93JP-00112515.
 XX PR 16-APR-1993; 93JP-00112515.
 XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX DR WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 8; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 1.2%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAAAAAATAAAAAAAAAA 1496
Db 19 CTAAAAAATAAAAAAAAAA 2

RESULT 127
AAQ75705/c
ID AAQ75705 standard; DNA; 21 BP.
XX AC AAQ75705;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 1.2%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAAAAAATAAAAAAAAAA 1496
Db 19 CTAAAAAATAAAAAAAAAA 2

RESULT 128
AAQ75706/c
ID AAQ75706 standard; DNA; 21 BP.
XX AC AAQ75706;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 1.2%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAAAAAATAAAAAAAAAA 1496
Db 19 CTAAAAAATAAAAAAAAAA 2

RESULT 129
AAQ75707/c
ID AAQ75707 standard; DNA; 21 BP.
XX AC AAQ75707;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.

XX 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
PR 16-APR-1993; 93JP-00112515.
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
DR
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 2 A; 0 C; 2 G; 17 T; 0 U; 0 Other;
Query Match 1.2%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1479 CTAAAAAATAAAAAAAAAA 1496
Db 19 CTAAAAAATAAAAAAAAAA 2
RESULT 130
AAQ75710/c
ID AAQ75710 standard; DNA; 21 BP.
XX
AC AAQ75710;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
XX JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 2 A; 0 C; 2 G; 17 T; 0 U; 0 Other;
Query Match 1.2%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1479 CTAAAAAATAAAAAAAAAA 1496
Db 19 CTAAAAAATAAAAAAAAAA 2
RESULT 130
AAQ75710/c
ID AAQ75710 standard; DNA; 21 BP.
XX
AC AAQ75710;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
XX JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of

CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;
Query Match 1.2%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1479 CTAAAAAATAAAAAAAAAA 1496
Db 19 CTAAAAAATAAAAAAAAAA 2
RESULT 131
AAQ75709/c
ID AAQ75709 standard; DNA; 21 BP.
XX
AC AAQ75709;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
XX JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
Query Match 1.2%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1479 CTAAAAAATAAAAAAAAAA 1496
Db 19 CTAAAAAATAAAAAAAAAA 2
RESULT 132
AAQ75711/c
ID AAQ75711 standard; DNA; 21 BP.
XX
AC AAQ75711;
XX

```

DT 04-AUG-1995 (first entry)
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
XX 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;
    Query Match 1.2%; Score 18; DB 1; Length 21;
    Best Local Similarity 100.0%; Pred. NO. 89;
    Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1479 CTAAAAA1496
DB 19 CTAAAAA1496

RESULT 133
AAQ75550/c
ID AAQ75550 standard; DNA; 19 BP.
XX
AC AAQ75550;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
XX 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;
    Query Match 1.2%; Score 18; DB 1; Length 21;
    Best Local Similarity 100.0%; Pred. NO. 89;
    Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1479 CTAAAAA1496
DB 19 CTAAAAA1496

RESULT 133
AAQ75550/c
ID AAQ75550 standard; DNA; 19 BP.
XX
AC AAQ75550;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
XX 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 0 A; 2 C; 1 G; 17 T; 0 U; 0 Other;
    Query Match 1.2%; Score 17.4; DB 1; Length 20;
    Best Local Similarity 94.7%; Pred. NO. 1.1e+02;
    Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1478 GCTAAAAA1496
DB 19 GCTAAAAA1496

RESULT 134
AAQ75574/c
ID AAQ75574 standard; DNA; 20 BP.
XX
AC AAQ75574;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
XX 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 19 BP; 0 A; 1 C; 1 G; 17 T; 0 U; 0 Other;
    Query Match 1.2%; Score 17.4; DB 1; Length 19;
    Best Local Similarity 94.7%; Pred. NO. 95;
    Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1478 GCTAAAAA1496
DB 19 GCTAAAAA1496

RESULT 134
AAQ75574/c
ID AAQ75574 standard; DNA; 20 BP.
XX
AC AAQ75574;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
XX 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 0 A; 2 C; 1 G; 17 T; 0 U; 0 Other;
    Query Match 1.2%; Score 17.4; DB 1; Length 20;
    Best Local Similarity 94.7%; Pred. NO. 1.1e+02;
    Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1478 GCTAAAAA1496
DB 19 GCTAAAAA1496

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```

Db      19  |||||||
          GCAAAAAAAAAAAAAAAAAA 1

RESULT 135
AAQ75586/c
ID  AAQ75586 standard; DNA; 20 BP.
XX
AC  AAQ75586;
XX
DT  04-AUG-1995 (first entry)
XX
DE  Reverse transcription primer used in cDNA analysis technique.
XX
KW  Analysis; gene expression; reverse transcription; primer; cDNA;
KW  aggregate; restriction enzyme; ss.
XX
OS  Synthetic.
XX
PN  JP06303997-A.
XX
PD  01-NOV-1994.
XX
PF  16-APR-1993; 93JP-00112515.
XX
PR  16-APR-1993; 93JP-00112515.
XX
PA  (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR  WPI; 1995-018287/03.
XX
PT  Analysis of cDNA and gene expression - by amplification of mRNA followed
PT  by digestion with restriction enzymes.
XX
PS  Disclosure; Page 5; 11pp; Japanese.
XX
CC  A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC  double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC  labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC  and using the aggregate of mRNAs as the template for each reverse
CC  transcription primer; (b) digesting each of the prepared aggregates of
CC  the double-stranded cDNAs with restriction enzyme and; (c)
CC  electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC  method can be used to analyse gene expression rapidly and easily.
XX
SQ  Sequence 20 BP; 0 A; 2 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 1.2%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1478 GCTAAAAAAAAAAAAAAAAA 1496
Db 20 GCAAAAAAAAAAAAAAAAAA 2

RESULT 137
AAQ75562/c
ID  AAQ75562 standard; DNA; 20 BP.
XX
AC  AAQ75562;
XX
DT  04-AUG-1995 (first entry)
XX
DE  Reverse transcription primer used in cDNA analysis technique.
XX
KW  Analysis; gene expression; reverse transcription; primer; cDNA;
KW  aggregate; restriction enzyme; ss.
XX
OS  Synthetic.
XX
PN  JP06303997-A.
XX
PD  01-NOV-1994.
XX
PF  16-APR-1993; 93JP-00112515.
XX
PR  16-APR-1993; 93JP-00112515.
XX
PA  (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR  WPI; 1995-018287/03.
XX
PT  Analysis of cDNA and gene expression - by amplification of mRNA followed
PT  by digestion with restriction enzymes.
XX
PS  Disclosure; Page 5; 11pp; Japanese.
XX
CC  A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC  double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC  labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC  and using the aggregate of mRNAs as the template for each reverse
CC  transcription primer; (b) digesting each of the prepared aggregates of
CC  the double-stranded cDNAs with restriction enzyme and; (c)
CC  electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC  method can be used to analyse gene expression rapidly and easily.
XX
SQ  Sequence 20 BP; 1 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 1.2%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1478 GCTAAAAAAAAAAAAAAAAA 1496
Db 20 GATAAAAAAAAAAAAAAAAA 2

RESULT 136
AAQ75594/c
ID  AAQ75594 standard; DNA; 20 BP.
XX
AC  AAQ75594;
XX
DT  04-AUG-1995 (first entry)
XX
DE  Reverse transcription primer used in cDNA analysis technique.
XX
KW  Analysis; gene expression; reverse transcription; primer; cDNA;
KW  aggregate; restriction enzyme; ss.
XX
OS  Synthetic.
XX
PN  JP06303997-A.
XX

```

```

CC electrophoresing the digested aggregate of cDNAs in seprate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 0 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

Query Match      1.2%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1478 GCTAATAAAAAAAAAAAAAA 1496
Db 20 GCCAATAAAAAAAAAAAAAA 2

RESULT 138
AAQ75573/c
ID AAQ75573 standard; DNA; 20 BP.
XX
AC AAQ75573;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-075798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in seprate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match      1.2%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1478 GCTAATAAAAAAAAAAAAAA 1496
Db 19 GCCAATAAAAAAAAAAAAAA 1

RESULT 139
AAQ75590/c
ID AAQ75590 standard; DNA; 20 BP.
XX
AC AAQ75590;
XX
DT 04-AUG-1995 (first entry)
XX

```

```

XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-075798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in seprate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 1 A; 2 C; 0 G; 17 T; 0 U; 0 Other;

Query Match      1.2%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1478 GCTAATAAAAAAAAAAAAAA 1496
Db 20 GCTAATAAAAAAAAAAAAAA 2

RESULT 140
AAQ75582/c
ID AAQ75582 standard; DNA; 20 BP.
XX
AC AAQ75582;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed

```

```

PT by digestion with restriction enzymes.
PS Disclosure; Page 5; 1lpp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75796)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 2 A; 1 C; 0 G; 17 T; 0 U; 0 Other;
  Query Match 1.2%; Score 17.4; DB 1; Length 20;
  Best Local Similarity 94.7%; Pred. No. 1.1e+02;
  Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1478 GCTAAAAAATAAAAAAAAAA 1496
DB 20 GTTAAAAAATAAAAAAAAAA 2

RESULT 141
AAQ75571/c
ID AAQ75571 standard; DNA; 20 BP.
XX
XX AAQ75571;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; Gene expression; Reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 5; 1lpp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75796)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 0 A; 1 C; 2 G; 17 T; 0 U; 0 Other;
  Query Match 1.2%; Score 17.4; DB 1; Length 20;
  Best Local Similarity 94.7%; Pred. No. 1.1e+02;
  Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1478 GCTAAAAAATAAAAAAAAAA 1496
DB 20 GTTAAAAAATAAAAAAAAAA 2

Db 19 GCAAAAAAAAAAAAAAAAAA 1
  RESULT 142
  AAC83128/c
  ID AAC83128 standard; DNA; 20 BP.
  XX
  XX AAC83128;
  XX
  XX 23-FEB-2001 (first entry)
  XX
  XX Cell cycle regulatory gene related oligonucleotide SEQ ID 31.
  XX
  XX Cell cycle regulation; corn; transgenic plant; cyclin; maize; soybean;
  KW cyclin-dependent kinase; sunflower; sorghum; canola; wheat; alfalfa;
  KW cotton; rice; barley; millet; ss.
  XX
  XX Zea mays.
  XX
  XX WO200065040-A2.
  XX
  XX 02-NOV-2000.
  XX
  XX 13-APR-2000; 2000WO-US009975.
  XX
  XX 22-APR-1999; 99US-0130849P.
  XX
  XX (PION-) PIONEER HI-BRED INT INC.
  XX
  XX Helentjaris TG, Habben JE, Sun Y;
  XX
  XX WPI; 2000-687333/67.
  XX
  XX Nucleic acids useful for producing transgenic plants, preferably maize,
  PT with increased cell cycle gene activity, preferably activity of cyclin
  PT and/or cyclin-dependent kinase.
  XX
  XX Disclosure; Page 107; 122pp; English.
  XX
  XX Polynucleotide sequences AAC83101 - AAC83113 encode proteins AAB35794 -
  CC AAB35806 which are involved in regulating the cell cycle. The protein and
  CC DNA sequences have been isolated from Zea mays (corn), and the invention
  CC also includes oligonucleotides AAC83114 - AAC83139 which are related to
  CC the cell cycle polynucleotides. The cell cycle polynucleotide sequences
  CC are useful for producing transgenic plants such as maize, soybean,
  CC sunflower, sorghum, canola, wheat, alfalfa, cotton, rice, barley and
  CC millet with increased levels of cell cycle gene activity, such as
  CC activity of cyclin and cyclin-dependent kinases. The DNA sequences are
  CC also useful as probes for detecting deficiencies in the level of mRNA in
  CC screening for desired transgenic plants, for detecting mutations in the
  CC gene, for monitoring upregulation of expression or changes in enzyme
  CC activity in screening assays of compounds, for detecting any number of
  CC allelic variants, orthologs or paralogues of the gene, and site-directed
  CC mutagenesis in eukaryotic cells. The DNA sequences are also useful for
  CC recombinant expression of the encoded polypeptides and as immunogens for
  CC preparing and screening antibodies. A transgenic plant comprising an
  CC expression cassette including a cell cycle regulatory gene is useful for
  CC assaying enzyme agonists and antagonists, and as immunogens or antigens
  CC to obtain antibodies. The antibodies are useful in assaying expression
  CC levels of cell cycle regulatory proteins, for identifying and isolating
  CC nucleic acids from expression libraries, for identifying homologues of
  CC polypeptides from other species, and for purification of the proteins
  XX
  XX Sequence 20 BP; 2 A; 5 C; 11 G; 2 T; 0 U; 0 Other;
  SQ
  Query Match 1.2%; Score 17.4; DB 1; Length 20;
  Best Local Similarity 94.7%; Pred. No. 1.1e+02;
  Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 222 CCGCCGCCGCCGCCGCAT 240
DB 19 CAGCCGCCGCCGCCGCAT 1

```

PI	Wang Y, Zhang H, Li H;
XX	WPI; 2001-550442/62.
XX	Hepatitis E virus gene sequence and its application.
PT	Example 1; Page 15(Disclosure); 34pp; Chinese.
PS	The present invention relates to a novel nucleotide sequence and protein
XX	of a new hepatitis E virus HEV-T1 and the application of the nucleotide
CC	sequence and protein in diagnosing, preventing and treating hepatitis.
CC	The present sequence is a PCR primer described in the exemplification of
CC	the invention
XX	Sequence 20 BP; 7 A; 6 C; 6 G; 1 T; 0 U; 0 Other;
SQ	Query Match 1.2%; Score 17.4; DB 1; Length 20;
	Best Local Similarity 94.7%; Pred. No. 1.1e+02;
	Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	700 TGACTGCTGTGGTCCAGC 718
DB	20 TGACTGCTGTGGTCCAGC 2
RESULT 145	
ABZ85532	
ID	ABZ85532 standard; DNA; 20 BP.
XX	ABZ85532;
AC	17-OCT-2003 (first entry)
DT	Human oligonucleotide sequence.
DE	Human; antisense; lung dysfunction; nasal airway dysfunction;
XX	antiinflammatory steroid; ubiqunone; antiinflammatory; antiallergic;
KW	antiasmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW	antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW	adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW	lung inflammation; respiratory disease; ds.
OS	Homo sapiens.
XX	WO200285308-A2.
PX	31-OCT-2002.
PD	23-APR-2002; 2002WO-US013135.
PF	24-APR-2001; 2001US-0286137P.
XX	(EPIG-) EPIGENESIS PHARM INC.
XX	Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI	Miller S, Tang L, Shahabuddin S;
PI	WPI; 2003-229219/22.
DR	Pharmaceutical composition for treating ailments associated with impaired
XX	respiration, has oligo(s) antisense to specific gene(s) or its
PT	corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT	ubiquinone.
XX	Claim 15; SEQ ID NO 774; 872pp; English.
PS	The invention relates to a novel pharmaceutical composition, which has a
XX	first active agent comprising an oligonucleotide antisense to the
CC	initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC	5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC	junctions of genes encoding a polypeptide associated with lung and/or
CC	nasal airway dysfunction and a second active agent comprising an

PI	Wang Y, Zhang H, Li H;
XX	WPI; 2001-550442/62.
XX	Hepatitis E virus gene sequence and its application.
PT	Example 1; Page 15(Disclosure); 34pp; Chinese.
PS	The present invention relates to a novel nucleotide sequence and protein
XX	of a new hepatitis E virus HEV-T1 and the application of the nucleotide
CC	sequence and protein in diagnosing, preventing and treating hepatitis.
CC	The present sequence is a PCR primer described in the exemplification of
CC	the invention
XX	Sequence 20 BP; 7 A; 6 C; 6 G; 1 T; 0 U; 0 Other;
SQ	Query Match 1.2%; Score 17.4; DB 1; Length 20;
	Best Local Similarity 94.7%; Pred. No. 1.1e+02;
	Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	700 TGACTGCTGTGGTCCAGC 718
DB	20 TGACTGCTGTGGTCCAGC 2
RESULT 144	
AAI69675/c	
ID	AAI69675 standard; DNA; 20 BP.
XX	AAI69675;
AC	10-JAN-2002 (first entry)
DT	Hepatitis E virus HEV-T1 sequence related PCR primer #44.
DE	Hepatitis E virus; HEV-T1; hepatitis infection; PCR primer; ss.
XX	Unidentified.
OS	CN1300771-A.
PN	27-JUN-2001.
PD	23-DEC-1999; 99CN-00125741.
XX	23-DEC-1999; 99CN-00125741.
XX	(CHME-) CHINESE MEDICINE & BIOLOGIC PROD APPRAIS.
PA	Wang Y, Zhang H, Li H;
XX	WPI; 2001-550442/62.
DR	Hepatitis E virus gene sequence and its application.
XX	Example 1; Page 15(Disclosure); 34pp; Chinese.
PS	The present invention relates to a novel nucleotide sequence and protein
XX	of a new hepatitis E virus HEV-T1 and the application of the nucleotide
CC	sequence and protein in diagnosing, preventing and treating hepatitis.
CC	The present sequence is a PCR primer described in the exemplification of
CC	the invention
XX	Sequence 20 BP; 7 A; 6 C; 6 G; 1 T; 0 U; 0 Other;
SQ	Query Match 1.2%; Score 17.4; DB 1; Length 20;
	Best Local Similarity 94.7%; Pred. No. 1.1e+02;
	Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	700 TGACTGCTGTGGTCCAGC 718
DB	20 TGACTGCTGTGGTCCAGC 2
RESULT 144	
AAI69675/c	
ID	AAI69675 standard; DNA; 20 BP.
XX	AAI69675;
AC	10-JAN-2002 (first entry)
DT	Hepatitis E virus HEV-T1 sequence related PCR primer #40.
DE	Hepatitis E virus; HEV-T1; hepatitis infection; PCR primer; ss.
XX	Unidentified.
OS	CN1300771-A.
PN	27-JUN-2001.
PD	23-DEC-1999; 99CN-00125741.
XX	23-DEC-1999; 99CN-00125741.
XX	(CHME-) CHINESE MEDICINE & BIOLOGIC PROD APPRAIS.
PA	

CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences

XX
 SQ Sequence 20 BP; 17 A; 2 C; 1 G; 0 T; 0 U; 0 Other;

Query Match 1.2%; Score 17.4; DB 1; Length 20;
 Best Local Similarity 94.7%; Pred. No. 1.1e+02; Indels 0; Gaps 0;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1478 GCTAAAAAATAAAAAAAAAA 1496
 |||||
 DB 2 GCCAAAAAATAAAAAAAAAA 20

RESULT 146
 AAT94667/C
 ID AAT94667 standard; DNA; 18 BP.
 XX
 AC AAT94667;
 XX
 XX 27-MAR-1998 (first entry)
 DT
 XX Anchored poly(T) oligonucleotide polyT-Ancha.
 DE
 XX Flavonoid 3'-hydroxylase; pigmentation; flower colour; transgenic plant;
 KW snapdragon; primer; ss.
 KW
 XX Synthetic.
 OS
 XX WO9732023-A1.
 PN
 XX 04-SEP-1997.
 PD
 XX 28-FEB-1997; 97WO-AU000124.
 PF
 XX 01-MAR-1996; 96AU-00008386.
 PR
 XX (FLOR-) FLORIGENE LTD.
 PA
 XX Brugliera F, Holton TA, Michael MZ;
 PI
 XX WPI; 1997-448691/41.
 DR
 XX Novel flavonoid 3'-hydroxylase(s) from flowering plants - and
 PT corresponding DNA, used in the manipulation of pigmentation in plants.
 PT
 XX Example 15; Page 59; 234pp; English.
 PS
 XX Anchored poly(T) oligonucleotides polyT-ancha (AAT94667), polyT-anchC
 CC (AAT94668) and polyT-anchG (AAT94669) are complementary to the upstream
 CC region of a polyadenylation sequence. They were used to prime cDNA
 CC synthesis from snapdragon (Antirrhinum majus) petal and leaf RNA, and
 CC were also utilised in the PCR amplification of plant cytochrome P450
 CC sequences (see also AAT94670-73). A cDNA clone (see AAT94657) encoding
 CC flavonoid 3'-hydroxylase (see AAT94657) was isolated using a differential
 CC display approach. This can be used to manipulate the pigmentation of
 CC transgenic plants
 CC
 XX
 SQ Sequence 18 BP; 1 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 1.1%; Score 17; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 1e+02; Indels 0; Gaps 0;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAAAAAAA 1496
 |||||
 DB 18 TAAAAAATAAAAAAAAAA 2

RESULT 147
 AAV54170/C
 ID AAV54170 standard; cDNA; 18 BP.
 XX
 AC AAV54170;
 XX
 DT 21-DEC-1998 (first entry)
 XX
 DE Nucleotide sequence PCR primer 7.
 XX
 KW PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
 KW immunohistological staining.
 XX
 OS Synthetic.
 OS
 PN WO9839437-A1.
 PN
 XX 11-SEP-1998.
 PD
 XX 05-MAR-1998; 98WO-JP000905.
 PF
 XX 05-MAR-1997; 97JP-00050302.
 PR
 XX (KYOW) KYOWA HAKKO KOGYO KK.
 PA
 XX Sakaki Y;
 PI
 XX WPI; 1998-495844/42.
 DR
 XX Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
 PT treating diseases associated with apoptosis.
 PT
 XX Example 1; Page 49; 70pp; Japanese.
 PS
 XX This is the nucleotide sequence of a PCR primer used in the method of the
 CC invention, involving the use of novel apoptosis-related DNAs and
 CC proteins. The inventions can be used as diagnostic reagents for apoptosis
 CC e.g. (monoclonal) antibodies for the protein, as a reagent in
 CC immunohistological staining, as apoptosis inhibitors. It can also be used
 CC for treatment of apoptosis-related diseases
 CC
 XX
 SQ Sequence 18 BP; 1 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 1.1%; Score 17; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1e+02; Indels 0; Gaps 0;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAAAAAATAAAAAAAAAA 1495
 |||||
 DB 18 CTAAAAAATAAAAAAAAAA 2

RESULT 148
 AAV16008
 ID AAV16008 standard; DNA; 18 BP.
 XX
 AC AAV16008;
 XX
 DT 21-MAY-1998 (first entry)
 XX
 DE PCR primer D-R used to identify Sox-3 gene mutations in mice.
 DE
 KW Mutation; Sox-3; ENU mutagenesis; mutational screening; recessive;
 KW single strand conformation polymorphism; SSCP; phenotypic alteration;
 KW PCR primer; amplify; ss.

XX OS Synthetic.
 XX OS Mus sp.
 XX PN WO9744485-A1.
 XX PD 27-NOV-1997.
 XX PF 16-MAY-1997; 97WO-GB001354.
 XX PR 17-MAY-1996; 96GB-00010355.
 XX PA (HEXA-) HEXAGEN TECHNOLOGY LTD.
 XX PI Goodfellow PN;
 XX XX WPI; 1998-018536/02.
 XX DR Identification of mutation(s) in genes of interest - without prior
 XX PT observation of phenotypic alteration in the mutated organism or cell.
 XX PS Example 4; Page 41; 56pp; English.
 XX XX PCR primers AAV16001-18 were used to identify mutations in Sox-3 using
 CC the method of the invention. The primers are located throughout the gene
 CC and are unique to Sox-3. The method comprises testing a nucleic acid
 CC sample from a mutated organism for a mutation in a gene of interest
 CC without the prior observation of a phenotypic alteration in the mutated
 CC organism resulting from the mutation. Sox-3 is a member of the Sox gene
 CC family, a family of about 20 genes which all encode a "HMG" box, which is
 CC a DNA-binding domain. Mice were mutagenised using ENU mutagenesis. The
 CC mutagenised mice were tested by PCR with each primer set and fluorescent
 CC single strand conformation polymorphism (SSCP), which identifies mice
 CC carrying mutations in Sox-3. The method provides mutational screening
 CC based on genomic and genetic techniques rather than on phenotypic
 CC observation. The method identifies and characterises genes via
 CC mutagenesis to identify genes encoding products which may have
 CC therapeutic benefit. The method also identifies the presence of mutations
 CC in a gene which do not rely solely upon prior matching of a gene with a
 CC disease. Heterozygotic organisms can also be screened to identify those
 CC carrying a mutation in a copy of a gene of interest even though the gene
 CC may be recessive and therefore causes no phenotypic alteration
 XX XX
 XX SQ Sequence 18 BP; 1 A; 6 C; 11 G; 0 T; 0 U; 0 Other;
 Query Match 1.1%; Score 17; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 25 CGCGCGCGACGCGCGC 41
 DB 2 CGCGCGCGACGCGCGC 18
 RESULT 149
 AAX18373/c
 ID AAX18373 standard; DNA; 18 BP.
 XX AC AAX18373;
 XX XX
 XX DT 11-MAY-1999 (first entry)
 XX DE RT-PCR primer of the invention SEQ ID 14.
 XX KW RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
 XX OS Synthetic.
 XX PN JP11032765-A.
 XX XX 09-FEB-1999.
 XX XX 18-JUL-1997; 97JJP-00208312.
 XX PF

XX PR 18-JUL-1997; 97JJP-00208312.
 XX XX (TAKI) TAKARA SHUZO CO LTD.
 XX XX WPI; 1999-183822/16.
 XX XX Peptides having at least two new nucleotides - useful as primers in RT-PCR.
 XX PT
 XX PS Disclosure; Page 11; 19pp; Japanese.
 XX XX This sequence represents a primer of the invention. The invention relates
 CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
 CC -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
 CC a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
 CC natural number indicating the repetition of alpha; beta, delta = V or N;
 CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
 CC thymine; gamma = thymine; k = natural number of 3 or over indicating the
 CC repetition of gamma, in which thymine expressed by gamma is composed of
 CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
 CC useful as primers for RT-PCR and determination of base sequences. The new
 CC sequences allow for reproductive and highly efficient analysis of gene
 CC sequences
 XX SQ Sequence 18 BP; 1 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
 Query Match 1.1%; Score 17; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1480 TAAAAAATAAAAAA 1496
 DB 17 TAAAAAATAAAAAA 1
 RESULT 150
 AAX18372/c
 ID AAX18372 standard; DNA; 18 BP.
 XX AC AAX18372;
 XX XX
 XX DT 11-MAY-1999 (first entry)
 XX DE RT-PCR primer of the invention SEQ ID 13.
 XX KW RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
 XX OS Synthetic.
 XX PN JP11032765-A.
 XX XX 09-FEB-1999.
 XX XX 18-JUL-1997; 97JJP-00208312.
 XX PR 18-JUL-1997; 97JJP-00208312.
 XX XX (TAKI) TAKARA SHUZO CO LTD.
 XX PA WPI; 1999-183822/16.
 XX DR Peptides having at least two new nucleotides - useful as primers in RT-PCR.
 XX PT
 XX PS Disclosure; Page 11; 19pp; Japanese.
 XX XX This sequence represents a primer of the invention. The invention relates
 CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
 CC -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
 CC a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
 CC natural number indicating the repetition of alpha; beta, delta = V or N;
 CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or

CC thymine; gamma = thymine; k = natural number of 3 or over indicating the
 CC repetition of gamma, in which thymine expressed by gamma is composed of
 CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
 CC useful as primers for RT-PCR and determination of base sequences. The new
 CC sequences allow for reproductive and highly efficient analysis of gene
 CC sequences
 XX
 SQ Sequence 18 BP; 2 A; 0 C; 0 G; 16 T; 0 U; 0 Other;
 Query Match 1.1%; Score 17; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1480 TAAAAAAAAAAAAAAAAA 1496
 DB 17 TAAAAAAAAAAAAAAAAA 1
 RESULT 151
 AAZ90640/C
 ID AAZ90640 standard; DNA; 18 BP.
 XX
 AC AAZ90640;
 XX
 DT 13-JUN-2000 (first entry)
 XX
 DE Human adipose tissue gene amplifying primer #1.
 XX
 KW Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
 KW arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
 OS Homo sapiens.
 XX
 PN JP2000037190-A.
 XX
 PD 08-FEB-2000.
 XX
 PF 23-JUL-1998; 98JP-00225228.
 XX
 PR 23-JUL-1998; 98JP-00225228.
 XX
 PA (NIPPON) JAPAN TOBACCO INC.
 XX
 DR WPI; 2000-306578/27.
 XX
 PT A physiologically active protein specifically derived from mammal tissue.
 PS Example 2; Page 18; 50pp; Japanese.
 XX
 CC The invention relates to identification of genes and proteins of adipose
 CC tissue relating to obesity, particularly complications of visceral
 CC obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
 CC hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
 CC proteins (AAZ90631-633) are used in the genetic diagnosis, prevention
 CC and treatment of adipose tissue related diseases. Sequences AAZ90640-51
 CC represent PCR primers amplifying the human adipose tissue genes
 XX
 SQ Sequence 18 BP; 1 A; 0 C; 2 G; 15 T; 0 U; 0 Other;
 Query Match 1.1%; Score 17; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1479 CTAAAAAAAAAAAAAAAAA 1495
 DB 18 CTAAAAAAAAAAAAAAAAA 2
 RESULT 152
 AAZ43267
 ID AAZ43267 standard; DNA; 18 BP.
 XX
 AC AAZ43267;
 XX

XX
 DT 11-FEB-2000 (first entry)
 XX
 DE Murine Sox3 gene PCR primer 8.
 XX
 KW Screening; mutation; treatment; disease; drug discovery; PCR primer; ss.
 XX
 OS Mus musculus.
 XX
 PN US5994075-A.
 XX
 PD 30-NOV-1999.
 XX
 PF 16-MAY-1997; 97US-00857946.
 XX
 PR 17-MAY-1996; 96US-0017824P.
 XX
 PA (HEXA-) HEXAGEN TECHNOLOGY LTD.
 XX
 PI Goodfellow PN;
 XX
 DR WPI; 2000-038255/03.
 XX
 PT Identifying a mutation in a gene of interest in an organism useful for
 PT identifying genes encoding products which may have therapeutic benefits.
 XX
 PS Example 5; Col 63-64; 70pp; English.
 XX
 CC This invention describes a novel mutational screening method based on
 CC genomic and genetic techniques to identify and characterize a mutation in
 CC a gene of interest without first selecting a phenotypic characteristic.
 CC The screening methods are useful for identifying genes encoding products
 CC which may have therapeutic benefit for treating human or animal diseases.
 CC The method can be used for the DNA mutation screening of a class or a
 CC family of genes providing a rapid assay for identifying mutant genes. The
 CC methods produce organisms which can be used for drug discovery e.g.
 CC providing a model for the study and treatment of a disease state, allow
 CC in vitro assessment of drug activity and interbreeding of mutants which
 CC allow investigation of gene interactions in the overall phenotype. A
 CC range of phenotypes associated with different mutations, and specified
 CC mutations in a gene of interest can be determined. The method can be
 CC adapted to screen for a mutation in two or more genes of interest in an
 CC organism. The methods allow mutations in a gene of interest to be
 CC identified without having to rely on matching a gene with a disease.
 CC AAZ43260-243421 represent PCR primers used in the method of the invention
 XX
 SQ Sequence 18 BP; 1 A; 6 C; 11 G; 0 T; 0 U; 0 Other;
 Query Match 1.1%; Score 17; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 25 CGCGCGCGCGCGCGCGCG 41
 DB 2 CGCGCGCGCGCGCGCGCG 18
 RESULT 153
 AA05252
 ID AA05252 standard; DNA; 18 BP.
 XX
 AC AA05252;
 XX
 DT 19-MAY-2000 (first entry)
 XX
 DE PCR primer D-R used in Sox-3 amplimer generation.
 XX
 KW PCR primer; Sox-2; Sox-3; T gene; Tyrosinase; MGF; Sry; C-kit; Tryp-1;
 KW Pax-6; mutation detection; therapeutic target identification; mouse;
 KW mast cell growth factor; ss.
 XX
 OS Mus sp.
 XX

PN US6015670-A.
 XX 18-JAN-2000.
 XX 14-NOV-1997; 97US-00970740.
 PF 17-MAY-1996; 96US-0017824P.
 PR 16-MAY-1997; 97US-00857946.
 XX (HEXA-) HEXAGEN TECHNOLOGY LTD.
 XX Goodfellow PN;
 XX WPI; 2000-181139/16.
 XX Detecting mutations in selected genes, useful e.g. for identifying
 PT therapeutic targets or products, by analyzing DNA in mutated embryonic
 PT stem cells without phenotypic characterization.
 XX
 PS Example 5; Col 31; 66pp; English.
 XX
 CC PCR primers AAA05245-A05406 are used to generate amplicons from the mouse
 CC Sox-3 gene, Sox-2 gene, T gene, tyrosinase gene, Tryp-1 gene, Sry gene,
 CC MGF (maest cell growth factor) gene, c-kit gene, and the Pax-6 gene. The
 CC primers are used in a method for the identification of a mutation in a
 CC selected gene in a tissue without the prior observation of a phenotypic
 CC alteration in the mutated organism or cell. The method is used to
 CC identify mutations in a selected gene that encode products of potential
 CC therapeutic activity or that are potential targets, particularly where
 CC the gene of interest has been identified as a candidate gene by
 CC positional cloning. Other applications are determining functions of genes
 CC in a particular gene and identification of particular mutations. Animals
 CC containing an identified mutation are used as models for studying
 CC diseases or their treatment, and cells from them for in vitro assessment
 CC of drug action. Interbreeding of mutant mice is used to investigate
 CC genetic interaction in the overall phenotype
 XX
 XX Sequence 18 BP; 1 A; 6 C; 11 G; 0 T; 0 U; 0 Other;
 SQ
 Query Match 1.1%; Score 17; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 25 CGCGCGCGGACGCGCGG 41
 DB 2 CGCGCGCGGACGCGCGG 18
 RESULT 154
 AAQ75552/c
 ID AAQ75552 standard; DNA; 19 BP.
 XX
 AC AAQ75552;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KW Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 PN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-00112515.
 XX
 PR 16-APR-1993; 93JP-00112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 DR WPI; 1995-018287/03.
 XX
 XX Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.
 XX
 PS Disclosure; Page 5; 11pp; Japanese.
 XX
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX
 XX Sequence 19 BP; 1 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
 SQ
 Query Match 1.1%; Score 17; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1480 TAAAAAATAAAAAA 1496
 DB 18 TAAAAAATAAAAAA 2
 RESULT 155
 AAQ75553/c
 ID AAQ75553 standard; DNA; 19 BP.
 XX
 AC AAQ75553;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KW Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 PN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-00112515.
 XX
 PR 16-APR-1993; 93JP-00112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 DR WPI; 1995-018287/03.
 XX
 XX Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.
 XX
 PS Disclosure; Page 5; 11pp; Japanese.
 XX
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX
 XX Sequence 19 BP; 1 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
 SQ
 Query Match 1.1%; Score 17; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;

XX WPI; 1995-018287/03.
 XX
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.
 XX
 PS Disclosure; Page 5; 11pp; Japanese.
 XX
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX
 XX Sequence 19 BP; 2 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
 SQ
 Query Match 1.1%; Score 17; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1480 TAAAAAATAAAAAA 1496
 DB 18 TAAAAAATAAAAAA 2
 RESULT 155
 AAQ75553/c
 ID AAQ75553 standard; DNA; 19 BP.
 XX
 AC AAQ75553;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KW Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 PN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-00112515.
 XX
 PR 16-APR-1993; 93JP-00112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 DR WPI; 1995-018287/03.
 XX
 XX Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.
 XX
 PS Disclosure; Page 5; 11pp; Japanese.
 XX
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX
 XX Sequence 19 BP; 1 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
 SQ
 Query Match 1.1%; Score 17; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;

CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily

XX SQ Sequence 20 BP; 1 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAAAAAAA 1496
 |||||
 Db 18 TAAAAAATAAAAAAAAAA 2

RESULT 159
 AAQ75579/c
 ID AAQ75579 standard; DNA; 20 BP.

XX AC AAQ75579;
 XX DT 04-AUG-1995 (first entry)
 XX DE Reverse transcription primer used in cDNA analysis technique.
 XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
 XX KW aggregate; restriction enzyme; ss.
 XX OS Synthetic.
 XX PN JP06303997-A.
 XX PD 01-NOV-1994.
 XX PF 16-APR-1993; 93JP-00112515.
 XX PR 16-APR-1993; 93JP-00112515.
 XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX DR WPI; 1995-018287/03.
 XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 XX PT by digestion with restriction enzymes.
 XX PS Disclosure; Page 5; 11pp; Japanese.

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily

XX SQ Sequence 20 BP; 1 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAAAAAAA 1496
 |||||
 Db 18 TAAAAAATAAAAAAAAAA 2

RESULT 161
 AAQ75588/c
 ID AAQ75588 standard; DNA; 20 BP.

XX AC AAQ75588;
 XX DT 04-AUG-1995 (first entry)
 XX DE Reverse transcription primer used in cDNA analysis technique.
 XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
 XX KW aggregate; restriction enzyme; ss.
 XX OS Synthetic.
 XX PN JP06303997-A.
 XX PD 01-NOV-1994.
 XX PF 16-APR-1993; 93JP-00112515.
 XX PR 16-APR-1993; 93JP-00112515.
 XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

Query Match 1.1%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAAAAAAA 1496
 |||||
 Db 18 TAAAAAATAAAAAAAAAA 2

RESULT 160
 AAQ75589/c
 ID AAQ75589 standard; DNA; 20 BP.

XX AC AAQ75589;
 XX DT 04-AUG-1995 (first entry)
 XX DE Reverse transcription primer used in cDNA analysis technique.
 XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
 XX KW aggregate; restriction enzyme; ss.
 XX OS Synthetic.
 XX PN JP06303997-A.
 XX PD 01-NOV-1994.
 XX PF 16-APR-1993; 93JP-00112515.
 XX PR 16-APR-1993; 93JP-00112515.
 XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

DR WPI; 1995-018287/03.
 XX Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.
 PT
 PS Disclosure; Page 5; 11pp; Japanese.
 XX
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX
 SQ Sequence 20 BP; 2 A; 1 C; 0 G; 17 T; 0 U; 0 Other;
 Query Match 1.1%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1480 TAAAAAAAAAAAAAAAAA 1496
 DB 18 TAAAAAAAAAAAAAAAAA 2
 RESULT 162
 AAQ75581/c
 ID AAQ75581 standard; DNA; 20 BP.
 XX
 AC AAQ75581;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KW Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 OS Synthetic.
 XX
 PN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-00112515.
 XX
 PR 16-APR-1993; 93JP-00112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 DR WPI; 1995-018287/03.
 XX
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.
 XX
 PS Disclosure; Page 5; 11pp; Japanese.
 XX
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX
 SQ Sequence 20 BP; 2 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
 Query Match 1.1%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1480 TAAAAAAAAAAAAAAAAA 1496
 DB 18 TAAAAAAAAAAAAAAAAA 2
 RESULT 164
 AAQ75580/c
 ID AAQ75580 standard; DNA; 20 BP.
 XX
 AC AAQ75580;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KW Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 OS Synthetic.
 XX

OY 1480 TAAAAAAAAAAAAAAAAA 1496
 DB 18 TAAAAAAAAAAAAAAAAA 2
 RESULT 163
 AAQ75583/c
 ID AAQ75583 standard; DNA; 20 BP.
 XX
 AC AAQ75583;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KW Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 OS Synthetic.
 XX
 PN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-00112515.
 XX
 PR 16-APR-1993; 93JP-00112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 DR WPI; 1995-018287/03.
 XX
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.
 XX
 PS Disclosure; Page 5; 11pp; Japanese.
 XX
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX
 SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
 Query Match 1.1%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1480 TAAAAAAAAAAAAAAAAA 1496
 DB 18 TAAAAAAAAAAAAAAAAA 2
 RESULT 164
 AAQ75580/c
 ID AAQ75580 standard; DNA; 20 BP.
 XX
 AC AAQ75580;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KW Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 OS Synthetic.
 XX

PN JP06303997-A.
 XX 01-NOV-1994.
 XX 16-APR-1993; 93JP-00112515.
 PF 16-APR-1993; 93JP-00112515.
 PR 16-APR-1993; 93JP-00112515.
 XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX WPI; 1995-018287/03.
 DR Analysis of cDNA and gene expression - by amplification of mRNA followed
 XX by digestion with restriction enzymes.
 PT Disclosure; Page 5; 11pp; Japanese.
 PS
 XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-075798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX
 SQ Sequence 20 BP; 3 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
 Query Match 1.1%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1480 TAAAAA AAAAAAAAAA 1496
 DB 18 TAAAAA AAAAAAAAAA 2

RESULT 165
 AAQ75587/C
 ID AAQ75587 standard; DNA; 20 BP.
 XX
 AC AAQ75587;
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KW Analysis; gene expression; reverse transcription; primer; cDNA;
 XX aggregate; restriction enzyme; ss.
 OS Synthetic.
 XX
 SS JP06303997-A.
 PN 01-NOV-1994.
 PD 16-APR-1993; 93JP-00112515.
 PF 16-APR-1993; 93JP-00112515.
 PR 16-APR-1993; 93JP-00112515.
 XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX WPI; 1995-018287/03.
 DR Analysis of cDNA and gene expression - by amplification of mRNA followed
 XX by digestion with restriction enzymes.
 PT Disclosure; Page 5; 11pp; Japanese.
 PS
 XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-075798)
 CC and using the aggregate of mRNAs as the template for each reverse

CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX
 SQ Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;
 Query Match 1.1%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1480 TAAAAA AAAAAAAAAA 1496
 DB 18 TAAAAA AAAAAAAAAA 2

RESULT 166
 AAQ7752/C
 ID AAQ7752 standard; DNA; 20 BP.
 XX
 AC AAQ7752;
 DT 07-DEC-1998 (first entry)
 XX
 DE Phosphorothioate oligonucleotide.
 XX
 KW phosphorothioate; sulphurisation; heterocycle; automated synthesis;
 KW antisense; EDITH; Beaucage reagent; ss.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT misc_feature 1..20
 FT /*tag= a
 FT /note= "phosphorothioate internucleotide linkages"
 XX
 PN W09741130-A2.
 XX
 PD 06-NOV-1997.
 XX
 PF 29-APR-1997; 97WO-US007118.
 XX
 PR 30-APR-1996; 96US-00641920.
 XX
 PA (MINU) UNIV MINNESOTA.
 PA (LOU) UNIV LOUISIANA STATE & AGRIC.
 XX
 PI Barany G, Musier-Forsyth K, Xu Q, Chen L, Hammer RP;
 XX WPI; 1997-549671/50.
 DR
 XX Sulphurisation of phosphorus-containing compounds, e.g.
 PT oligo:nucleotide(s) - by contacting the compound with a di:sulphide-
 PT containing five-membered heterocycle.
 XX
 PS Example 7; Page 30; 51pp; English.
 XX
 CC The present invention provides a method for sulphurising phosphorus-
 CC containing compounds. It comprises contacting the phosphorus-containing
 CC compound which a 1,2,4-dithiazolidine-2,5-dione compound or a 3-
 CC substituted-1,2,4-dithiazolin-5-one compound. The method is especially
 CC useful for incorporation of phosphorothioate linkages into biologically
 CC important molecules such as DNA, RNA and phosphopeptides. Molecules
 CC containing such linkages are useful e.g. as antisense compounds for
 CC inhibiting gene expression, as reagents for studying DNA-protein or RNA-
 CC protein interactions, or as catalytic RNA. The present sequence
 CC represents an oligonucleotide with phosphorothioate linkages prepared by
 CC the method of the invention
 XX
 SQ Sequence 20 BP; 1 A; 0 C; 0 G; 0 T; 19 U; 0 Other;
 Query Match 1.1%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;

		Matches	17;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1480	TAAAAAAAAAAAAAAAAA 1496									
Db	20	TAAAAAAAAAAAAAAAAA 4									
RESULT 167											
ABZ89546											
ID	ABZ89546	standard; DNA; 20 BP.									
XX	AC	ABZ89546;									
XX	DT	17-OCT-2003 (first entry)									
XX	DE	Human oligonucleotide sequence.									
XX	KW	Human; antisense; lung dysfunction; nasal airway dysfunction;									
XX	KW	antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;									
XX	KW	antiallergic; hypotensive; immunosuppressive; cytotstatic; gene therapy;									
XX	KW	antisense gene therapy; respiratory; lung; adenosine sensitivity;									
XX	KW	adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;									
XX	KW	lung inflammation; respiratory disease; ds.									
OS	Homo sapiens.										
XX	XX	WO200285308-A2.									
PD	31-OCT-2002.										
XX	23-APR-2002; 2002WO-US013135.										
XX	24-APR-2001; 2001US-0286137P.										
XX	(EPIG-) EPIGENESIS PHARM INC.										
PI	Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;										
PI	Miller S, Tang L, Shahabuddin S;										
XX	WPI; 2003-229219/22.										
XX	Pharmaceutical composition for treating ailments associated with impaired										
PT	respiration, has oligo(s) antisense to specific gene(s) or its										
PT	corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or										
PT	ubiquinone.										
PS	Disclosure; SEQ ID NO 4788; 872pp; English.										
XX	The invention relates to a novel pharmaceutical composition, which has a										
CC	first active agent comprising an oligonucleotide antisense to the										
CC	initiation codon, coding region, 5' or 3' end genomic flanking regions,										
CC	5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of										
CC	junctions of genes encoding a polypeptide associated with lung and/or										
CC	nasal airway dysfunction and a second active agent comprising an										
CC	antiinflammatory steroid and ubiquinone. A composition of the invention										
CC	has antiinflammatory, antiallergic, antiasthmatic, hypotensive,										
CC	immunosuppressive, and cytostatic activity. The composition may have a										
CC	use in antisense gene therapy. The composition is useful for treating or										
CC	preventing a respiratory, lung or malignant disease or condition, also										
CC	for enhancing the prophylactic or therapeutic respiratory effect of an										
CC	antiinflammatory steroid in a subject, for reducing or depleting levels										
CC	of, or reducing sensitivity to adenosine, reducing levels of adenosine										
CC	receptor, producing bronchodilation, increasing levels of ubiquinone or										
CC	lung surfactant in a subject's tissue, or treating bronchoconstriction,										
CC	lung inflammation, lung allergies, or a respiratory disease or condition.										
CC	Note: The sequence data for this patent is not represented in the printed										
CC	specification, but was obtained in electronic format directly from WIPO										
CC	at ftp.wipo.int/pub/published_pct_sequences										
XX	Sequence 20 BP; 18 A; 0 C; 0 G; 2 T; 0 U; 0 Other;										
Query Match											
Best Local Similarity 1.1%; Score 17; DB 1; Length 20;											
Pred. No. 1.2e+02;											

Query Match 1.1%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;

```

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAAA 1496
    |||||
Db 1 TAAAAAAAAAAAAA 17

RESULT 169
ABZ89179
ID ABZ89179 standard; DNA; 20 BP.
XX
AC ABZ89179;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiqunone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; lung; adenosine sensitivity;
KW lung inflammation; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIC-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiqunone.
XX
PS Disclosure; SEQ ID NO 4421; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiqunone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiqunone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 19 A; 0 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 1.1%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAAA 1496
    |||||
Db 1 TAAAAAAAAAAAAA 17

RESULT 170
ABZ92865
ID ABZ92865 standard; DNA; 20 BP.
XX
AC ABZ92865;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiqunone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; lung; adenosine sensitivity;
KW lung inflammation; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIC-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiqunone.
XX
PS Disclosure; SEQ ID NO 8107; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiqunone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiqunone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 18 A; 0 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 1.1%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;

```

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAAA 1496
 |||||
 Db 4 TAAAAAAAAAAAAA 20

RESULT 171
 ABZ89703
 ID ABZ89703 standard; DNA; 20 BP.
 XX AC ABZ89703;
 XX DT 17-OCT-2003 (first entry)
 XX DE Human oligonucleotide sequence.
 XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.
 XX OS Homo sapiens.
 XX PN WO200285308-A2.
 XX PD 31-OCT-2002.
 XX PF 23-APR-2002; 2002WO-US013135.
 XX PR 24-APR-2001; 2001US-0286137P.
 XX PA (EPIG-) EPIGENESIS PHARM INC.
 XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 XX WPI; 2003-229219/22.
 XX PT Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.
 XX PS Disclosure; SEQ ID NO 4945; 872pp; English.
 XX CC The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 20 BP; 16 A; 0 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 1.1%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAAA 1496
 |||||
 Db 4 TAAAAAAAAAAAAA 20

RESULT 172
 ABZ88694
 ID ABZ88694 standard; DNA; 20 BP.
 XX AC ABZ88694;
 XX DT 17-OCT-2003 (first entry)
 XX DE Human oligonucleotide sequence.
 XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.
 XX OS Homo sapiens.
 XX PN WO200285308-A2.
 XX PD 31-OCT-2002.
 XX PF 23-APR-2002; 2002WO-US013135.
 XX PR 24-APR-2001; 2001US-0286137P.
 XX PA (EPIG-) EPIGENESIS PHARM INC.
 XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 XX WPI; 2003-229219/22.
 XX PT Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.
 XX PS Disclosure; SEQ ID NO 3936; 872pp; English.
 XX CC The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 20 BP; 17 A; 0 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 1.1%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;

```
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAAAAAAA 1496
Db 3 TAAAAAAAAAAAAAAAAA 19

RESULT 173
ABZ89014
ID ABZ89014 standard; DNA; 20 BP.
XX
AC ABZ89014;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiqunone; antiinflammatory; antiallergic;
KW antiaesthetic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiqunone.
XX
PS Disclosure; SEQ ID NO 4256; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding regions, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiqunone. A composition of the invention
CC has antiinflammatory, antiallergic, antiaesthetic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiqunone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 16 A; 2 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 1.1%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAATAAAAAAAAAAAAAA 1495
Db 4 CTAATAAAAAAAAAAAAAA 20

RESULT 174
AAD44128
ID AAD44128 standard; DNA; 18 BP.
XX
AC AAD44128;
XX
DT 13-DEC-2002 (first entry)
XX
DE PCR primer #3 designed to bind human MMP PPR region.
XX
KW Sequential consensus region-directed amplification; gene expression;
KW disease diagnosis; gene analysis; human; matrix metalloproteinase; MMP;
KW propeptide region; PPR; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN US6277571-B1.
XX
PD 21-AUG-2001.
XX
PF 30-SEP-1998; 98US-00163485.
XX
PR 03-OCT-1997; 97US-00943162.
XX
PR 03-OCT-1997; 97US-0108152P.
XX
PA (UYVI-) UNIV VIRGINIA COMMONWEALTH INTELLECTUAL.
XX
PI Fillmore H, Broadus W, Gillies G;
XX
DR WPI; 2002-412824/44.
XX
PT Sequential consensus region-directed amplification for sorting mixture of
PT DNAs into 2 or more subsets or distinguishing gene expression patterns in
PT 2 samples, useful for disease diagnosis and gene analysis.
XX
PS Example; Col 12; 19pp; English.
XX
CC The invention relates to a method of sequential consensus region-directed
CC amplification for sorting a mixture of DNAs into 2 or more subsets or
CC distinguishing gene expression patterns in 2 samples. The methods, kits
CC and oligonucleotides are useful for sorting a mixture of DNAs into 2 or
CC more subsets or distinguishing gene expression patterns in 2 samples e.g.
CC for disease diagnosis and gene analysis. The present sequence is a PCR
CC primer designed to bind to human matrix metalloproteinase (MMP)
CC propeptide region (PPR). This primer is used to illustrate the method of
CC the invention
XX
SQ Sequence 18 BP; 6 A; 2 C; 5 G; 3 T; 0 U; 2 Other;

Query Match 1.1%; Score 16.6; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.2e+02;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 599 AAGGATGTGAAGCAGTTC 616
Db 1 AAGGATGTNAGCAGTTC 18

RESULT 175
AAT69640/c
ID AAT69640 standard; DNA; 19 BP.
XX
AC AAT69640;
XX
DT 20-FEB-1998 (first entry)
XX
```


DE Telomerase Oligo-dT-Primer P3.
 XX Telomerase; substrate; primer; detection; 5'-region; retrovirus;
 KW long terminal repeat 2; LTR-2; diagnosis; tumour; screening;
 KW effector compound; PCR; amplification; Oligo-dT-Primer; ss.
 XX Synthetic.
 XX DE19644302-A1.
 XX 05-JUN-1997.
 XX 24-OCT-1996; 96DE-01044302.
 XX 28-NOV-1995; 95DE-01044317.
 XX (BOEF) BOEHRINGER MANNHEIM GMBH.
 XX Enrich T, Leying H, Hinzpeter M, Karl G;
 XX WPI; 1997-299542/28.
 XX Measuring telomerase activity, useful for tumour diagnosis and compound
 PT screening - by extending substrate primer, followed by amplification and
 PT immobilising product for detection.
 XX Example; Page 11; 21pp; German.
 XX The present sequence is a telomerase Oligo-dT-Primer, which can be used
 CC in a novel method for detecting telomerase activity. The method comprises
 CC adding to a test sample a 1st primer, that serves as telomerase
 CC substrate, and nucleoside triphosphate (dNTP) and incubating to allow
 CC primer extension by the telomerase, amplifying the extension product,
 CC immobilising the amplification product (AP) on a solid phase and
 CC qualitative and/or quantitative detection of AP, where the substrate
 CC primer is preferably from the 5'-region of the long terminal repeat 2
 CC (LTR-2) sequence of a retrovirus. The method can be used to diagnose
 CC tumours and screen compounds for effector activity. Immobilisation of AP
 CC provides a signal that is reproducibly representative of telomerase
 CC activity, eliminates the need for gel electrophoretic separation and
 CC provides high sensitivity. Radioactive labels are not required and the
 CC method can be automated for routine use. Specific detection is achieved
 CC by proper choice of hybridisation conditions, without separation of the
 CC telomerase extension product. A specific signal is generated by 1-10 cell
 CC equivalents, but for tumour analysis 10-1000 ng of tissue is usually used
 XX
 SQ Sequence 19 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 2 Other;
 Query Match 1.1%; Score 16.6; DB 1; Length 19;
 Best Local Similarity 94.1%; Pred. No. 1.3e+02;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1480 TAAAAAAAAAAAAAAAAA 1496
 Db 18 KAAAAAAAAAAAAAAAAA 2
 RESULT 176
 AAN30173
 ID AAN30173 standard; DNA; 18 BP.
 XX
 AC AAN30173;
 XX
 DT 05-APR-1992 (first entry)
 XX
 DE Sequence derived from the L1 region of the bovine papillomavirus (bpv)
 DE type 1a genome.
 XX
 KW Diagnostic reagent; vaccine; medicine; wart; tumour; ss.
 XX Bovine papillomavirus.
 OS
 XX Key Location/Qualifiers

FT CDS 1. .18
 FT /*tag= a
 XX
 PN BP92456-A.
 XX
 PD 26-OCT-1983.
 XX
 XX 01-APR-1983; 83EP-00901081.
 XX
 PR 05-APR-1982; 82PR-00005887.
 XX
 XX (INSP) INST PASTEUR.
 PA (DANO/) DANOS O.
 XX
 XX Danos O, Katinka M, Yaniv M;
 XX WPI; 1983-802979/44.
 DR P-PSDB; AAP30313.
 DR
 XX DNA fragment coding for Papillomavirus antigenic proteins - and derived
 PT immunogen, vaccine and antibody.
 PT
 XX Claim 6; Page 16; 25pp; French.
 XX
 CC The inventors claim DNA fragments capable of expressing, in a host, a
 CC prod. contg. at least one antigenic determinant of papillomavirus (PV),
 CC (see AAN30170-N30173). Also claimed are immunogens consisting of at least
 CC one peptide sequence coded for by the DNA fragments (see AAP30310-
 CC P30313), vaccines contg. the immunogens and antibodies raised from them.
 CC The vaccines are useful in human and veterinary medicine and the
 CC antibodies are useful as diagnostic reagents. The DNA fragments are most
 CC esp. derived from the L1 region of human PV type 1a
 XX
 SQ Sequence 18 BP; 16 A; 1 C; 1 G; 0 T; 0 U; 0 Other;
 Query Match 1.1%; Score 16.4; DB 1; Length 18;
 Best Local Similarity 94.4%; Pred. No. 1.3e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1478 GCTAAAAAAAAAAAAAAAAA 1495
 Db 1 GAAAAAAAAAAAAAAAAA 18
 RESULT 177
 AAT94669/C
 ID AAT94669 standard; DNA; 18 BP.
 XX
 AC AAT94669;
 XX
 DT 27-MAR-1998 (first entry)
 XX
 DE Anchored poly(T) oligonucleotide polyT-AnchG.
 XX
 KW Flavonoid 3' hydroxylase; pigmentation; flower colour; transgenic plant;
 KW snapdragon; primer; ss.
 XX
 OS Synthetic.
 XX
 PN WO9732023-A1.
 XX
 PD 04-SEP-1997.
 XX
 XX 28-FEB-1997; 97WO-AU000124.
 XX
 PR 01-MAR-1996; 96AU-00008386.
 XX
 XX (FLOR-) FLORIGENE LTD.
 PA
 XX Brugliera F, Holton TA, Michael MZ;
 XX WPI; 1997-448691/41.
 XX

PT Novel flavonoid 3'-hydroxylase(s) from flowering plants - and
PT corresponding DNA, used in the manipulation of pigmentation in plants.
XX
PS Example 15; Page 59; 234pp; English.

XX Anchored poly(T) oligonucleotides polyT-anchA (AAT94667), polyT-anchC
CC (AAT94668) and polyT-anchG (AAT94669) are complementary to the upstream
CC region of a polyadenylation sequence. They were used to prime cDNA
CC synthesis from snapdragon (Antirrhinum majus) petal and leaf RNA, and
CC were also utilised in the PCR amplification of plant cytochrome P450
CC sequences (see also AAT94670-73). A cDNA clone (see AAT94657) encoding
CC flavonoid 3' hydroxylase (see AAW35704) was isolated using a differential
CC display approach. This can be used to manipulate the pigmentation of
CC transgenic plants
XX
SQ Sequence 18 BP; 0 A; 0 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 1.1%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1479 CTAAATAAAAAAAAAAAAAA 1496
Db 18 CAAAAAAAAAAAAAAAAAAAAA 1

RESULT 178
AAF75596/c
ID AAF75596 standard; DNA; 18 BP.
XX
AC AAF75596;
XX
DT 10-MAY-2001 (first entry)
XX
DE Binary encoded sequence tag method anchored primer #1.
XX
KW Binary encoded sequence tag; BEST; nucleic acid analysis;
KW gene expression; adaptor; PCR primer; ss.
XX
OS Synthetic.
XX
XX WO200112855-A2.
PN
XX
PD 22-FEB-2001.
XX
XX 11-AUG-2000; 2000WO-US022164.
PF
XX
PR 13-AUG-1999; 99US-0148870P.
PR
PR 06-APR-2000; 2000US-00544713.
XX
XX (UYVA) UNIV YALE.
PA
XX Kaufman JC, Roth ME, Lizardi PM, Feng L, Latimer DR;
PI WPI; 2001-202878/20.
XX
DR
XX Producing binary sequence tags, useful for analyzing nucleic acid
PT sequence tags, gene expression or gene-expression patterns, involves
PT generating nucleic acid fragments, which are mixed with offset adaptors
PT and adaptor-indexers.
XX
XX Disclosure; Page 100; 101pp; English.

XX The present invention describes a method of producing binary sequence
CC tags from nucleic acid fragments in a sample, involving incubating the
CC sample with cleaving reagents, mixing offset adaptors with the sample,
CC incubating with more cleaving reagents and mixing the sample with adaptor
CC -indexers where the adaptors are coupled to binary sequence tags. The
CC method is useful in sequence analysis, including analysis and comparison
CC of gene expression, nucleic acid samples and genomes
XX
SQ Sequence 18 BP; 0 A; 1 C; 1 G; 16 T; 0 U; 0 Other;

Query Match 1.1%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1479 CTAAATAAAAAAAAAAAAAA 1496
Db 18 CAAAAAAAAAAAAAAAAAAAAA 1

RESULT 179
ABK13935/c
ID ABK13935 standard; DNA; 18 BP.
XX
AC ABK13935;
XX
DT 21-MAY-2002 (first entry)
XX
DE 5'-PCR primer used to produce single pattern characteristic by HaeII.
XX
KW Identification of transcribed gene; mRNA profile; gene expression;
KW cellular processes; fingerprinting; susceptibility to external factor;
KW development; disease; PCR; primer; ss.
XX
OS Synthetic.
XX
XX WO200208461-A2.
PN
XX
PD 31-JAN-2002.
XX
XX 23-JUL-2001; 2001WO-IB001539.
PF
XX
PR 21-JUL-2000; 2000GB-00018016.
PR
PR 21-JUL-2000; 2000US-0219925P.
XX
XX (GLOB-) GLOBAL GENOMICS AB.
PA
XX Linnarsson S, Ernfors P, Bauren G;
PI WPI; 2002-217065/27.
XX
DR
XX Providing mRNA profile, by generating two independent patterns
PT characteristic of sample mRNA population, analyzing patterns, comparing
PT gene expression by cell types under varied conditions, and identifying
PT genes.
XX
XX Disclosure; Fig 1; 67pp; English.

XX The present invention relates to a method for providing a profile of mRNA
CC molecules present in a sample. The method comprises generating two
CC independent patterns characteristic of the population of mRNA molecules
CC expressed in the sample and analysing the patterns using a combinatorial
CC algorithm, comparing gene expression by different or same cell types
CC under different conditions, and identifying genes having a role in
CC various cellular processes. The method is useful for the analysis and
CC identification of transcribed genes, and fingerprinting. The method can
CC be used to identify genes which play a role in determining various
CC cellular processes, including susceptibility to external factors,
CC development, and disease. The present sequence for a PCR primer is used
CC in the production of a single pattern characteristic of a sample,
CC employing a Type II restriction enzyme (i.e. HaeII) in the methods of the
CC present invention
XX
SQ Sequence 18 BP; 0 A; 1 C; 1 G; 16 T; 0 U; 0 Other;

Query Match 1.1%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1479 CTAAATAAAAAAAAAAAAAA 1496
Db 18 CAAAAAAAAAAAAAAAAAAAAA 1

RESULT 180
ACF36339/C
ID ACF36339 standard; DNA; 18 BP.
XX AC ACF36339;
XX DT 04-DEC-2003 (first entry)
XX DE Nucleotide sequence of a double stranded product DNA fragment.
XX DE Gene variant identification; restriction enzyme; HaeII; ds.
XX KW Gene variant identification; restriction enzyme; HaeII; ds.
XX OS Synthetic.
XX PN WO2003064689-A2.
XX PD 07-AUG-2003.
XX PF 28-JAN-2003; 2003WO-IB000255.
XX PR 29-JAN-2002; 2002US-0352245P.
XX PA (GLOB-) GLOBAL GENOMICS AB.
XX PI Lonnarberg P, Oldin M, Linnarsson S, Ernfors P;
XX WPI; 2003-627619/59.
XX DR Determining polyadenylation sites within transcribed gene sequences
XX PT present in a sample comprises assigning to gene fragments gene candidates
XX PT within a database by comparing signals in the dataset with the database.
XX PS Example; Fig 2; 81pp; English.
XX CC The invention relates to determining the presence of and/or identifying a
XX CC polyadenylation site within a sequence of a transcribed gene or variants
XX CC present in a sample. The method involves assigning to gene fragments gene
XX CC candidates within a database by comparing signals in the dataset with the
XX CC database, the database comprising data representing mRNAs with known
XX CC polyA sites and/or 'virtual genes' representing a possible
XX CC polyadenylation site within an actual gene. The method is useful for
XX CC determining the presence of and/or identifying a polyadenylation site or
XX CC alternative polyadenylation sites within a sequence of a transcribed gene
XX CC or sequences of transcribed gene variants present or potentially present
XX CC in a sample, in identifying gene features, particularly in identifying
XX CC differences between sequence variants that occur in a population of
XX CC nucleic acid molecules, especially in identifying or discovering polyA
XX CC site usage or determining polyA site usage in a nucleic acid sample, and
XX CC gene variants arising from alternative polyA sites. The present sequence
XX CC represents a double stranded product DNA fragment
XX SQ Sequence 18 BP; 0 A; 1 C; 1 G; 16 T; 0 U; 0 Other;
Query Match 1.1%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1479 CTAAGAAAAA 1496
DB 18 CGAAAAA 1

RESULT 181
ACF36364/C
ID ACF36364 standard; DNA; 18 BP.
XX AC ACF36364;
XX DT 04-DEC-2003 (first entry)
XX DE Nucleotide sequence of a double stranded product DNA.
XX DE Nucleic acid manipulation; mRNA profiling; polymerase chain reaction;
KW

XX electrophoresis; type II restriction enzyme; HaeII; ds.
XX Synthetic.
XX PN WO2003064691-A2.
XX PD 07-AUG-2003.
XX PF 28-JAN-2003; 2003WO-IB000843.
XX PR 29-JAN-2002; 2002US-0352215P.
XX PA (GLOB-) GLOBAL GENOMICS AB.
XX PI Linnarsson S, Ernfors P, Bauren G, Metsis A, Pihlak A;
XX PI Montelius A;
XX WPI; 2003-618365/59.
XX PT Producing a population of double-stranded product DNA molecules, useful
XX PT for mRNA profiling, comprises amplification by nested polymerase chain
XX PT reaction.
XX PS Example; Fig 1; 105pp; English.
XX CC The invention relates to producing a population of double-stranded
XX CC product DNA molecules comprising amplification by a nested PCR method.
XX CC The method is useful in profiling mRNA transcribed in a system under
XX CC investigation. The oligonucleotides are used as size standards in
XX CC electrophoresis, and as internal controls allowing for calculation of
XX CC relative amounts of material present. The present sequence represents a
XX CC double stranded product DNA, which aids in outlining an approach to
XX CC production of a single pattern characteristic of a sample, employing a
XX CC type II restriction enzyme (HaeII)
XX SQ Sequence 18 BP; 0 A; 1 C; 1 G; 16 T; 0 U; 0 Other;
Query Match 1.1%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1479 CTAAGAAAAA 1496
DB 18 CGAAAAA 1

RESULT 182
AAQ75549/C
ID AAQ75549 standard; DNA; 19 BP.
XX AC AAQ75549;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.

PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.

PS Disclosure; Page 5; 11pp; Japanese.

XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 19 BP; 0 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1479 CTAAAAAATAAAAAAAAAA 1496
DB 18 CAAAAAATAAAAAAAAAA 1

RESULT 183
AAQ75548/c
ID AAQ75548 standard; DNA; 19 BP.

XX
AC AAQ75548;
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.

XX JP06303997-A.

XX 01-NOV-1994.

XX 16-APR-1993; 93JP-00112515.

XX 16-APR-1993; 93JP-00112515.

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.

PS Disclosure; Page 5; 11pp; Japanese.

XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 19 BP; 1 A; 0 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 1.1%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1479 CTAAAAAATAAAAAAAAAA 1496

DB 18 CAAAAAATAAAAAAAAAA 1

RESULT 184

AAQ75547/c
ID AAQ75547 standard; DNA; 19 BP.

XX
AC AAQ75547;

XX 04-AUG-1995 (first entry)

XX Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.

XX Synthetic.

XX JP06303997-A.

XX 01-NOV-1994.

XX 16-APR-1993; 93JP-00112515.

XX 16-APR-1993; 93JP-00112515.

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.

XX Disclosure; Page 5; 11pp; Japanese.

XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 19 BP; 0 A; 0 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 1.1%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1479 CTAAAAAATAAAAAAAAAA 1496
DB 19 CAAAAAATAAAAAAAAAA 2

RESULT 185

AAQ75555/c
ID AAQ75555 standard; DNA; 19 BP.

XX
AC AAQ75555;

XX 04-AUG-1995 (first entry)

XX Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.

XX Synthetic.

XX JP06303997-A.

XX

PD 01-NOV-1994.
 XX 16-APR-1993; 93JP-00112515.
 XX 16-APR-1993; 93JP-00112515.
 XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX WPI; 1995-018287/03.
 XX Analysis of cDNA and gene expression - by amplification of mRNA followed
 XX by digestion with restriction enzymes.
 XX Disclosure; Page 5; 11pp; Japanese.
 XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
 XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 XX labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 XX and using the aggregate of mRNAs as the template for each reverse
 XX transcription primer; (b) digesting each of the prepared aggregates of
 XX the double-stranded cDNAs with restriction enzyme and; (c)
 XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
 XX method can be used to analyse gene expression rapidly and easily
 XX Sequence 19 BP; 0 A; 1 C; 1 G; 17 T; 0 U; 0 Other;
 Query Match 1.1%; Score 16.4; DB 1; Length 19;
 Best Local Similarity 94.4%; Pred. No. 1.5e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1479 CTAATAAAAAAAAAAAAAA 1496
 Db 19 CGAAAAAAAAAAAAAAAAAA 2
 RESULT 186
 AAX18389/C
 ID AAX18389 standard; DNA; 18 BP.
 XX AAX18389;
 XX 11-MAY-1999 (first entry)
 XX RT-PCR primer of the invention SEQ ID 30.
 XX RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
 XX Synthetic.
 XX JP11032765-A.
 XX 09-FEB-1999.
 XX 18-JUL-1997; 97JP-00208312.
 XX 18-JUL-1997; 97JP-00208312.
 XX (TAKI) TAKARA SHUZO CO LTD.
 XX WPI; 1999-183822/16.
 XX Peptides having at least two new nucleotides - useful as primers in RT-
 XX PCR.
 XX Example 1; Page 12; 19pp; Japanese.
 XX This sequence represents a primer of the invention. The invention relates
 XX to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
 XX -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
 XX a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
 XX natural number indicating the repetition of alpha; beta, delta = V or N;
 XX V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
 XX thymine; gamma = thymine; k = natural number of 3 or over indicating the

CC repetition of gamma, in which thymine expressed by gamma is composed of
 CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
 CC useful as primers for RT-PCR and determination of base sequences. The new
 CC sequences allow for reproductive and highly efficient analysis of gene
 CC sequences
 XX Sequence 18 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 2 Other;
 Query Match 1.1%; Score 16.2; DB 1; Length 18;
 Best Local Similarity 94.1%; Pred. No. 1.4e+02;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1480 TAAAAAAAAAAAAAAAAA 1496
 Db 17 BAAAAAAAAAAAAAAAAA 1
 RESULT 187
 AAT94431
 ID AAT94431 standard; mRNA; 19 BP.
 XX AAT94431;
 XX 02-MAR-1998 (first entry)
 XX Template mRNA poly-A tail SEQ ID NO:1 from WO9729211.
 XX Primer; detection; characterisation; mRNA; restriction display PCR;
 XX synthesis; cDNA; ss.
 XX Synthetic.
 XX Homo sapiens.
 XX WO9729211-A1.
 XX 14-AUG-1997.
 XX 07-FEB-1997; 97WO-US002009.
 XX 09-FEB-1996; 96US-0011379P.
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX Weinstein JN, Boulamwini J;
 XX WPI; 1997-415362/38.
 XX Detection and characterisation of mRNA by restriction display PCR -
 XX comprising synthesis of cDNA, digestion with a restriction endonuclease,
 XX ligation to an adaptor DNA and PCR amplification.
 XX Disclosure; Page 24; 40pp; English.
 XX A method has been improved for detecting and characterising mRNA
 XX molecules which includes synthesising a double stranded (ds) cDNA from
 XX isolated mRNA, digesting the ds cDNA with a restriction endonuclease to
 XX produce cDNA fragments in which at least one end of the cDNA fragments
 XX has a sequence capable of hybridising to an adaptor DNA sequence. The
 XX improvement comprises: (a) hybridising adaptor DNA sequences to at least
 XX one end of the cDNA fragments; (b) ligating the adaptor DNA sequences to
 XX the cDNA fragments; (c) amplifying the cDNA fragments having ligated
 XX adaptor DNA sequences by a PCR using primers that hybridise to the ends
 XX of the cDNA fragments, where the primers have at least one nucleotide at
 XX the 3' end that specifically hybridises to a subset of cDNA molecules;
 XX and (d) detecting the presence of the resulting amplified cDNA fragments.
 XX The present sequence represent a template poly-A tail used in the present
 XX specification. The method designate restriction display PCR can be used
 XX for characterising cells based on their mRNA content, for representing
 XX expressed genes, and for discovery of therapeutics that alter cellular
 XX gene expression. The method is also useful for characterising cells of a
 XX variety of types and under a variety of physiological conditions. The
 XX method is also useful for identifying cells or tissue from particular
 XX individuals or species based on the fingerprint obtained from the mRNA

```
CC content of isolated cells or tissue and comparing it to cells or tissue
CC from a known source
XX
SQ Sequence 19 BP; 17 A; 0 C; 0 G; 0 T; 0 U; 2 Other;

Query Match      1.1%; Score 16.2; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 1.6e+02;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAAAAAAA 1496
DB 2 BAAAAAATAAAAAAAAAA 18

RESULT 188
AA18390/C
ID AA18390 standard; DNA; 19 BP.
XX
AC AA18390;
XX
DT 11-MAY-1999 (first entry)
XX
DE RT-PCR primer of the invention SEQ ID 31.
XX
KW RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
OS Synthetic.
XX
FN JP11032765-A.
XX
PD 09-FEB-1999.
XX
PF 18-JUL-1997; 97JP-00208312.
XX
PR 18-JUL-1997; 97JP-00208312.
XX
PA (TAKI ) TAKARA SHUZO CO LTD.
XX
DR WPI; 1999-183822/16.
XX
PT Peptides having at least two new nucleotides - useful as primers in RT-PCR.
XX
PS Example 1; Page 12; 19pp; Japanese.
XX
CC This sequence represents a primer of the invention. The invention relates
CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC -N3'; or (X)m5'-(gamma)k-delta-N3'; where x = a labelled compound and/or
CC a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC natural number indicating the repetition of alpha; beta, delta = V or N;
CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC repetition of gamma, in which thymine expressed by gamma is composed of
CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC useful as primers for RT-PCR and determination of base sequences. The new
CC sequences allow for reproductive and highly efficient analysis of gene
CC sequences
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 0 T; 0 U; 2 Other;

Query Match      1.1%; Score 16.2; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 1.6e+02;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAAAAAAA 1496
DB 18 BAAAAAATAAAAAAAAAA 2

RESULT 189
AA06572/C
ID AA06572 standard; DNA; 19 BP.
XX
```

```
AC AAX06572;
XX
DT 06-APR-1999 (first entry)
XX
DE (-)-limonene-6-hydroxylase primer 3.B.
XX
KW (-)-limonene-6-hydroxylase; (-)-limonene-3-hydroxylase; L3H; L6H;
KW spear mint; peppermint; enzyme; limonene hydroxylase; trans-carveol;
KW trans-isopiperitenol; pathogen defense mechanism; attractant;
KW environmental signal; monoterpene hydroxylase; PCR primer; ss.
XX
OS Synthetic.
OS Mentha spicata.
XX
PN WO9859042-A1.
XX
PD 30-DEC-1998.
XX
PF 15-JUN-1998; 98WO-US012581.
XX
PR 24-JUN-1997; 97US-00881784.
XX
PA (UNIW ) UNIV WASHINGTON STATE RES FOUND.
XX
PI Croteau RB, Lupien SL, Karp F;
XX
DR WPI; 1999-105618/09.
XX
PT New isolated limonene hydroxylase nucleic acids - which encode limonene-6
PT -hydroxylase and limonene-3-hydroxylase, which can be used to produce
PT trans-carveol and trans-isopiperitenol.
XX
PS Example 4; Page 27; 80pp; English.
XX
CC The invention relates to nucleotide sequences encoding spearmint (-)-
CC limonene-6-hydroxylase (L6H) and peppermint (-)-limonene-3- hydroxylase
CC (L3H). Host cells containing a vector comprising the nucleotide sequences
CC can be used for the recombinant production of limonene hydroxylases or of
CC primary enzyme products. The primary enzyme products are trans-carveol in
CC the case of (-)-L6H or trans-isopiperitenol in the case of (-)-L3H, which
CC are of subsequent use, to obtain enhanced expression of limonene
CC hydroxylase in plants to attain enhanced trans- carveol or trans-
CC isopiperitenol production as a predator or pathogen defense mechanism,
CC attractant or environmental signal. The limonene hydroxylase cDNAs also
CC provide a useful tool for isolating other monoterpene hydroxylase genes
CC and for examining the developmental regulation of monoterpene
CC biosynthesis. Sequences AAX06564-73 represent primers for the PCR
CC amplification of (-)-limonene-6-hydroxylase cDNA
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 0 T; 0 U; 1 Other;

Query Match      1.1%; Score 16.2; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 1.6e+02;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAAAAAAA 1496
DB 19 DAAAAAATAAAAAAAAAA 3

RESULT 190
AAZ99489/C
ID AAZ99489 standard; DNA; 19 BP.
XX
AC AAZ99489;
XX
DT 03-JUL-2000 (first entry)
XX
DE Primer HOOK for cDNA encoding a C-20 oxidase polypeptide.
XX
KW Gibberellic acid; copalyl diphosphate synthase; 3beta-hydroxylase;
KW 2-oxidase; phytoene synthase; C-20 oxidase; 2beta,3beta-hydroxylase;
KW seed germination; seedling growth; gibberellin biosynthetic pathway;
```

KW transgenic plant; hypocotyl; epicotyl; PCR primer; ss.

XX

OS Cucurbita maxima.

XX

PN WO200009722-A2.

XX

PD 24-FEB-2000.

XX

PF 10-AUG-1999; 99WO-US018066.

XX

PR 10-AUG-1998; 98US-0096111P.

XX

PR 07-JUN-1999; 99US-0137977P.

XX

PA (MONS) MONSANTO CO.

XX

PI Brown SM, Ellich TD, Heck GR, Kishore GM, Logusch EW, Logusch SJ;

XX

PI Pillar KJ, Rao S, Ream JE;

XX

DR WPI; 2000-224351/19.

XX

XX Obtaining transgenic plant useful for controlling seed germination and
PT seedling growth comprises transgene comprising a sequence expressing
PT altered levels of an essential hormone.

XX

PS Example 17; Page 262; 267pp; English.

XX

XX The present primer was used to reverse transcribe cDNA encoding a C-20
CC oxidase. The amplification fragment is used in the method of the invention.
CC The specific method describes methods for the inhibition and control of
CC gibberellic acid levels. Gibberellic acid levels may be inhibited or
CC controlled by use of a chimeric expression construct expressing a RNA or
CC protein which suppresses the gibberellin biosynthetic pathway sequence,
CC diverts substrate from the pathway, or degrades pathway substrates or
CC products. The methods uses copalyl diphosphate synthase, 3beta-
CC hydroxylase, 2-oxidase, phytoene synthase, C-20 oxidase, and a
CC 3beta-hydroxylase polynucleotides to achieve this. The method is
CC used to control seed germination and seedling growth especially to
CC regulate gene products of gibberellin biosynthetic pathway and
CC restoration of normal seed germination, in transgenic plants. The plants
CC produced are gibberellin deficient, and have shortened hypocotyl and/or
CC epicotyl phenotypes compared to normal plants

XX

SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

XX

Query Match 1.1%; Score 16.2; DB 1; Length 19;

Best Local Similarity 94.1%; Pred. No. 1.6e+02;

Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAAAAAAA 1496

XX

DB 19 BAAAAAATAAAAAAAAAA 3

XX

RESULT 191

AAD15201/C

ID AAD15201 standard; DNA; 19 BP.

XX

AC AAD15201;

XX

DT 01-NOV-2001 (first entry)

XX

DE 3' sequencing primer #1 to identify and characterise polynucleotides.

XX

KW Fatty lesion development; atherosclerosis; Alzheimer's disease;
KW nervous system disorder; Parkinson's disease; immune system disorder;
KW ischaemia; lymphopaenia; leukocyte adhesion deficiency syndrome;
KW haemoglobinuria; anaemia; hyperproliferative disorder; Gaucher's disease;
KW coagulation disorder; blood platelet disorder; autoimmune disorder;
KW dermatitis; herpes simplex; Addison's disease; rheumatoid arthritis;
KW Grave's disease; gene therapy; antiarteriosclerotic; immunostimulant;
KW cardiovascular; antiviral; primer; ss.

XX

OS Unidentified.

XX

XX WO200154651-A2.

XX 02-AUG-2001.

XX 25-JAN-2001; 2001WO-US002439.

XX 25-JAN-2000; 2000US-0177963P.

XX (DIGI-) DIGITAL GENE TECHNOLOGIES INC.

XX Leonardi A, Sartani A, Glass JR, Sutcliffe JG, Hasel KW;

XX WPI; 2001-514526/56.

XX New polynucleotides regulated by fatty lesion development and their
XX encoded polypeptides, useful for preventing, treating or ameliorating
XX atherosclerosis, as well as for immune or hyperproliferative disorders.

XX Example 1; Page 79; 188pp; English.

XX The present invention relates to an isolated nucleic acid regulated by
XX fatty lesion development, which comprises any of 55 polynucleotide
XX sequences from Oryctolagus cuniculus. The polynucleotide, polypeptide or
XX antibody is useful for preventing, treating, modulating or ameliorating a
XX medical condition, particularly atherosclerosis. The invention is used as
XX a marker or detector of nervous system disorder or disease (e.g.
XX Parkinson's disease, Alzheimer's disease, ischaemia, dementia). The
XX invention may also be useful for treating deficiencies or disorders of
XX the immune system (e.g. lymphopaenia, leukocyte adhesion deficiency
XX syndrome or haemoglobinuria, anaemia), hyperproliferative disorders
XX (e.g. Gaucher's disease), infectious disease (e.g. herpes simplex),
XX coagulation disorders, blood platelet disorders and autoimmune disorders
XX (Addison's disease, rheumatoid arthritis, dermatitis, Grave's disease).
XX The polynucleotide sequence is also used in gene therapy. The present
XX sequence is a 3' sequencing primer used in the identification and
XX characterisation of polynucleotides up-regulated by fatty lesion
XX development

XX Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

XX Query Match 1.1%; Score 16.2; DB 1; Length 19;

XX Best Local Similarity 94.1%; Pred. No. 1.6e+02;

XX Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAAAAAAA 1496

DB 19 BAAAAAATAAAAAAAAAA 3

XX RESULT 192

XX AAH21968/C

XX ID AAH21968 standard; DNA; 19 BP.

XX AC AAH21968;

XX 16-AUG-2001 (first entry)

XX Mouse total gene expression analysis (TOGA) 3' sequencing primer SEQ.92.

XX Mouse; human; total gene expression analysis; TOGA; DST; EST;

XX digital sequence tag; expressed sequence tag; neuroleptic; antimanic;

XX central nervous system; antidepressant; gene therapy; diagnosis;

XX neuropsychiatric disorder; schizophrenia; bipolar disorder;

XX addiction-related behaviour; chromosome identification; immune response;

XX PCR primer; probe; ss.

XX Mus musculus.

XX WO200130972-A2.

XX 03-MAY-2001.

XX

PF 26-OCT-2000; 2000WO-US029690.
 XX
 PR 26-OCT-1999; 99US-0161379P.
 XX
 PA (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
 XX Thomas EA, Sutcliffe JG, Pribyl TW, Hilbush B, Hasel KW;
 XX WPI; 2001-300499/31.
 DR
 XX
 XX New neuroleptic-regulated polynucleotides expressed in the central
 PT nervous system for diagnosing and treating neuropsychiatric disorders
 PT such as schizophrenia, bipolar disorder and addiction-related behavior.
 XX
 XX Example 1; Page 87; 210pp; English.
 XX
 CC The present invention describes isolated neuroleptic-regulated nucleic
 CC acid molecules. (I) have neuroleptic, antimanic and antidepressant
 CC activities, and can be used in gene therapy. (I), polypeptides (II)
 CC encoded by (I), or a host cell (III) comprising (I), are useful for
 CC preventing, treating, modulating or ameliorating a medical condition such
 CC as a neuropsychiatric disorder. (I) are useful as diagnostic agents for
 CC diagnosing a pathological condition or susceptibility to a pathological
 CC condition such as neuropsychiatric disorder e.g. schizophrenia, a bipolar
 CC disorder or addiction-related behaviour. (I) are useful for detecting the
 CC presence of a nucleic acid encoding a protein in a mammalian tissue
 CC sample. (I) can be used as probes and primers, for chromosome
 CC identification, to control gene expression through triple helix formation
 CC or antisense DNA or RNA, in gene therapy to treat the above mentioned
 CC disorders, identifying individuals from minute biological samples, as an
 CC alternative to restriction fragment length polymorphism (RFLP) and as
 CC polymorphic markers for forensic purposes. (I) is also useful as
 CC molecular weight markers on Southern gels, diagnostic probes for the
 CC presence of specific mRNA in a particular cell type, as a probe to
 CC subtract-out known sequences in the process of discovering novel
 CC polynucleotides, for selecting and making oligomers for attachment to a
 CC gene chip or other support, to raise anti-DNA antibodies using DNA
 CC immunisation technique, and as an antigen to elicit an immune response.
 CC AAX21877 to AAX21984, AAB98083 and AAB98084 represent sequences used in
 CC the exemplification of the present invention
 XX
 XX Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;
 Query Match 1.1%; Score 16.2; DB 1; Length 19;
 Best Local Similarity 94.1%; Pred. No. 1.6e+02;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1480 TAAAAAATAAAAAAAAAA 1496
 Db 19 BAAAAAATAAAAAAAAAA 3
 RESULT 193
 AAF76617/c
 ID AAF76617 standard; DNA; 19 BP.
 XX
 AC AAF76617;
 XX
 DT 15-MAY-2001 (first entry)
 XX
 XX Spearmint (-)-limonene-6-hydroxylase PCR primer SEQ ID NO: 18.
 DE
 XX Spearmint; peppermint; (-)-limonene-6-hydroxylase;
 KW (-)-limonene-3-hydroxylase; flavour; aroma; probe; PCR primer; ss.
 XX
 OS Mentha spicata.
 XX
 XX US6194185-B1.
 PN
 XX 27-FEB-2001.
 PD
 XX 14-APR-1999; 99US-00292768.
 XX
 XX

PR 24-JUN-1997; 97US-00881784.
 XX (UNIW) UNIV WASHINGTON STATE RES FOUND.
 XX
 PI Croteau RB, Lupien SL, Karp F;
 XX WPI; 2001-243405/25.
 DR
 XX Novel isolated limonene hydroxylase encoding nucleic acid molecule,
 PT useful for altering production of limonene-6-hydroxylase or limonene-3-
 PT hydroxylase in suitable host cell.
 XX
 PS Example 4; Col 55; 57pp; English.
 XX
 CC The present invention provides the protein and coding sequences of the
 CC peppermint and spearmint (-)-limonene-3-hydroxylase and the spearmint (-)
 CC -limonene-6-hydroxylase. Also provided are a number of probes and PCR
 CC primers which were used to isolate the sequences. These are useful in the
 CC production of transgenic plants with altered flavour and aroma
 XX
 SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;
 Query Match 1.1%; Score 16.2; DB 1; Length 19;
 Best Local Similarity 94.1%; Pred. No. 1.6e+02;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1480 TAAAAAATAAAAAAAAAA 1496
 Db 19 DAAAAAATAAAAAAAAAA 3
 RESULT 194
 AAS06525/c
 ID AAS06525 standard; DNA; 19 BP.
 XX
 AC AAS06525;
 XX
 DT 07-SEP-2001 (first entry)
 XX
 DE Mouse microglia and macrophage regulatory gene primer #60.
 XX
 KW Mouse; microglia; macrophage; regulatory gene; digital sequence tag; DST;
 KW PCR-based total gene expression analysis; TOGA; infectious disorder;
 KW neuroinflammatory pathology; neurodegenerative disease; gene therapy;
 KW hyperproliferative disorder; autoimmune; inflammatory disorder; primer;
 XX ss.
 XX Mus musculus.
 OS
 XX WO200134770-A2.
 PN
 XX 17-MAY-2001.
 PD
 XX
 XX 06-NOV-2000; 2000WO-US030585.
 PF
 XX 12-NOV-1999; 99WO-US026824.
 PR
 XX 03-MAR-2000; 2000US-0186770P.
 PR
 XX 19-JUN-2000; 2000US-0212465P.
 XX
 PA (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
 XX
 XX Carson MJ, Sutcliffe JG, Almazan MT, Tobal GM;
 PI WPI; 2001-308782/32.
 XX
 XX New regulated genes of microglia and macrophages, useful for diagnosing,
 PT preventing or treating neuroinflammatory pathology and neurodegenerative
 PT disease.
 XX
 XX Example 1; Page 88; 244pp; English.
 PS
 XX The present sequence represents a primer used to isolate novel mouse
 CC microglia and macrophage regulatory gene DST (digital sequence tag)

sequences. AAS06401-AAS06590 represent these novel sequences and the primer sequences used to isolate them. The PCR-based total gene expression analysis (TOGA) system is used to examine the expression pattern of molecules corresponding to genes that are regulated in unstimulated microglia, activated microglia, unstimulated macrophage and activated macrophage. The polynucleotides of the invention, the polypeptides encoded by them and antibodies that bind to these polypeptides are useful for the diagnosis, prevention, treatment or amelioration of a medical condition, preferably a neuroinflammatory pathology or a neurodegenerative disease such as Alzheimer's disease, senile dementia, Parkinson's disease, obsessive compulsive disorders, epilepsy, schizophrenia, multiple sclerosis, depression and bipolar manic-depressive disorder. The sequences and methods of the invention can also be used for detecting or treating infectious disorders (e.g. AIDS), hyperproliferative disorders (e.g. cancer), immune disorders (e.g. severe combined immunodeficiency, SCID) autoimmune diseases (e.g. insulin dependent diabetes mellitus), inflammatory disorders (e.g. arthritis). The polynucleotides can be used for gene therapy

SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

Query Match 1.1%; Score 16.2; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 1.6e+02;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAAAAAAA 1496
DB 19 BAAAAAATAAAAAAAAAA 3

RESULT 195
ABK71509/c
ID ABK71509 standard; DNA; 19 BP.
XX AC ABK71509;
XX 30-JUL-2002 (first entry)
XX CNS related 3' sequencing primer.
XX Central nervous system; CNS; neuroleptic; mouse; human; psychoses;
XX neuropsychiatric disorder; psychiatric disorder; Alzheimer's disease;
XX Pick's disease; Binswanger's disease; senile dementia; encephalopathy;
XX Parkinson's disease; obsessive compulsive disorder; epilepsy; ischaemia;
XX addiction; multiple sclerosis; depression; manic-depressive disorder;
XX primer; ss.
XX Synthetic.
XX WO200226936-A2.
XX 04-APR-2002.
XX 01-OCT-2001; 2001WO-US030695.
XX 29-SEP-2000; 2000US-0236790P.
XX 18-JAN-2001; 2001US-0263084P.
XX (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
XX Thomas EA, Sutcliffe JG, Pribyl TM, Hilbush BS, Hasel KW;
XX WPI; 2002-383271/41.
XX New polynucleotide useful in gene therapy for preventing, treating
XX modulating or ameliorating a medical condition such as psychoses or a
XX neuro psychiatric disorder e.g. schizophrenia, or a bipolar disorder in a
XX mammal.
XX Example 1; Page 40; 254pp; English.
XX This invention relates to the cDNA sequences of novel isolated

polynucleotides associated with psychoses or other neuropsychiatric disorders. The sequences of the invention may act as blockers of D₂ receptors in the meso-limbic dopamine system. The nucleotide sequences of the invention and the polypeptides encoded by them are useful in the manufacture of a medicament useful for preventing, treating, modulating or ameliorating a medical condition e.g. a neuropsychiatric disorder. An antibody that binds the proteins of the invention is useful for preventing, treating, modulating or ameliorating neurological disorders such as psychoses or other neuropsychiatric disorders in a subject. The sequences are also useful for diagnosing neurological disorders or a susceptibility to a neurological disorder such as psychoses and other neuro psychiatric disorders in a subject by determining the presence or absence of mutation in the nucleotide sequence of apolipoprotein D or by determining the alteration (increase or decrease) in the expression of apolipoprotein D. The sequences of the invention are useful in treating deficiencies or disorders of the central nervous system or peripheral nervous system by activating or inhibiting the proliferation, differentiation or mobilisation (chemotaxis) of neuroblasts, stem cells or glial cells. The sequences are useful as a marker or detector of a particular nervous system disease or disorder such as Alzheimer's disease, Pick's disease, Binswanger's disease, other senile dementia, Parkinson's disease, obsessive compulsive disorders, epilepsy, encephalopathy, ischaemia, addiction, multiple sclerosis, depression and manic-depressive disorder. The present sequence represents an oligonucleotide primer used in the identification of the cDNA sequences of the invention

SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

Query Match 1.1%; Score 16.2; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 1.6e+02;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAAAAAAA 1496
DB 19 BAAAAAATAAAAAAAAAA 3

RESULT 196
ABQ73231/c
ID ABQ73231 standard; DNA; 19 BP.
XX AC ABQ73231;
XX 27-SEP-2002 (first entry)
XX Rabbit atherosclerosis related TOGA primer SEQ ID NO:26.
XX Rabbit; Oryctolagus cuniculus; atherosclerosis; intimal hyperplasia;
XX TOGA primer; ss.
XX Oryctolagus cuniculus.
XX Synthetic.
XX WO200242420-A2.
XX 30-MAY-2002.
XX 21-NOV-2001; 2001WO-US044072.
XX 21-NOV-2000; 2000US-0252216P.
XX (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
XX Leonardi A, Sartani A, Glass JR, Hasel KW;
XX WPI; 2002-575233/61.
XX New polynucleotides related to regulated genes characteristic of
XX atherosclerosis, useful for diagnosing, preventing, treating, modulating
XX or ameliorating atherosclerosis in a mammalian subject.
XX Disclosure; Page 28; 130pp; English.

XX The present invention describes an isolated polynucleotide (I) and its
 CC complements, and degenerate variants, comprising a sequence selected from
 CC those given in ABQ73206 to ABQ73222 (NS), which is a digital sequence tag
 CC (DST) corresponding to mRNAs whose expression is regulated by
 CC proliferative lesion development caused by mechanically induced intimal
 CC hyperplasia, or by lecanidipine treatment, or by proliferative lesions
 CC and reversed by lecanidipine treatment. (I) has antiatherosclerotic
 CC activity and can be used in gene therapy. (I) can be used for diagnosing
 CC a medical condition (e.g. atherosclerosis) in a subject which involves
 CC determining the presence or absence of a mutation in (I) and diagnosing
 CC the medical condition based on the presence or absence of the mutation.
 CC (I) is also useful for diagnosing atherosclerosis, or the susceptibility
 CC to atherosclerosis in a subject which involves detecting an alteration
 CC (an increase or decrease) in amount of expression of (I). (I) is also
 CC useful for diagnosing or monitoring the effects of treating a subject
 CC with dihydropyridine calcium antagonist e.g., lercanidipine. (I) can also
 CC be used for preventing, treating, modulating, or ameliorating a medical
 CC condition such as atherosclerosis in a mammalian subject. The present
 CC sequence represents a TOGA primer which is used in the exemplification of
 CC the present invention
 XX

SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;
 Query Match 1.1%; Score 16.2; DB 1; Length 19;
 Best Local Similarity 94.1%; Pred. No. 1.6e+02;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAAAAAAA 1496
 :|||||
 Db 19 BAAAAAATAAAAAAAAAA 3

RESULT 197
 AAD34663/c
 ID AAD34663 standard; DNA; 19 BP.
 XX
 AC AAD34663;
 XX

DT 16-JUL-2002 (first entry)
 XX

DE PCR primer #4 used for direct sequencing of TOGA generated PCR products.
 XX

KW Hepatitis B virus; HBV infection; chronic hepatitis; toxicity; virucide;
 KW acute hepatitis; therapeutic; gene therapy; vaccine; infectious disease;
 KW TOGA; Total Gene expression Analysis; PCR; primer; ss.
 XX

OS Unidentified.
 XX

PN WO200222783-A2.
 XX

PD 21-MAR-2002.
 XX

XX 17-SEP-2001; 2001WO-US029123.
 XX

PR 15-SEP-2000; 2000US-0233176P.
 XX

PA (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
 XX

PI Chisari FV, Wieland SF, Guidotti LGDVM, Mueller R, Hilbush BS;
 XX

DR WPI; 2002-339865/37.
 XX

PT Preventing and treating hepatitis viral infection in a mammal, comprises
 PT administering nucleic acid molecules that up- or down-regulate in
 PT hepatitis B virus infection or polypeptides encoded by the nucleic acid
 PT molecules.
 XX

PS Disclosure; Page 28; 125pp; English.
 XX

CC The present invention relates to a method for preventing, treating,
 CC modulating or ameliorating a medical condition. The method involves
 CC administering one or more nucleic acid molecules up- or down-regulated in

CC hepatitis B virus (HBV) infection or polypeptides encoded by the nucleic
 CC acid molecules or antibodies that bind to the polypeptide. The method is
 CC useful for preventing, treating, modulating or ameliorating a medical
 CC condition. It is also useful for determining the presence or absence of a
 CC mutation in the nucleic acid molecules or detecting an alteration in
 CC expression of the polypeptide which is useful for the diagnosis of
 CC hepatitis viral infection. The method is useful for assessing the stage
 CC of hepatitis viral infection (e.g., acute hepatitis versus chronic
 CC hepatitis) or assessing the efficacy or toxicity of therapeutic treatment
 CC for hepatitis viral infection and a gene expression profile is useful for
 CC identifying polypeptides and polynucleotides which are associated with
 CC hepatitis viral infection. Sequences of the invention are used in gene
 CC therapy and as vaccines. Nucleic acid sequences are useful as a
 CC diagnostic markers for HBV infection and for treating infectious
 CC diseases. The present DNA sequence is a PCR primer which is used for
 CC direct sequencing of TOGA (Total Gene expression Analysis) generated PCR
 CC products
 XX

SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;
 Query Match 1.1%; Score 16.2; DB 1; Length 19;
 Best Local Similarity 94.1%; Pred. No. 1.6e+02;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAAAAAAA 1496
 :|||||
 Db 19 BAAAAAATAAAAAAAAAA 3

RESULT 198
 AAD40279/c
 ID AAD40279 standard; DNA; 19 BP.
 XX
 AC AAD40279;
 XX

DT 22-OCT-2002 (first entry)
 XX

DE HOOK PCR primer used to isolate pumpkin 2beta-3beta hydroxylase cDNA.
 XX

KW Gibberellin; transgenic plant; seed germination; seedling growth; GA;
 KW transgenic; 2beta-3beta hydroxylase; enzyme; pumpkin; PCR; primer; ss.
 XX

OS Cucurbita pepo.
 XX

PN US2002053095-A1.
 XX

PD 02-MAY-2002.
 XX

PF 10-AUG-1999; 99US-00371307.
 XX

PR 10-AUG-1999; 99US-00371307.
 XX

PA (BROW/) BROWN S M.
 XX

PI Brown SM, Elich TD, Heck GR, Kishore GM, Logusch EW, Logusch SJ;
 PI Piller KJ, Rac S, Ream JE;
 XX

DR WPI; 2002-489107/52.
 XX

PT Control of gibberellin levels in plants useful to avoid unfavorable
 PT conditions in crops to increase yields, using transgenic plants having
 PT reduced seed germination and early seedling growth then treatment to
 PT restore these properties.
 XX

XX Example 19; Page 104; 155pp; English.
 XX

CC The invention relates to control of gibberellin (GA) levels in plants.
 CC The method involves producing transgenic plants having a phenotype of
 CC reduced seed germination and reduced early seedling growth, then
 CC restoring seed germination and early seedling growth by treating plants
 CC with an appropriate compound when conditions are favourable. The method
 CC is useful to control seed germination and/or early seedling growth in
 CC agricultural production so that unfavorable environmental conditions

CC normally reducing agronomic output can be avoided and yields increased.
 CC Plants also demonstrate increased uniformity of germination, emergence
 CC and seedling vigor, so increasing yields at harvest. The method is
 CC especially useful in crop plants such as e.g. canola, soybean, cotton,
 CC etc., and is also useful in storage and transport of seeds to reduce
 CC premature germination which may affect agronomic or food quality of the
 CC seeds. The present sequence is a PCR primer used to isolate pumpkin 2beta
 CC -3beta hydroxylase cDNA. This primer is used in the exemplification of
 CC the invention

SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

Query Match 1.1%; Score 16.2; DB 1; Length 19;
 Best Local Similarity 94.1%; Pred. No. 1.6e+02;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAAAAAAA 1496
 :|||||
 Db 19 BAAAAAATAAAAAAAAAA 3

RESULT 199
 ABZ68389/c
 ID ABZ68389 standard; DNA; 19 BP.

XX AC ABZ68389;

XX DT 22-APR-2003 (first entry)

XX DE Reverse transcription primer used to produce yeast cDNA.

XX KW Histone acetyltransferase; histone deacetylase; gene expression profile;
 XX chromatin-associated protein; gene expression; primer; ss.

XX OS Synthetic.

XX PN WO2003000715-A1.

XX PD 03-JAN-2003.

XX PF 21-JUN-2002; 2002WO-US019750.

XX PR 22-JUN-2001; 2001US-0300135P.

XX PA (CERE-) CERES INC.

XX PI Dang V, Okamuro J;

XX DR WPI; 2003-175280/17.

XX PT New chimeric polypeptide comprising a histone acetyltransferase

PT polypeptide segment and a segment comprising a histone deacetylase
 PT chromatin-associated protein complex subunit, useful for modulating gene
 PT expression in cells.

XX PS Example 10; Page 54; 85pp; English.

XX CC The specification describes chimeric histone acetyltransferase
 CC polypeptides. The chimeric polypeptides comprise a polypeptide segment
 CC that exhibits histone acetyltransferase activity, and a polypeptide
 CC segment having 40% or greater sequence identity to a subunit of a histone
 CC deacetylase chromatin-associated protein complex. The chimeric
 CC polypeptides are useful for determining gene expression profiles in
 CC specific cells, for modulating gene expression in specific cells, and for
 CC making genetically modified eukaryotes. The present sequence represents a
 CC reverse transcription primer used in the method of the invention

SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

Query Match 1.1%; Score 16.2; DB 1; Length 19;
 Best Local Similarity 94.1%; Pred. No. 1.6e+02;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAAAAAAA 1496
 :|||||
 Db 19 BAAAAAATAAAAAAAAAA 3

RESULT 200
 ACC79402/c
 ID ACC79402 standard; DNA; 19 BP.

XX AC ACC79402;

XX DT 04-AUG-2003 (first entry)

XX DE M13 sequencing primer 3' primer SEQ ID NO:84.

XX KW Pathological condition; ataxia telangiectasia; AT; tumour; cancer;
 XX cytostatic; vaccine; gene therapy; PCR primer; ss.

XX OS Enterobacteria phage M13.

XX OS Synthetic.

XX PN WO2003033668-A2.

XX PD 24-APR-2003.

XX PF 17-OCT-2002; 2002WO-US033311.

XX PR 17-OCT-2001; 2001US-0330206P.

XX PA (DIGI-) DIGITAL GENE TECHNOLOGIES INC.

XX PI Barlow C, Winrow CJ, Callahan MLA, Pankratz DG, Vibat CRT;

XX PI Warren AJ;

XX DR WPI; 2003-393520/37.

XX PT Preventing or treating a pathological condition e.g., ataxia
 PT telangiectasia (AT), AT tumors or other cancers comprises administering
 PT polynucleotides.

XX PS Example 1; Page 76; 184pp; English.

XX CC The present invention describes a method for preventing or treating a
 CC pathological condition (comprising ataxia telangiectasia (AT), AT tumors
 CC or other cancers), which comprises administering to a mammalian subject
 CC at least one of: (a) a first polynucleotide comprising a sequence having
 CC 38-889 bp (consisting of the sequences in ACC79319 to ACC79392 (I)) or a
 CC second polynucleotide at least 95% identical to the first polynucleotide;
 CC (b) a third polynucleotide comprising at least 10-bp sequence that is
 CC hybridisable to the first polynucleotide under stringent conditions; or
 CC (c) a gene corresponding to any of (1)-(2) or another gene at least 95%
 CC identical to the gene. (1) have cytostatic activities, and can be used in
 CC vaccines and in gene therapy. The method is useful for preventing or
 CC treating e.g., ataxia telangiectasia (AT), AT tumors or other cancers.
 CC ACC79393 to ACC79423 represent primers used in the exemplification of the
 CC present invention

SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

Query Match 1.1%; Score 16.2; DB 1; Length 19;
 Best Local Similarity 94.1%; Pred. No. 1.6e+02;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAAAAAAA 1496
 :|||||
 Db 19 BAAAAAATAAAAAAAAAA 3

RESULT 201
 AAD49149/c
 ID AAD49149 standard; DNA; 19 BP.

XX AC AAD49149;

```

XX 07-MAR-2003 (first entry)
DT
XX
XX 3' sequencing primer #1 used in the invention.
DE
XX
XX Atherosclerosis; vaccine; nervous system disorder; Alzheimer's disease;
KW Parkinson's disease; multiple sclerosis; immune disorder; gene therapy;
KW autoimmune disorder; rheumatoid arthritis; hyperproliferative disorder;
KW haemolytic anaemia; graft-versus-host disease; inflammation; infection;
KW epilepsy; Addison's disease; neoplasm; tissue regeneration; chemotaxis;
KW food additive; food preservative; primer; ss.
XX
XX Unidentified.
OS
XX
XX WO200281726-A2.
PN
XX
XX 17-OCT-2002.
PD
XX
XX 15-NOV-2001; 2001WO-US043741.
PF
XX 15-NOV-2000; 2000US-0248992P.
PR
XX 28-NOV-2000; 2000US-0253623P.
PR
XX
XX (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
PA
XX Leonardi A, Sartani A, Glass J, Sutcliffe JG, Hasel KW;
PI
XX WPI; 2003-058561/05.
DR
XX
XX New polypeptide associated with atherosclerosis, useful for treating
PT atherosclerosis, nervous system disorders, immune disorders,
PT hyperproliferative disorders and infectious diseases.
XX
XX Disclosure; Page 139; 146pp; English.
XX
XX The invention relates to polynucleotides and polypeptides associated with
CC atherosclerosis. Polynucleotides of the invention are useful for delivery
CC of genes, DNA vaccines, diagnostic reagents, peptides, proteins or
CC macromolecules. Sequences of the invention are useful for treating
CC nervous system disorders (e.g., Alzheimer's disease, Parkinson's disease,
CC multiple sclerosis, epilepsy), immune disorders (e.g., autoimmune
CC disorders such as rheumatoid arthritis, Addison's disease, haemolytic
CC anaemia, graft-versus-host disease, inflammation), hyperproliferative
CC disorders (e.g., neoplasms) and infectious diseases (e.g., viral,
CC bacterial, fungal or parasite infection). They are used for regeneration
CC of tissues, to repair, replace or protect damage tissues, for increasing
CC chemotaxis activity of cells, for increasing or decreasing the
CC differentiation or proliferation of embryonic stem cells from a lineage,
CC for modulating mammalian characteristics, (such as body weight or
CC height), for modulating mammalian metabolism affecting catabolism,
CC anabolism, processing utilisation and storage of energy, to change a
CC mammal's mental or physical state, or as a food additive or preservative.
CC The invention is useful in gene therapy. The present sequence is a
CC sequencing primer used in the invention
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;
SQ
Query Match 1.1%; Score 16.2; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 1.6e+02;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1480 TAAAAAAAAAAAAAAAAA 1496
Db 19 BAAAAAAAAAAAAAAAAA 3
RESULT 202
AAD50267/C
ID AAD50267 standard; DNA; 19 BP.
XX
XX AAD50267;
AC
XX
XX 24-MAR-2003 (first entry)
DT
XX
XX 07-MAR-2003 (first entry)
DT
XX
XX 3' sequencing primer #1 used in the invention.
DE
XX
XX Atherosclerosis; vaccine; nervous system disorder; Alzheimer's disease;
KW Parkinson's disease; multiple sclerosis; immune disorder; gene therapy;
KW autoimmune disorder; rheumatoid arthritis; hyperproliferative disorder;
KW haemolytic anaemia; graft-versus-host disease; inflammation; infection;
KW epilepsy; Addison's disease; neoplasm; tissue regeneration; chemotaxis;
KW food additive; food preservative; primer; ss.
XX
XX Unidentified.
OS
XX
XX WO200281726-A2.
PN
XX
XX 17-OCT-2002.
PD
XX
XX 15-NOV-2001; 2001WO-US043741.
PF
XX 15-NOV-2000; 2000US-0248992P.
PR
XX 28-NOV-2000; 2000US-0253623P.
PR
XX
XX (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
PA
XX Leonardi A, Sartani A, Glass J, Sutcliffe JG, Hasel KW;
PI
XX WPI; 2003-058561/05.
DR
XX
XX New polypeptide associated with atherosclerosis, useful for treating
PT atherosclerosis, nervous system disorders, immune disorders,
PT hyperproliferative disorders and infectious diseases.
XX
XX Disclosure; Page 139; 146pp; English.
XX
XX The present invention relates to a novel simplified TOGA (RTM) method for
CC simultaneous sequence-specific identification of multiple mRNA molecules
CC in a RNA population. The method involves characterising each of the
CC sequence-specific polymerase chain reaction (PCR) products by partial
CC patterns and length. The method is useful for determining tissue-specific
CC patterns of gene expression or mechanisms of drug interaction. It is also
CC useful for drug screening, studying physiological processes, genomic
CC mapping or manufacture of diagnostic, prognostic or therapeutic reagents.
CC The present sequence is a primer used to illustrate the method of the
CC invention
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;
SQ
Query Match 1.1%; Score 16.2; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 1.6e+02;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1480 TAAAAAAAAAAAAAAAAA 1496
Db 19 BAAAAAAAAAAAAAAAAA 3
RESULT 203
ADC21495/C
ID ADC21495 standard; DNA; 19 BP.
XX
XX ADC21495;
AC
XX
XX 18-DEC-2003 (first entry)
DT
XX
XX Human PRDI-BF1 RT-PCR primer.
DE
XX
XX tumor; antigen; CD8+ cytotoxic T lymphocyte; CTL; CTL-induced lysis;
KW multiple myeloma cell; human; PRDI-BF1;
KW positive regulatory domain I-binding factor-1; MHC;
KW major histocompatibility complex Class I; cytostatic; vaccine; ss;
KW primer; PCR.
XX
XX Homo sapiens.
OS
XX
XX WO2003029282-A2.
PN
XX

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PD 10-APR-2003.
PF 24-SEP-2002; 2002WO-EP010701.
XX
XX
PR 29-SEP-2001; 2001DE-01048236.
XX
XX (IMMU-) IMMUGENICS AG.
XX
XX Theobald M, Lotz C;
XX
XX WPI; 2003-354724/33.
XX
XX New tumor-associated oligopeptide, useful particularly for treating
PT multiple myeloma, is recognized by CD8 cytotoxic T cells, also
PT derivatives and related nucleic acid.
XX
XX Disclosure; Page 22; 64pp; German.
XX
XX This invention describes a novel tumor-associated oligopeptide that is
CC recognized as an antigen by CD8+ cytotoxic T lymphocytes (CTL) and causes
CC CTL-induced lysis and/or apoptosis of tumor cells, especially multiple
CC myeloma cells. The oligopeptide is derived from human PRDI-BF1 (positive
CC regulatory domain I-binding factor-1) which is able to induce an MHC
CC (major histocompatibility complex) Class I allele variant A2-restricted
CC immune response of CD8+ CTL against tumor cells. The products of the
CC invention have cytostatic activity and can be used in a vaccine. The
CC peptide of the invention, also related retro-inverse and pseudopeptides,
CC fusion proteins (FP), polynucleotides, vectors, host cells and antibodies
CC and T cell receptors specific for PRDI-BF1 peptides are useful for
CC treating diseases associated with PRDI-BF1, particularly tumors. The
CC products of the invention are also useful as diagnostic, therapeutic and
CC prophylactic agents for detecting, modifying, generating, expanding
CC and/or regulating activation and functional status of T cells, and for
CC preparation of poly- or mono-clonal or recombinant A2-restricted T cell
CC receptors and their functional equivalents. This sequence represents an
CC RT-PCR primer used to amplify the human PRDI-BF1 gene described in the
CC invention.
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;
SQ
Query Match 1.1%; Score 16.2; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 1.6e+02;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1480 TAAAAAATAAAAAAAAAA 1496
Db 19 BAAAAAATAAAAAAAAAA 3
RESULT 204
AA18368/c
ID AA18368 standard; DNA; 16 BP.
XX
XX
AC AA18368;
XX
XX 11-MAY-1999 (first entry)
DT
XX
XX RT-PCR primer of the invention SEQ ID 9.
DE
XX
XX RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
KW
XX
XX Synthetic.
OS
XX
XX JF11032765-A.
PN
XX
XX 09-FEB-1999.
PD
XX
XX 18-JUL-1997; 97JP-00208312.
PF
XX
XX 18-JUL-1997; 97JP-00208312.
PR
XX
XX (TAKI ) TAKARA SHUZO CO LTD.
PA
XX
XX

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DR WPI; 1999-183822/16.
XX
XX Peptides having at least two new nucleotides - useful as primers in RT-
PT PCR.
XX
XX Disclosure; Page 10; 19pp; Japanese.
XX
XX This sequence represents a primer of the invention. The invention relates
CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
CC a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC natural number indicating the repetition of alpha; beta, delta = V or N;
CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC repetition of gamma, in which thymine expressed by gamma is composed of
CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC useful as primers for RT-PCR and determination of base sequences. The new
CC sequences allow for reproductive and highly efficient analysis of gene
CC sequences
XX
XX Sequence 16 BP; 1 A; 0 C; 1 G; 14 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1479 CTAAAAAATAAAAAAAAAA 1494
Db 16 CTAAAAAATAAAAAAAAAA 1
RESULT 205
AA18368
ID AA18368 standard; cDNA; 16 BP.
XX
XX
AC AA18368;
XX
XX 21-JUN-1999 (first entry)
DT
XX
XX Homo sapiens fetal kidney clone AK647 secreted protein gene 3' end.
DE
XX
XX Secreted protein; fetal kidney; ds.
KW
XX
XX Homo sapiens.
OS
XX
XX WO9900405-A1.
PN
XX
XX 07-JAN-1999.
PD
XX
XX 29-JUN-1998; 98WO-US013530.
PF
XX
XX 30-JUN-1997; 97US-00885610.
PR
XX
XX (GEMY ) GENETICS INST INC.
PA
XX
XX Jacobs K, McCooy JM, Lavallie ER, Racie LA, Merberg D, Treacy M;
PI Evans C, Agostino MJ;
XX
XX WPI; 1999-095671/08.
DR
XX
XX New polynucleotides encoding secreted human proteins - are derived from
PT foetal kidney or adult retina cDNA libraries, used as; e.g. potential
PT vaccines.
PT
XX
XX Disclosure; Page 54; 76pp; English.
XX
XX The sequence is that of the 3' end of a sequence encoding a secreted
CC protein from a human fetal kidney clone AK296. Such a sequence is
CC predicted to have biological activities which would make them suitable
CC for treating, preventing or ameliorating medical conditions in humans and
CC animals, although no supporting data is given. Suggested activities
CC include nutritional activity, cytokine and cell
CC proliferation/differentiation activity, immune stimulating (e.g. as

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CC vaccines) or suppressing activity, haematopoiesis regulating activity,
CC tissue growth activity, activin/inhibin activity,
CC chemotactic/chemokinetic activity, haemostatic and thrombolytic activity,
CC receptor/ligand activity, anti-inflammatory activity, cadherin/tumour
CC invasion suppressor activity, and tumour inhibition activity. It is also
CC stated to be useful for gene therapy
XX
SQ Sequence 16 BP; 16 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
    Query Match          1.1%; Score 16; DB 1; Length 16;
    Best Local Similarity 100.0%; Pred. No. 1.3e+02;
    Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
Db 1 AAAAAAAAAAAAAA 16

RESULT 206
AAC66068
ID AAC66068 standard; DNA; 16 BP.
XX
AC AAC66068;
XX
DT 22-FEB-2001 (first entry)
XX
DE DNA chip primer #4.
XX
KW DNA chip; primer; nucleoside derivative; photolabile protecting group;
KW photolithographic nucleic acid chip; ss.
XX
OS Synthetic.
XX
PN WO200061594-A2.
XX
PD 19-OCT-2000.
XX
PF 07-APR-2000; 2000WO-DE001148.
XX
PR 08-APR-1999; 99DE-01015867.
XX
PT 28-JAN-2000; 2000DB-01003631.
XX
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
PI Beier M, Hoheisel J;
XX
DR WPI; 2000-679457/66.
XX
PT New nucleoside derivatives with photolabile protecting groups, useful in
PT oligonucleotide synthesis, particularly on solid phases, e.g. for
PT hybridization testing.
XX
PS Disclosure; Fig 9; 48pp; German.
XX
CC This invention describes nucleoside derivatives (I) with photolabile
CC protecting groups. (I) are used to synthesize oligonucleotides using the
CC photolithographic nucleic acid chip method, particularly where these are
CC intended for performing enzymatic reactions initiated from a free 3'-
CC hydroxy (especially solid-phase polymerase reactions or ligase reactions,
CC but also reverse transcription, cDNA synthesis etc.), also for
CC hybridization testing, sequencing and in DNA computing. (I) are produced
CC with high selectivity by reaction with a mild acylating agent that has
CC high specificity for the 3'-position, without significant side-reactions
CC (cf. more reactive acylating agents such as chloroformates)
XX
SQ Sequence 16 BP; 16 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
    Query Match          1.1%; Score 16; DB 1; Length 16;
    Best Local Similarity 100.0%; Pred. No. 1.3e+02;
    Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
|||||

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```

Db 1 AAAAAAAAAAAAAA 16

RESULT 207
ABA04585/c
ID ABA04585 standard; DNA; 16 BP.
XX
AC ABA04585;
XX
DT 15-FEB-2002 (first entry)
XX
DE Oligonucleotide #5.
XX
KW Analytical support; genomic sequencing; mutation detection;
KW pharmaceutical development; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER = Fl(CH2)6-PO-thymine, where Fl is flavine
FT and PO is a phosphate group"
XX
PN FR2805348-A1.
XX
PD 24-AUG-2001.
XX
PF 23-FEB-2000; 2000FR-00002236.
XX
PR 23-FEB-2000; 2000FR-00002236.
XX
PA (COMS ) COMMISSARIAT ENERGIE ATOMIQUE.
XX
PI Cuzin M, Peltie P, Fontecave M, Decout JL, Dueymes C;
XX
DR WPI; 2001-628265/73.
XX
PT Support for hybridization analysis of nucleic acids for sequencing
PT techniques, comprises an array of oligonucleotides having a label where
PT the fluorescence changes follow hybridization.
XX
PS Example 1; Page 12; 33pp; French.
XX
CC The present invention relates to an analytical support, to which a number
CC of oligonucleotides are fixed. The oligonucleotides are labelled with a
CC fluorescent compound, the fluorescence of which varies when the
CC oligonucleotide hybridises to its complement. The analytical support is
CC useful in hybridisation testing for identification of specific nucleic
CC acids, such as genomic sequencing, detecting mutations or pharmaceutical
CC development. The present oligonucleotide was used to illustrate the
CC invention
XX
SQ Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;
    Query Match          1.1%; Score 16; DB 1; Length 16;
    Best Local Similarity 100.0%; Pred. No. 1.3e+02;
    Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
|||||
Db 16 AAAAAAAAAAAAAA 1

RESULT 208
AAF30895/c
ID AAF30895 standard; DNA; 16 BP.
XX
AC AAF30895;
XX
DT 09-JUL-2001 (first entry)
XX

```

DE Oligonucleotide-minor groove binder complex.

KW ODN-MGB-LF; oligonucleotide; minor groove binder; latent fluorophore;

KW hybridisation; detection; fluorescence; probe; ss.

XX Synthetic.

OS

FH Key Location/Qualifiers

FT modified_base 1

FT /*tag= a

FT /note= "thymine modified by a minor groove binder (2-

FT dimethylaminonaphthalene-6- sulfonamide"

XX

PN WO200131063-A1.

XX

PD 03-MAY-2001.

XX

PF 26-OCT-2000; 2000WO-US029786.

XX

PR 26-OCT-1999; 99US-00428236.

XX

PA (EPOC-) EPOCH BIOSCIENCES INC.

XX

PI Dempcy RO, Afonina IA, Vermeulen NMJ;

XX

DR WPI; 2001-328656/34.

XX

XX Conjugate of oligonucleotide, minor groove binder and latent fluorophore,

PT useful for detecting specific nucleic acids, e.g. for single-nucleotide

PT mismatch discrimination.

XX

PS Disclosure; Page 101; 105pp; English.

XX

CC The present sequence is that of an oligonucleotide (ODN)-minor groove

CC binder (MGB) complex. MGBs bind in a non-intercalating manner to the

CC minor groove of non-single-stranded DNA, RNA or their hybrids. ODN-MGB-LF

CC conjugates of the invention also comprise a latent fluorophore (LF),

CC which binds similarly to the MGB but in an intercalating manner, or lies

CC in the minor groove, or is oriented in some other way to the DNA molecule

CC by MGB, such that it becomes fluorescent (or its fluorescent properties

CC change detectably). The conjugates are used as hybridisation probes and

CC amplification primers for fluorescent detection of specifically

CC hybridising sequences, for analysis or diagnosis, especially (real-time)

CC PCR, for single-nucleotide mismatch discrimination, target or signal

CC amplification, array-based assays and sequencing, including detection of

CC double-stranded DNA by triplex formation

XX

SQ Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

Query Match 1.1%; Score 16; DB 1; Length 16;

Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496

Db 16 AAAAAAAAAAAAAA 1

RESULT 209

AAF30880/C

ID AAF30880 standard; DNA; 16 BP.

XX

AC AAF30880;

XX

DT 09-JUL-2001 (first entry)

XX

DE Oligonucleotide portion of ODN-MGB-LF conjugate.

XX

KW ODN-MGB-LF; oligonucleotide; minor groove binder; latent fluorophore;

KW hybridisation; detection; fluorescence; probe; ss.

XX

OS Synthetic.

XX

PN WO200131063-A1.

XX

PD 03-MAY-2001.

XX

PF 26-OCT-2000; 2000WO-US029786.

XX

PR 26-OCT-1999; 99US-00428236.

XX

PA (EPOC-) EPOCH BIOSCIENCES INC.

XX

PI Dempcy RO, Afonina IA, Vermeulen NMJ;

XX

DR WPI; 2001-328656/34.

XX

XX Conjugate of oligonucleotide, minor groove binder and latent fluorophore,

PT useful for detecting specific nucleic acids, e.g. for single-nucleotide

PT mismatch discrimination.

XX

PS Disclosure; Page 101; 105pp; English.

XX

CC The present sequence is that of an oligonucleotide (ODN) component of an

CC ODN-MGB (minor groove binder)-LF (latent fluorophore) conjugate of the

CC invention. MGBs bind in a non-intercalating manner to the minor groove of

CC non-single-stranded DNA, RNA or their hybrids, while a LF binds similarly

CC but in an intercalating manner, or lies in the minor groove, or is

CC oriented in some other way to the DNA molecule by MGB, such that it

CC becomes fluorescent (or its fluorescent properties change detectably).

CC The conjugates are used as hybridisation probes and amplification primers

CC for fluorescent detection of specifically hybridising sequences, for

CC analysis or diagnosis, especially (real-time) PCR, for single-nucleotide

CC mismatch discrimination, target or signal amplification, array-based

CC assays and sequencing, including detection of double-stranded DNA by

CC triplex formation. Many different targets can be detected a single

CC reaction vessel. The present ODN-MGB-LF conjugate was used to demonstrate

CC hybridisation-triggered fluorescence. Upon hybridisation to the

CC complementary target sequence there was an increase in fluorescence

CC yield, measured as the ratio of the fluorescence emitted by the hybrid

CC between the ODN-MGB-LF conjugate and its target sequence to the

CC fluorescence emitted by unhybridised (i.e. single-stranded) ODN-MGB-LF,

CC of 8.3

XX

SQ Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

Query Match 1.1%; Score 16; DB 1; Length 16;

Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496

Db 16 AAAAAAAAAAAAAA 1

RESULT 210

AAH42481/C

ID AAH42481 standard; DNA; 16 BP.

XX

AC AAH42481;

XX

DT 01-OCT-2001 (first entry)

XX

DE Oligonucleotide used to produce branched chain compounds.

XX

KW Branched chain compound; nucleic acid synthesis; primer extension;

KW reverse transcription; nucleic acid hybridization;

KW nucleic acid amplification; ss.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT modified_base 1

FT /*tag= a

FT /note= "COOH attached"

FT misc_feature 2.3

```

FT      /*tag= c
FT      /note= "branch present"
FT      modified_base 2 /*tag= b
FT      /note= "COOH attached"
FT      EP1111068-A1.
PN      XX
XX      PD
XX      27-JUN-2001.
XX      XX
XX      21-DEC-1999; 99EP-00125484.
XX      PR
XX      21-DEC-1999; 99EP-00125484.
XX      PA (LION-) LION BIOSCIENCE AG.
XX      PA (VBCG-) VBC GENOMICS GMBH.
XX      PI Schmidt W, Hiller R, Huber M, Mueller M;
XX      DR WPI; 2001-466959/51.
XX      XX
XX      Branded compounds useful in e.g. nucleic acid synthesis reaction
PT      comprises nucleic acid moieties optionally extended by a polymerase.
XX      PS
XX      Example 1; Page 10; 31pp; English.
XX      CC
XX      The specification describes branched compounds containing nucleic acid
XX      moieties optionally extended by a polymerase. The branched chain
XX      compounds of the invention are used in nucleic acid synthesis reaction,
XX      primer extension reaction, reverse transcription reaction of RNA into
XX      DNA, nucleic acid hybridization experiment (for identifying sequence of a
XX      nucleic acid), and nucleic acid amplification experiment (for analysing
XX      the expression pattern of genes). The compounds are also used in solid-
XX      phase enzymatic reactions. The present sequence was used in the course of
XX      the invention to produce branched chain compounds
XX      SQ
XX      Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

Query Match      1.1%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAA 1496
Db      16 AAAAAAAAAAAAAA 1

RESULT 212
AAD56451/c
ID      AAD56451 standard; DNA; 16 BP.
XX      AC
XX      AAD56451;
XX      DT
XX      07-AUG-2003 (first entry)
XX      DE
XX      2'-F-ANA antisense oligo #6, to elicit RNase H degradation of target RNA.
XX      KW
XX      Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
XX      antisense; ss.
XX      OS
XX      Unidentified.
XX      FH
XX      Key      Location/Qualifiers
XX      modified_base 1..16
XX      FT      /*tag= a
XX      FT      /mod_base= OTHER
XX      FT      /note= "2'-deoxy-2'-fluoroarabinothymidine"
XX      FT      misc_feature 8..9
XX      FT      /*tag= b
XX      FT      /note= "Bases 8 and 9 are linked by two secouridine
XX      FT      linkers which is represented as s in page 49 and x in
XX      FT      page 57 and Fig 7 and 8 of the specification"
XX      PN
XX      WO2003037909-A1.
XX      PD
XX      08-MAY-2003.
XX      XX
XX      29-OCT-2002; 2002WO-CA001628.
XX      PR
XX      29-OCT-2001; 2001US-0330719P.
XX      PA (UYMC-) UNIV MCGILL.
XX      XX

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PI Danha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;
XX WPI; 2003-421516/39.
XX
XX Novel acyclic linker-containing oligonucleotide useful for preventing or
XX decreasing translation, reverse transcription and/or replication of a
XX target RNA in a system, comprises a modified deoxyribonucleotide.
XX
XX Example 2; Fig 7; 104pp; English.
XX
XX The invention relates to an acyclic linker-containing oligonucleotide
XX comprising at least one modified deoxyribonucleotide. Oligonucleotides of
XX the invention are useful for preventing or decreasing translation,
XX reverse transcription and/or replication of a target RNA in a system.
XX They are useful for selectively preventing gene expression in a sequence-
XX specific manner, for hybridising to complementary RNA such as cellular
XX mRNA or viral RNA, to hybridise to and induce cleavage of complementary
XX RNA. They are also useful therapeutically in formulations or medicaments
XX to prevent or treat a disease characterised by the expression of a
XX particular target RNA. The invention is used in gene therapy. The present
XX sequence is an antisense oligo used to elicit human RNase (ribonuclease)
XX H degradation of target RNA. This sequence is used in the exemplification
XX of the invention
XX
XX Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 16; DB 1; Length 16;
XX Best Local Similarity 100.0%; Pred. No. 1.3e+02;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1481 AAAAAAAAAAAAAA 1496
DB 16 AAAAAAAAAAAAAA 1
XX
RESULT 213
AAL54078/c
ID AAL54078 standard; DNA; 16 BP.
XX
XX AAL54078;
XX
XX 06-MAR-2003 (first entry)
XX
XX Oligo-homodexyribonucleotide sequence, oligo dT.
XX
XX Detection; single-stranded sensor; detectable fluorescence emission;
XX forensic testing; paternity testing; tissue typing; hereditary disorder;
XX human population genetics; human evolutionary history; cystic fibrosis;
XX human haplotype diversity; Tay-Sachs; sickle-cell anaemia; ss.
XX
XX Unidentified.
XX
XX WO200284271-A2.
XX
XX 24-OCT-2002.
XX
XX 16-APR-2002; 2002WO-US012176.
XX
XX 16-APR-2001; 2001US-00836579.
XX
XX (REGC ) UNIV CALIFORNIA.
XX (CHAJ/) CHA J N.
XX
XX Cha JN, Morse DE, Stucky GD;
XX
XX WPI; 2003-103378/09.
XX
XX Detecting polynucleotides, for pharmacogenetic testing, comprises
XX contacting a target polynucleotide with a complementary single-stranded
XX sensor polynucleotide and an agent that allows the sensor to fluoresce
XX upon excitation.
XX
XX Example 1; Page 25; 41pp; English.
XX

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XX
XX The invention relates to a novel assay for detecting a polynucleotide in
XX a sample, which comprises: contacting a sample suspected of containing a
XX target polynucleotide with a predetermined single-stranded sensor
XX polynucleotide complementary to the target polynucleotide, in a solution
XX comprising an agent that is a nonequeous solvent that allows the sensor
XX polynucleotide to produce a detectable fluorescence emission; exciting
XX the sensor polynucleotide; and determining fluorescence emission. The
XX assay is useful for detecting a single or double-stranded target
XX polynucleotide, such as, DNA or RNA in a sample. The assay finds use in a
XX wide variety of different applications including pharmacogenetic testing,
XX forensic testing to identify the species or individual which was the
XX source of a forensic specimen, in anthropological setting, paternity
XX testing, testing for compatibility between prospective tissue or blood
XX donors and patients and in screening for hereditary disorders. The method
XX is also useful to study alterations of gene expression in response to a
XX stimulus, disease, drug or medication, and other applications include
XX human population genetics, analyses of human evolutionary history and
XX characterisation of human haplotype diversity. The method is useful for
XX detecting polynucleotide sequences from contaminants or pathogens
XX including bacteria, yeast, and viruses to detect single nucleotide
XX polymorphisms, which may be associated with particular alleles or subsets
XX of alleles. The method is useful for detection of mutations and to detect
XX nucleotide sequences associated with increased risk of diseases or
XX disorders including cystic fibrosis, Tay-Sachs, and sickle-cell anaemia.
XX This polynucleotide sequence represents an oligonucleotide sequence used
XX in a fluorescence technique of the invention
XX
XX Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 16; DB 1; Length 16;
XX Best Local Similarity 100.0%; Pred. No. 1.3e+02;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1481 AAAAAAAAAAAAAA 1496
DB 16 AAAAAAAAAAAAAA 1
XX
RESULT 214
ADB68519/c
ID ADB68519 standard; DNA; 16 BP.
XX
XX ADB68519;
XX
XX 04-DEC-2003 (first entry)
XX
XX DNA hybridisation oligomer SEQ ID 9.
XX
XX hydroxyproline nucleic acid; HypNA; PNA; peptide nucleic acid;
XX gene expression; respiration; secretion; signalling;
XX ion-channel activity; cell motility; developmental phenotype;
XX tumour regression; hybridisation; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX misc_difference 1 /tag= a
XX /note= "Optional N-terminal acetyl"
XX
XX WO2003068798-A2.
XX
XX 21-AUG-2003.
XX
XX 07-FEB-2003; 2003WO-US003904.
XX
XX 09-FEB-2002; 2002US-00072975.
XX
XX (ACTI-) ACTIVE MOTIF.
XX
XX Efimov V, Fernandez J, Archdeacon D, Archdeacon J, Choob M;
XX

```

```

DR WPI; 2003-689653/65.
XX
PT Method of inhibiting expression of genes or RNA transcripts, useful for
PT therapy and determining effects of genes, by administering oligomers
PT containing hydroxyproline nucleic acid.
XX
PS Example 17; Page 233; 240pp; English.
XX
PS The invention relates to a novel method of inhibiting the expression of
CC one or more genes or RNA transcripts by administering at least one
CC oligonucleotide analogue that includes at least one hydroxyproline
CC nucleic acid (HyPNA) monomer to a cell or organism or their extracts. The
CC oligonucleotides of the invention may be used to monitor properties
CC including gene expression, respiration, secretion, signalling, ion-
CC channel activity, cell motility, developmental phenotype and tumour
CC regression. Furthermore, they may be utilised to determine the effects of
CC particular genes, as antisense or homologous recombination constructs
CC e.g. for creating animal models of disease and finally, for increasing
CC the activity of some enzymes, such as polymerases. The current sequence
CC is that of the DNA hybridisation oligomer SEQ ID 9 of the invention. This
CC sequence may also comprise a peptide nucleic acid (PNA).
XX
SQ Sequence 16 BP; 0 A; 0 C; 0 G; 0 T; 16 U; 0 Other;
Query Match 1.1%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1496
DB 16 AAAAAAAAAAAAAA 1
RESULT 215
AAAX69800/c
ID AAAX69800 standard; RNA; 17 BP.
AC AAAX69800;
XX
XX 28-JUL-1999 (first entry)
XX
DE Human flt1 VEGF receptor hammerhead ribozyme substrate #1095.
XX
KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.
XX
OS Homo sapiens.
XX
XX WO9715662-A2.
XX
PD 01-MAY-1997.
XX
XX 25-OCT-1996; 96WO-US017480.
XX
XX 26-OCT-1995; 95US-0005974P.
XX
XX 11-JAN-1996; 96US-00584040.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX (CHIR ) CHIRON CORP.
XX
XX Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX
XX WPI; 1997-259017/23.
XX
XX 25-OCT-1996; 96WO-US017480.
XX
XX 26-OCT-1995; 95US-0005974P.
XX
XX 11-JAN-1996; 96US-00584040.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX (CHIR ) CHIRON CORP.
XX
XX Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX
XX WPI; 1997-259017/23.
XX
XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
XX stability - useful for treating e.g. tumour angiogenesis, psoriasis,
XX rheumatoid arthritis, etc., in a human patient.
XX
XX Claim 4; Page 79; 218pp; English.
XX
CC The present invention describes nucleic acid molecules which modulate the
CC synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention
XX
SQ Sequence 17 BP; 0 A; 1 C; 0 G; 0 T; 16 U; 0 Other;
Query Match 1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1496
DB 17 AAAAAAAAAAAAAA 2
RESULT 216
AAAX69801/c
ID AAAX69801 standard; RNA; 17 BP.
XX
XX AAAX69801;
XX
XX 28-JUL-1999 (first entry)
XX
DE Human flt1 VEGF receptor hammerhead ribozyme substrate #1096.
XX
KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.
XX
OS Homo sapiens.
XX
XX WO9715662-A2.
XX
PD 01-MAY-1997.
XX
XX 25-OCT-1996; 96WO-US017480.
XX
XX 26-OCT-1995; 95US-0005974P.
XX
XX 11-JAN-1996; 96US-00584040.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX (CHIR ) CHIRON CORP.
XX
XX Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX
XX WPI; 1997-259017/23.
XX
XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
XX stability - useful for treating e.g. tumour angiogenesis, psoriasis,
XX rheumatoid arthritis, etc., in a human patient.
XX
XX Claim 4; Page 79; 218pp; English.
XX
CC The present invention describes nucleic acid molecules which modulate the
CC synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention
XX

```

SQ Sequence 17 BP; 0 A; 1 C; 0 G; 0 T; 16 U; 0 Other;
 Query Match 1.1%; Score 16; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1481 AAAAAAAAAAAAAA 1496
 16 AAAAAAAAAAAAAA 1
 DB
 RESULT 217
 AAV49503/c
 ID AAV49503 standard; cDNA to mRNA; 17 BP.
 XX
 AAV49503;
 XX
 18-NOV-1998 (first entry)
 XX
 Human eosinophil cell activator HVC002 primer #1.
 DE
 Eosinophil cell activator; treatment; diagnosis; malignant tumour;
 KW
 parasitic infection; allergic inflammation; eosinophilic pneumonia;
 KW
 rapid onset eosinophilia; autoimmune disease; gene therapy; primer; ss.
 XX
 Synthetic.
 OS
 Homo sapiens.
 OS
 WO9824817-A1.
 PN
 11-JUN-1998.
 XX
 05-DEC-1997; 97WO-JP004470.
 XX
 05-DEC-1996; 96JP-00325762.
 XX
 (KYOW) KYOWA HAKKO KOGYO KK.
 XX
 Yoshiue H, Saito A, Nakagawa S, Kuga T, Shinkai A, Koike M;
 PI
 Nishi T;
 XX
 WPI; 1998-333261/29.
 DR
 DNA and encoded protein which activates eosinophil cells - for treatment
 of cancer, parasite infection, autoimmune disease and allergic
 inflammation.
 PT
 Example 1; Page 64; 92pp; Japanese.
 PS
 AAV49503-V49507 are primers used in the isolation of a human eosinophil
 cell activator. This protein and antibodies generated from the protein
 can be used for treatment and diagnosis of malignant tumours, parasitic
 infections, allergic inflammation, eosinophilic pneumonia, rapid onset
 eosinophilia, and autoimmune diseases. DNA can be used for diagnosis, and
 the antisense DNA in gene therapy of these disorders. The protein can be
 used for screening of potential agonists or antagonists of its activity
 XX
 Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
 SQ
 Query Match 1.1%; Score 16; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1480 TAAAAAAAAAAAAA 1495
 17 TAAAAAAAAAAAAA 2
 DB
 RESULT 218
 AAX18371/c
 ID AAX18371 standard; DNA; 17 BP.
 XX
 AAX18371;
 AC

SQ Sequence 17 BP; 0 A; 1 C; 0 G; 0 T; 16 U; 0 Other;
 Query Match 1.1%; Score 16; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1481 AAAAAAAAAAAAAA 1496
 16 AAAAAAAAAAAAAA 1
 DB
 RESULT 217
 AAV49503/c
 ID AAV49503 standard; cDNA to mRNA; 17 BP.
 XX
 AAV49503;
 XX
 18-NOV-1998 (first entry)
 XX
 Human eosinophil cell activator HVC002 primer #1.
 DE
 Eosinophil cell activator; treatment; diagnosis; malignant tumour;
 KW
 parasitic infection; allergic inflammation; eosinophilic pneumonia;
 KW
 rapid onset eosinophilia; autoimmune disease; gene therapy; primer; ss.
 XX
 Synthetic.
 OS
 Homo sapiens.
 OS
 WO9824817-A1.
 PN
 11-JUN-1998.
 XX
 05-DEC-1997; 97WO-JP004470.
 XX
 05-DEC-1996; 96JP-00325762.
 XX
 (KYOW) KYOWA HAKKO KOGYO KK.
 XX
 Yoshiue H, Saito A, Nakagawa S, Kuga T, Shinkai A, Koike M;
 PI
 Nishi T;
 XX
 WPI; 1998-333261/29.
 DR
 DNA and encoded protein which activates eosinophil cells - for treatment
 of cancer, parasite infection, autoimmune disease and allergic
 inflammation.
 PT
 Example 1; Page 64; 92pp; Japanese.
 PS
 AAV49503-V49507 are primers used in the isolation of a human eosinophil
 cell activator. This protein and antibodies generated from the protein
 can be used for treatment and diagnosis of malignant tumours, parasitic
 infections, allergic inflammation, eosinophilic pneumonia, rapid onset
 eosinophilia, and autoimmune diseases. DNA can be used for diagnosis, and
 the antisense DNA in gene therapy of these disorders. The protein can be
 used for screening of potential agonists or antagonists of its activity
 XX
 Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
 SQ
 Query Match 1.1%; Score 16; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1480 TAAAAAAAAAAAAA 1495
 17 TAAAAAAAAAAAAA 2
 DB
 RESULT 218
 AAX18371/c
 ID AAX18371 standard; DNA; 17 BP.
 XX
 AAX18371;
 AC

XX WPI; 1999-183822/16.
XX Peptides having at least two new nucleotides - useful as primers in RT-
PT PCR.
XX
PS Disclosure; Page 11; 19pp; Japanese.
XX
CC This sequence represents a primer of the invention. The invention relates
CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
CC a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC natural number indicating the repetition of alpha; beta, delta = V or N;
CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC repetition of gamma, in which thymine expressed by gamma is composed of
CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC useful as primers for RT-PCR and determination of base sequences. The new
CC sequences allow for reproductive and highly efficient analysis of gene
CC sequences
XX
SQ Sequence 17 BP; 2 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAAAAAAA 1495
DB 16 TAAAAAATAAAAAAAAAA 1
|||||||

RESULT 220
AA30179/C
ID AAA30179 standard; DNA; 17 BP.
XX
AC AAA30179;
DT 16-AUG-2000 (first entry)
XX
DE PCR primer GT15A used in pollenosis associated gene identification.
XX
KW Pollenosis-associated protein; high pollen-specific immunoglobulin E;
KW IGE; diagnose; cedar pollenosis; treatment; human; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200020575-A1.
XX
PD 13-APR-2000.
XX
PF 06-OCT-1999; 99WO-JP005506.
XX
PR 06-OCT-1998; 98JP-00284610.
XX
PA (GENO-) GENOX RES INC.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Lu N, Ogawa K;
XX
DR WPI; 2000-317712/27.
XX
PT Gene highly expressed in patients with high cedar pollen-specific IGE
PT levels, useful for diagnosing pollenosis, and screening candidate
PT compounds for pollenosis treatment.
XX
PS Example 6; Page 38; 44pp; Japanese.
XX
CC This sequence represents a PCR primer used in the identification of a
CC human pollenosis associated gene. The gene is highly expressed in
CC individuals with high pollen-specific immunoglobulin E (IGE) levels. The
CC invention relates to the nucleotide sequence encoding the pollenosis
CC associated protein, diagnosing pollenosis and screening candidate

CC compounds for treating pollenosis. The gene can be used in diagnosing
CC pollenosis, particularly cedar pollenosis, and screening candidate
CC compounds for pollenosis treatment
XX
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAAAAAAA 1495
DB 17 TAAAAAATAAAAAAAAAA 2
|||||||

RESULT 221
AA82720/C
ID AA82720 standard; DNA; 17 BP.
XX
AC AA82720;
XX
DT 10-NOV-2000 (first entry)
XX
DE Human IGA nephropathy-associated cDNA primer #61.
XX
KW IGA nephropathy-associated protein; diagnosis; treatment; antisense;
KW human; primer; ss.
XX
OS Homo sapiens.
XX
PN WO963085-A1.
XX
PD 09-DEC-1999.
XX
PF 28-MAY-1999; 99WO-JP002855.
XX
PR 02-JUN-1998; 98JP-00152603.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Ishiwa T, Sakurada M, Kawabata A, Nakagawa S, Nishi T, Kuga T;
PI Sawada S, Takei M, Shibata K, Furuya A;
XX
DR WPI; 2000-097328/08.
XX
PT DNA sequences preferentially expressed in IGA nephropathy patients,
PT proteins encoded by them, and antibodies to those proteins.
XX
PS Claim 3; Page 169; 180pp; Japanese.
XX
CC This invention describes novel DNA sequences preferentially expressed in
CC IGA nephropathy patients, and DNA sequences stringently hybridizing to
CC them. Independent claims cover diagnostic reagents for IGA nephropathy
CC incorporating the antisense sequences; the treatment of IGA nephropathy
CC using the antisense sequences for mRNA inhibition; proteins associated
CC with IGA nephropathy, containing sequences encoded by the DNA sequences;
CC antibodies recognizing these proteins; the production of the proteins by
CC culture of host cells transfected with DNA encoding them; diagnostic
CC reagents for IGA nephropathy containing the antibodies; and compositions
CC for the treatment of IGA nephropathy which contain the antibodies. The
CC products of the invention can be used for the diagnosis and treatment of
CC IGA nephropathy. This sequence represents a primer used in the isolation
CC and identification of the human IGA nephropathy-associated proteins
CC described in the method of the invention
XX
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAAAAAAA 1495
|||||||

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Db      17 TAAAAAAAAAAAAAAAAA 2

RESULT 222
AAZ36739/c
ID      AAZ36739 standard; DNA; 17 BP.
XX
XX
AC      AAZ36739;
XX
XX
DT      13-MAR-2000 (first entry)
DE
DE      Anchored oligo(dT) primer AT15A used for modified differential display.
KW
KW      Stimulus-regulated nucleic acid; sequence profile; nucleic acid level;
KW      differentially expressed nucleic acid; disease state; cancer;
KW      autoimmune disease; infectious disease; aging; developmental disorder;
KW      proliferative disorder; neurological disorder; toxicity; primer;
KW      treatment resistance; differential expression; drug discovery;
KW      growth factor; epidermal growth factor; radiation; stress; pathogen; ss.
XX
XX      Synthetic.
OS
XX
XX
PN      WO9955913-A2.
XX
XX      04-NOV-1999.
XX
XX      27-APR-1999; 99WO-US009119.
XX
XX      27-APR-1998; 98US-0083331P.
PR      27-AUG-1998; 98US-0098070P.
PR      04-FEB-1999; 99US-0118624P.
XX
XX      (KIMM-) KIMMEL CANCER CENT SIDNEY.
PA
XX
XX      McClelland M, Welsh J, Trenkle T;
PI
XX
XX      WPI; 2000-086388/07.
DR
XX
XX      Measuring expression of low abundance reduced complexity target nucleic
XX      acid molecules.
PT
XX
XX      Example 3; Page 91; 187pp; English.
PS
XX
XX      AAZ36739-41 represent oligo(dT) primers used for modified differential
XX      display, in the method of the invention. The specification describes a
XX      method for measuring the level of two or more nucleic acid molecules in a
XX      target. The method comprises contacting a probe with an arbitrarily or
XX      statistically sampled target and detecting the amount of specific binding
XX      of the target to the probe. The methods can be used to identify
XX      differentially expressed nucleic acid molecules associated with disease
XX      states, such as cancer, autoimmune disease, infectious disease, aging,
XX      developmental disorder, proliferative disorder or neurological disorder.
XX      Alternatively the methods can be used to assess the efficacy or toxicity
XX      of or a resistance to a treatment. Also the methods can be used to
XX      determine differential expression of nucleic acid molecules in response
XX      to a stimulus, e.g. a chemical, drug or growth factor (especially
XX      epidermal growth factor), radiation, stress or a pathogen. The methods
XX      can also be used to determine co-regulated genes that can be potential
XX      targets for drug discovery
XX
SQ      Sequence 17 BP; 2 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match      1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1480 TAAAAAAAAAAAAAAAAA 1495
Db      17 TAAAAAAAAAAAAAAAAA 2

RESULT 223
AAZ25450/c
ID      AAZ25450 standard; DNA; 17 BP.
XX
XX
AC      AAZ25450;
XX
XX
DT      19-JUL-2000 (first entry)
DE
DE      Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1948.
KW
KW      Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
KW      hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW      gene expression modification; cancer; phosphorothioate; endonuclease;
KW      anticancer; breast cancer; endometrium cancer; ss.
XX
XX      Homo sapiens.
OS
XX
XX      WO9954459-A2.
PN
XX
XX      28-OCT-1999.
PD
XX
XX      19-APR-1999; 99WO-US008547.
XX
XX      20-APR-1998; 98US-0082404P.
PR      23-JUN-1998; 98US-00103636.
XX
XX      (RIBO-) RIBOZYME PHARM INC.
PA
XX
XX      Thompson JD, Beigelman L, McSwiggen JA, Karpeisky A, Bellon L;
XX      Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;
XX      Matulic-Adamic J;
PI
XX
XX      WPI; 2000-013248/01.
DR
XX
XX      New nucleic acids that interact, and optionally cleave, target sequences,
XX      used to treat cancer.
PT
XX
XX      Claim 77; Page 79; 148pp; English.
PS
XX
XX      The present invention describes nucleic acids (A) that interact stably
XX      with a target sequence and contain at least one phosphoro(di)thioate
XX      link, having endonuclease activity. (A), and more generally any catalytic
XX      nucleic acid (A') that modulates expression of the oestrogen receptor
XX      gene, are used to treat cancer (particularly of breast or endometrium),
XX      in vivo or by transforming cells ex vivo and implanting treated cells, or
XX      for other conditions associated with levels of oestrogen receptor.
XX      Because of the high selectivity for targeted RNA, (A) can also be used to
XX      correlate inhibition of gene expression with alterations in phenotype,
XX      particularly for identification of therapeutic targets, and as research
XX      reagents (for RNA, in the same way that restriction endonucleases are
XX      used with DNA). The combination of modifications in (A) improves
XX      resistance to nucleases, binding affinity and/or activity. AAZ23503 to
XX      AAZ24748 represent oestrogen receptor hammerhead ribozyme sequences, and
XX      AAZ25993 to AAZ26105 represent oestrogen receptor hairpin ribozyme
XX      sequences, and AAZ26107 to AAZ26218 represent their corresponding target
XX      sequences. AAZ26219 to AAZ26271 represent other ribozyme sequences and
XX      antisense oligonucleotides used in the exemplification of the present
XX      invention
XX
SQ      Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

Query Match      1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAAAAAA 1496
Db      17 AAAAAAAAAAAAAAAAAA 2

RESULT 224
AAZ25449/c
ID      AAZ25449 standard; DNA; 17 BP.
XX
XX

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AC AAA25449;
DE 19-JUL-2000 (first entry)
DE Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1947.
DE Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW gene expression modification; cancer; phosphorothioate; endonuclease;
KW anticancer; breast cancer; endometrium cancer; ss.
XX Homo sapiens.
XX OS
XX PN WO9954459-A2.
XX PD 28-OCT-1999.
XX PF 19-APR-1999; 99WO-US008547.
XX PR 20-APR-1998; 98US-0082404P.
XX PR 23-JUN-1998; 98US-00103636.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PI Thompson JD, Beigelman L, Mcswiggen JA, Karpeisky A, Bellon L;
XX PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;
XX PI Matulic-Adamic J;
XX DR WPI; 2000-013248/01.
XX DR New nucleic acids that interact, and optionally cleave, target sequences,
XX PT used to treat cancer.
XX PS Claim 77; Page 79; 148pp; English.
XX CC The present invention describes nucleic acids (A) that interact stably
XX CC with a target sequence and contain at least one phosphorodithioate
XX CC link, having endonuclease activity. (A), and more generally any catalytic
XX CC nucleic acid (A') that modulates expression of the oestrogen receptor
XX CC gene, are used to treat cancer (particularly of breast or endometrium),
XX CC in vivo or by transforming cells ex vivo and implanting treated cells, or
XX CC for other conditions associated with levels of oestrogen receptor.
XX CC Because of the high selectivity for targeted RNA, (A) can also be used to
XX CC correlate inhibition of gene expression with alterations in phenotype,
XX CC particularly for identification of therapeutic targets, and as research
XX CC reagents (for RNA, in the same way that restriction endonucleases are
XX CC used with DNA). The combination of modifications in (A) improves
XX CC resistance to nucleases, binding affinity and/or activity. AAA23503 to
XX CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
XX CC AAA25993 to AAA26105 represent their corresponding target sequences.
XX CC sequences, and AAA26107 to AAA26218 represent their corresponding target
XX CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
XX CC antisense oligonucleotides used in the exemplification of the present
XX CC invention
XX SQ Sequence 17 BP; 0 A; 0 C; 1 G; 16 T; 0 U; 0 Other;

Query Match 1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
DB 17 AAAAAAAAAAAAAA 2

RESULT 225
AAA25451/C
ID AAA25451 standard; DNA; 17 BP.
XX AC
XX AC AAA25451;
XX DT
XX 30-JAN-2001 (first entry)

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DT 19-JUL-2000 (first entry)
DE Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1949.
DE Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW gene expression modification; cancer; phosphorothioate; endonuclease;
KW anticancer; breast cancer; endometrium cancer; ss.
XX Homo sapiens.
XX OS
XX PN WO9954459-A2.
XX PD 28-OCT-1999.
XX PF 19-APR-1999; 99WO-US008547.
XX PR 20-APR-1998; 98US-0082404P.
XX PR 23-JUN-1998; 98US-00103636.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PI Thompson JD, Beigelman L, Mcswiggen JA, Karpeisky A, Bellon L;
XX PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;
XX PI Matulic-Adamic J;
XX DR WPI; 2000-013248/01.
XX DR New nucleic acids that interact, and optionally cleave, target sequences,
XX PT used to treat cancer.
XX PS Claim 77; Page 79; 148pp; English.
XX CC The present invention describes nucleic acids (A) that interact stably
XX CC with a target sequence and contain at least one phosphorodithioate
XX CC link, having endonuclease activity. (A), and more generally any catalytic
XX CC nucleic acid (A') that modulates expression of the oestrogen receptor
XX CC gene, are used to treat cancer (particularly of breast or endometrium),
XX CC in vivo or by transforming cells ex vivo and implanting treated cells, or
XX CC for other conditions associated with levels of oestrogen receptor.
XX CC Because of the high selectivity for targeted RNA, (A) can also be used to
XX CC correlate inhibition of gene expression with alterations in phenotype,
XX CC particularly for identification of therapeutic targets, and as research
XX CC reagents (for RNA, in the same way that restriction endonucleases are
XX CC used with DNA). The combination of modifications in (A) improves
XX CC resistance to nucleases, binding affinity and/or activity. AAA23503 to
XX CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
XX CC AAA25993 to AAA26105 represent their corresponding target sequences.
XX CC sequences, and AAA26107 to AAA26218 represent their corresponding target
XX CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
XX CC antisense oligonucleotides used in the exemplification of the present
XX CC invention
XX SQ Sequence 17 BP; 0 A; 0 C; 1 G; 16 T; 0 U; 0 Other;

Query Match 1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
DB 16 AAAAAAAAAAAAAA 1

RESULT 226
AAA98232/C
ID AAA98232 standard; DNA; 17 BP.
XX AC
XX AC AAA98232;
XX DT
XX 30-JAN-2001 (first entry)

```

DE Human retrovirus HERV LTR PCR primer #31.
 XX Cell-specific expression; tissue-specific expression; gene therapy; LTR;
 KW U3-R segment; long terminal repeat; retroviral expression vector;
 KW PCR primer; ss.
 XX
 OS Human endogenous retrovirus.
 XX
 XX WO200053789-A2.
 XX
 XX 14-SEP-2000.
 XX
 XX 09-MAR-2000; 2000WO-EP002064.
 XX
 XX 10-MAR-1999; 99DE-01010650.
 XX
 XX (GSFU-) GSF FORSCHUNGSZENTRUM UMWELT & GESUNDHEIT.
 XX
 XX Leib-Moesch C, Schoen U, Baust C;
 XX
 XX WPI; 2000-587442/55.
 XX
 XX Retroviral expression vector, useful in gene therapy, contains a promoter
 PT from a human endogenous retrovirus to provide cell-specific expression.
 XX
 XX Disclosure; Page 27; 67pp; German.
 XX
 XX This invention describes a novel retroviral expression vector (A)
 CC containing DNA sequences (I) for packaging vector RNA and for cell-
 CC specific expression of proteins or peptides encoding by heterologous DNA
 CC (II). The sequences controlling cell-specific expression contain a cell-
 CC specific regulatable promoter region (P) from a human endogenous
 CC retrovirus (HERV) DNA sequence. The invention also describes (a) mRNA and
 CC RNA of (A); (b) prokaryotic and eukaryotic cells containing (A); (c)
 CC eukaryotic cells containing (A) in integrated form; (d) virions
 CC containing a retroviral expression vector RNA derived from (A); (e) a
 CC method for producing the virions of (d); (f) a method for incorporating
 CC protein-encoding nucleic acid sequences into a eukaryotic cell by
 CC infection with the virions of (d); and (g) a retroviral vector system
 CC containing (A) and a packaging cell line, that contains at least one
 CC (recombinant) retrovirus construct that encodes for the packaging
 CC proteins of (A). (A) are used for cell- or tissue-specific expression of
 CC foreign genes for gene therapy and to produce virions for introducing
 CC (II) into the chromosomal DNA of eukaryotic cells, preferably mammalian
 CC and specifically human. (A) retain the advantages of usual retroviral
 CC promoters with all the signal structures required for transcription in a
 CC small region within the U3-R segment, but without their disadvantages
 CC (excessive strength and limited cell specificity). Since (A) are derived
 CC from endogenous (harmless) viral sequences, they do not introduce any new
 CC viral sequences into the genome and recombination will not create new
 CC types of retroviruses. The promoters provide cell or tissue specific
 CC expression, according to which HERV they are derived from
 XX
 SQ Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
 Query Match 1.1%; Score 16; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1481 AAAAAAAAAAAAAA 1496
 Db 17 AAAAAAAAAAAAAA 2
 RESULT 227
 AAAS0197/c
 ID AAAS0197 standard; DNA; 17 BP.
 XX
 AC AAAS0197;
 XX
 DT 07-NOV-2000 (first entry)
 XX
 DE 2'-Methoxyethoxy-modified phosphorothioate oligonucleotide.

XX Phosphorothioate oligonucleotide; H-phosphonate chemistry; ss.
 KW Synthetic.
 OS
 PH Key Location/Qualifiers
 FT modified_base 1..19
 FT /tag= a
 FT /note= "2'-methoxyethoxy modified thymidine"
 FT modified_base 1..17
 FT /tag= b
 FT /note= "phosphorothioate internucleoside linkages"
 XX
 PN WO200047593-A1.
 XX
 XX 17-AUG-2000.
 XX
 XX 11-FEB-2000; 2000WO-US003543.
 XX
 XX 12-FEB-1999; 99US-00250075.
 XX
 XX (ISIS-) ISIS PHARM INC.
 XX
 XX Manoharan M, Maier MA;
 PI
 XX WPI; 2000-558189/51.
 XX
 XX Preparation of mixed backbone oligomeric compounds useful as e.g. primers
 PT for diagnostic tests, involves oxidation of H-phosphonate internucleoside
 PT linkages to phosphodiester internucleoside linkages.
 XX
 XX Example 12; Page 34; 49pp; English.
 XX
 XX The present sequence is that of a phosphorothioate oligonucleotide
 CC containing 20 T nucleobases, each having a 2'-methoxyethoxy group on its
 CC 5' ribosyl sugar moiety. It is an example of an oligomeric compound
 CC produced according to the methods of the invention. The invention
 CC provides compounds and methods for the preparation of mixed backbone
 CC oligomeric, or chimeric, compounds having phosphodiester internucleoside
 CC linkages in addition to phosphorothioate and/or phosphoramidate
 CC internucleoside linkages. The methods also include incorporation of
 CC boranophosphate internucleoside linkages. The methods utilize H-
 CC phosphonate intermediates that are coupled together forming contiguous
 CC regions of 1 or more H-phosphonate internucleoside linkages. Each
 CC contiguous region is subsequently oxidized to phosphodiester,
 CC phosphorothioate, phosphoramidate or boranophosphate internucleoside
 CC linkages prior to further elongation. Mixed backbone oligomeric compounds
 CC are prepared in this manner by oxidizing adjacent regions with different
 CC reagents. Oligomeric compounds of the invention are prepared using novel
 CC oxidation steps that oxidize a region of 1 or more H-phosphonate
 CC internucleoside linkages without degrading existing linkages that have
 CC been previously oxidized. The oligonucleotides obtained are useful as
 CC primers in PCR, probes, linkers, gene fragments and for other diagnostic
 CC tests on e.g. biological tissue, fluid, cells etc., as research reagents,
 CC and as antiviral agents
 XX
 SQ Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
 Query Match 1.1%; Score 16; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1481 AAAAAAAAAAAAAA 1496
 Db 17 AAAAAAAAAAAAAA 2
 RESULT 228
 AAC64202/c
 ID AAC64202 standard; DNA; 17 BP.
 XX
 AC AAC64202;
 XX

```

DT 21-FEB-2001 (first entry)
DE PCR anchor primer, SEQ ID NO:3, used in human gene 373 isolation.
XX
KW Human; pollinosis-associated gene 373; IgE; immunoglobulin E;
KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
KW drug screening; allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200065046-A1.
XX
PD 02-NOV-2000.
XX
PF 26-APR-2000; 2000WO-JP002730.
XX
PD 02-NOV-2000.
XX
PF 26-APR-2000; 2000WO-JP002730.
XX
PR 27-APR-1999; 99JP-00120489.
XX
PA (GENO-) GENOX RES INC.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX
DR WPI; 2000-687339/67.
XX
PT Pollinosis-associated gene 373 undergoing significantly low expression in
PT subjects with high cedar pollen-specific immunoglobulin-E levels, useful
PT in diagnosis of allergic diseases and screening drug candidates.
XX
PS Example 6; Page 69; 80pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 373 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC was isolated from T-cells from individuals allergic to cedar pollen using
CC the differential display method. The invention also relates also relates
CC to the protein encoded by pollinosis gene 373; expression constructs and
CC host cells comprising pollinosis-associated gene 373 nucleic acids;
CC pollinosis-associated gene 373 primers and probes; antibodies against the
CC protein encoded by the gene; methods of detection of pollinosis-
CC associated gene 373 nucleic acids; and a method of diagnosis of allergic
CC diseases via the detection of pollinosis-associated gene 373 nucleic
CC acids. The invention additionally encompasses methods of screening drug
CC candidates for the treatment of allergic disease by measuring the
CC expression of pollinosis-associated gene 373 in pollen antigen-stimulated
CC T-cells in the presence of a test compound relative to a control.
CC Pollinosis-associated gene 373 is useful in the diagnosis of allergic
CC diseases and in the screening of drug candidates for the treatment of
CC such diseases. The present sequence represents a PCR primer used in the
CC isolation of human pollinosis-associated gene 373 cDNA
XX
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAAAAAAA 1495
Db |||||
17 TAAAAAATAAAAAAAAAA 2

RESULT 229
AAC64181/c
ID AAC64181 standard; DNA; 17 BP.
XX
AC AAC64181;
XX
DT 21-FEB-2001 (first entry)
DE PCR anchor primer, SEQ ID NO:2, used in human gene 419 isolation.
XX
KW Human; pollinosis-associated gene 419; FAF-1 homologue;
XX
KW Human; pollinosis-associated gene 513; IgE; immunoglobulin E;
KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
KW drug screening; allergic disease; PCR primer; ss.
XX
XX

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```

KW Fas-associated factor-1; IgE; immunoglobulin E; cedar pollen allergy;
KW T-cell; reduced expression; detection; diagnosis; drug screening;
KW allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200065045-A1.
XX
PD 02-NOV-2000.
XX
PF 26-APR-2000; 2000WO-JP002729.
XX
PR 27-APR-1999; 99JP-00120490.
XX
PA (GENO-) GENOX RES INC.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX
DR WPI; 2000-687338/67.
XX
PT Pollinosis-associated gene 419 undergoing significantly low expression in
PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis
PT of allergic diseases and screening drug candidates.
XX
PS Example 6; Page 49; 77pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 419 which
CC exhibits reduced expression in the T-cells of individuals with high cedar
CC pollen-specific IgE (immunoglobulin E) levels. The gene was isolated from
CC T-cells from individuals allergic to cedar pollen using the differential
CC display method. Pollinosis-associated gene 419 has homology with the gene
CC encoding human Fas-associated factor-1 (FAF-1). The invention also
CC relates to the protein encoded by pollinosis gene 419; expression
CC constructs and host cells comprising pollinosis- associated gene 419
CC nucleic acids; pollinosis-associated gene 419 primers and probes;
CC antibodies against the protein encoded by the gene; methods of detection
CC of pollinosis-associated gene 419 nucleic acids; and a method of
CC diagnosis of allergic diseases via the detection of pollinosis-
CC associated gene 419 nucleic acids. The invention additionally encompasses
CC methods of screening drug candidates for the treatment of allergic
CC disease by measuring the expression of pollinosis-associated gene 419 in
CC pollen antigen-stimulated T-cells in the presence of a test compound
CC relative to a control. Pollinosis-associated gene 419 is useful in the
CC diagnosis of allergic diseases and in the screening of drug candidates
CC for the treatment of such diseases. The present sequence represents a PCR
CC primer used in the isolation of human pollinosis-associated gene 419 cDNA
XX
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAAAAAAA 1495
Db |||||
17 TAAAAAATAAAAAAAAAA 2

RESULT 230
AAC64171/c
ID AAC64171 standard; DNA; 17 BP.
XX
AC AAC64171;
XX
DT 21-FEB-2001 (first entry)
DE PCR anchor primer, SEQ ID NO:2, used in human gene 513 isolation.
XX
KW Human; pollinosis-associated gene 513; IgE; immunoglobulin E;
KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
KW drug screening; allergic disease; PCR primer; ss.
XX
XX

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XX WPI; 2000-687344/67.
XX
XX Pollinosis-associated gene 627 undergoing significantly low expression in
PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis
PT of allergic diseases and screening drug candidates.
XX
XX Example 6; Page 41; 51pp; Japanese.
XX
XX The invention relates to the human pollinosis-associated gene 627 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC was isolated from T-cells from individuals allergic to cedar pollen using
CC the differential display method. The invention also relates to methods of
CC detection of pollinosis-associated gene 627 nucleic acids; a method of
CC diagnosis of allergic diseases via the detection of pollinosis-associated
CC gene 627 nucleic acids; and a method of screening drug candidates for the
CC treatment of allergic disease by measuring the expression of pollinosis-
CC associated gene 627 in pollen antigen-stimulated T-cells in the presence
CC of a test compound relative to a control. Pollinosis-associated gene 627
CC is useful in the diagnosis of allergic diseases and in the screening of
CC drug candidates for the treatment of such diseases. The present sequence
CC represents a PCR primer used in the isolation of human pollinosis-
CC associated gene 627 cDNA
XX
XX Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1480 TAAAAAATAAAAAA 1495
DB 17 TAAAAAATAAAAAA 2
RESULT 233
AAC64230/C
ID AAC64230 standard; DNA; 17 BP.
XX
XX AAC64230;
AC
XX
XX 21-FEB-2001 (first entry)
DT
XX
XX PCR anchor primer, SEQ ID NO:2, used in human gene 795 isolation.
DE
XX
XX Human; pollinosis-associated gene 795; vimentin homologue; IgE;
KW immunoglobulin E; cedar pollen allergy; T-cell; reduced expression;
KW detection; diagnosis; drug screening; allergic disease; PCR primer; ss.
XX
XX Synthetic.
OS
XX
XX WO200065050-A1.
PN
XX
XX 02-NOV-2000.
PD
XX
XX 26-APR-2000; 2000WO-JP002734.
PF
XX
XX 27-APR-1999; 99JP-00120494.
PR
XX
XX (GENO-) GENOX RES INC.
PA (EISA) EISAI CO LTD.
XX
XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;
PI Yokoi A;
XX
XX WPI; 2000-687343/67.
XX
XX Pollinosis-associated gene 795 undergoing significantly low expression in
PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis
PT of allergic diseases and screening drug candidates.
XX
XX Example 6; Page 43; 61pp; Japanese.
XX
XX The invention relates to the human pollinosis-associated gene 795 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC was isolated from T-cells from individuals allergic to cedar pollen using
CC the differential display method. The invention also relates to methods of
CC detection of pollinosis-associated gene 795 nucleic acids; and a method of
CC diagnosis of allergic diseases via the detection of pollinosis-associated
CC gene 795 nucleic acids. The invention additionally encompasses methods of
CC screening drug candidates for the treatment of allergic disease by
CC measuring the expression of pollinosis-associated gene 795 in pollen
CC antigen-stimulated T-cells in the presence of a test compound relative to
CC a control. Pollinosis-associated gene 795 is useful in the diagnosis of
CC allergic diseases and in the screening of drug candidates for the
CC treatment of such diseases. The present sequence represents a PCR primer
CC used in the isolation of human pollinosis-associated gene 795 cDNA
XX
XX Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1480 TAAAAAATAAAAAA 1495
DB 17 TAAAAAATAAAAAA 2
RESULT 234
AAC92292/C
ID AAC92292 standard; DNA; 17 BP.
XX
XX AAC92292;
AC
XX
XX 22-MAR-2001 (first entry)
DT
XX
XX Human pollinosis-associated gene 465 related PCR primer SEQ ID NO:2.
DE
XX
XX Human; pollinosis-associated gene 465; pollen scattering; allergy;
KW allergic disease; PCR primer; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200073439-A1.
PN
XX
XX 07-DEC-2000.
PD
XX
XX 18-MAY-2000; 2000WO-JP003191.
PF
XX
XX 27-MAY-1999; 99JP-00148784.
PR
XX
XX (GENO-) GENOX RES INC.
PA (EISA) EISAI CO LTD.
XX
XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;
PI Yokoi A;
XX
XX WPI; 2001-061528/07.
XX
XX Pollinosis-associated gene 465 undergoing significantly low expression in
PT subjects after pollen scattering, useful in diagnosis of allergic
PT diseases and screening candidate compounds to regulate response of T
PT cells to antigen stimulus.
XX
XX Example 6; Page 43; 61pp; Japanese.
XX
XX

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CC The present invention describes the human pollinosis-associated gene 465
 CC which has a nucleic acid sequence of 3442 base pairs (bp), given in
 CC (AAC92291), that undergoes significantly low expression in subjects after
 CC pollen scattering, and is useful in the diagnosis of allergic diseases
 CC and screening candidate compounds for remedies capable of regulating the
 CC response of T cells to the stimulus by an antigen. The gene is useful in
 CC the diagnosis of allergic diseases and screening candidate compounds for
 CC remedies capable of regulating the response of T cells to the stimulus by
 CC an antigen. The present sequence represents a PCR primer which is used in
 CC an example from the present invention
 XX
 SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 1.1%; Score 16; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1480 TAAAAAATAAAAAAAAAA 1495
 DB 17 TAAAAAATAAAAAAAAAA 2

RESULT 235
 AAC91719/c
 ID AAC91719 standard; DNA; 17 BP.

XX AAC91719;
 AC
 XX
 DT 27-MAR-2001 (first entry)
 XX
 DE PCR anchor primer, SEQ ID NO:2, used in human gene 787 isolation.
 XX
 KW Human; pollinosis-associated gene 787; pollen allergy; T-cell;
 KW reduced expression; detection; diagnosis; drug screening;
 KW allergic disease; PCR primer; ss.
 XX
 OS Synthetic.

XX
 PN WO200073440-A1.
 XX
 PD 07-DEC-2000.
 XX
 PF 18-MAY-2000; 2000WO-JP003192.
 XX
 PR 27-MAY-1999; 99JP-00148785.
 XX
 PA (GENO-) GENOX RES INC.
 PA (EISA) EISAI CO LTD.

XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
 PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;
 PI Yokoi A;
 XX
 DR WPI; 2001-032159/04.

XX
 PT Pollinosis-associated gene 787 undergoing significantly low expression in
 PT subjects after pollen scattering, useful in diagnosis of allergic
 PT diseases and screening candidate compounds to regulate response of T
 PT cells to antigen stimulus.

XX Example 6; Page 40; 54pp; Japanese.

XX The invention relates to the human pollinosis-associated gene 787 which
 CC exhibits significantly reduced expression in the T-cells of individuals
 CC after the pollen-scattering season, relative to expression levels in T-
 CC cells before the pollen-scattering season. The gene was isolated from T-
 CC cells from individuals allergic to pollen using the differential display
 CC method. The invention also relates to pollinosis-associated gene 787
 CC primers and probes; methods of detection of pollinosis-associated gene
 CC 787 nucleic acids; and a method of diagnosis of allergic diseases via the
 CC detection of pollinosis-associated gene 787 nucleic acids. The invention
 CC additionally encompasses a method of screening drug candidates for the
 CC treatment of allergic disease by measuring the expression of pollinosis-

CC associated gene 787 in pollen antigen-stimulated T-cells in the presence
 CC of a test compound relative to a control. Pollinosis-associated gene 787
 CC is useful in the diagnosis of allergic diseases and in the screening of
 CC drug candidates for the treatment of such diseases. The present sequence
 CC represents a PCR primer used in the isolation of human pollinosis-
 CC associated gene 787 cDNA

SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
 Query Match 1.1%; Score 16; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1480 TAAAAAATAAAAAAAAAA 1495
 DB 17 TAAAAAATAAAAAAAAAA 2

RESULT 236
 AAC82874/c
 ID AAC82874 standard; DNA; 17 BP.

XX AAC82874;
 AC
 XX
 DT 20-MAR-2001 (first entry)
 XX
 DE Human pollinosis-associated gene 441 primer #1.
 XX
 KW Pollinosis; pollinosis-associated gene 441; allergy; T cell;
 KW pollen scattering; antigen; primer; ss.

XX Homo sapiens.

PN WO200073435-A1.

XX 07-DEC-2000.

PF 18-MAY-2000; 2000WO-JP003190.

PR 27-MAY-1999; 99JP-00148783.

XX (GENO-) GENOX RES INC.

XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
 PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
 XX
 DR WPI; 2001-061526/07.

XX Pollinosis-associated gene 441 which undergoes lower expression in
 PT subjects after pollen scattering, useful in diagnosis of allergic
 PT diseases and screening candidate compounds to regulate response of T
 PT cells to antigen stimulus.

XX Example 6; Page 35; 42pp; Japanese.

XX This invention describes a novel nucleic acid molecule comprising a
 CC sequence (I) which undergoes significantly low expression in subjects
 CC after pollen scattering, and is useful in diagnosis of allergic diseases
 CC and screening candidate compounds for remedies capable of regulating the
 CC response of T cells to the stimulus by an antigen

SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
 Query Match 1.1%; Score 16; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1480 TAAAAAATAAAAAAAAAA 1495
 DB 17 TAAAAAATAAAAAAAAAA 2

RESULT 237

```
AAH47126/c
ID AAH47126 standard; DNA; 17 BP.
AC AAH47126;
XX
DT 30-NOV-2001 (first entry)
DE
DE Nucleotide sequence of primer GT15A.
XX
KW B1001; B1466; B1072; B1151; T-cell; allergy; atopic dermatitis; human;
KW PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200165259-A1.
XX
PD 07-SEP-2001.
XX
PF 23-FEB-2001; 2001WO-JP001372.
XX
PR 02-MAR-2000; 2000JP-00061832.
XX
PA (GENO-) GENOX RES INC.
PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX
PI Nagasu T, Oshida T, Obayashi I, Matsui K, Saito H;
XX
DR WPI; 2001-557789/62.
XX
PT Diagnosis of allergies including atopic dermatitis.
XX
PS Example 6; Page 65; 83pp; Japanese.
XX
CC The invention provides a method of diagnosis of allergies that involves:
CC assaying the levels of expression of genes B1001, B1466, B1072 or B1151
CC in T-cells; and comparing them with the level of expression in healthy T-
CC cells. The method is useful for diagnosing allergies, particularly atopic
CC dermatitis. The present sequence represents a PCR primer used for
CC analysis of the expression of the above genes
XX
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAAAAAAA 1495
Db 17 TAAAAAAAAAAAAAAAAA 2

RESULT 238
ABK13941/c
ID ABK13941 standard; DNA; 17 BP.
XX
AC ABK13941;
XX
DT 21-MAY-2002 (first entry)
DE
DE 5'-PCR primer used to produce single pattern characteristic by FokI.
XX
KW Identification of transcribed gene; mRNA profile; gene expression;
KW cellular process; fingerprinting; susceptibility to external factor;
KW development; disease; PCR; primer; ss.
XX
OS Synthetic.
XX
PN WO200208461-A2.
XX
PD 31-JAN-2002.
XX
PF 23-JUL-2001; 2001WO-IB001539.
XX
```

```
PR 21-JUL-2000; 2000GB-00018016.
PR 21-JUL-2000; 2000US-0219925P.
XX
PA (GLOB-) GLOBAL GENOMICS AB.
XX
PI Linnarsson S, Ernfors P, Bauren G;
XX
XX WPI; 2002-217065/27.
DR
DR
XX
PT Providing mRNA profile, by generating two independent patterns
PT characteristic of sample mRNA population, analyzing patterns, comparing
PT gene expression by cell types under varied conditions, and identifying
PT genes.
XX
PS Disclosure; Fig 2; 67pp; English.
XX
CC The present invention relates to a method for providing a profile of mRNA
CC molecules present in a sample. The method comprises generating two
CC independent patterns characteristic of the population of mRNA molecules
CC expressed in the sample and analysing the patterns using a combinatorial
CC algorithm, comparing gene expression by different or same cell types
CC under different conditions, and identifying genes having a role in
CC various cellular processes. The method is useful for the analysis and
CC identification of transcribed genes, and fingerprinting. The method can
CC be used to identify genes which play a role in determining various
CC cellular processes, including susceptibility to external factors,
CC development, and disease. The present sequence for a PCR primer is used
CC in the production of a single pattern characteristic of a sample,
CC employing a Type IIS restriction enzyme (i.e. FokI) in the methods of the
CC present invention
XX
SQ Sequence 17 BP; 0 A; 1 C; 0 G; 16 T; 0 U; 0 Other;

Query Match 1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAAAAAA 1496
Db 16 AAAAAAAAAAAAAAAAAA 1

RESULT 239
ABK49634/c
ID ABK49634 standard; DNA; 17 BP.
XX
AC ABK49634;
XX
DT 15-JUL-2002 (first entry)
DE
DE Human Acetyltransferase-like protein 20-90-05 PCR primer GT15A.
XX
KW Human; ss; PCR; acetyltransferase; 20-90-05; allergic disease; primer;
KW differential display; eosinophil; antiallergic; atopic dermatitis; GT15A.
XX
OS Homo sapiens.
XX
PN WO200224903-A1.
XX
PD 28-MAR-2002.
XX
PF 21-SEP-2001; 2001WO-JP008246.
XX
PR 25-SEP-2000; 2000JP-00291318.
XX
PA (GENO-) GENOX RES INC.
PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
PA (EISA ) EISAI CO LTD.
XX
PI Sugita Y, Hashida R, Ogawa K, Fujishima T, Nagasu T, Tsujimoto G;
PI Takahashi E;
XX
DR WPI; 2002-315738/35.
```

XX Examining allergic diseases by differential display of gene showing
PT different expression particularly increased expression in remission stage
PT in eosinophils of patients, also applicable in screening candidate
PT compounds for remedies.
XX Example 1; Page 56; 72pp; Japanese.
XX
XX The invention relates to a method for examining allergic diseases
CC comprises determining the expression level of a gene containing, the
CC human cDNA appearing as ABK49633 which has homology with
CC acetyltransferases in the eosinophils of a patient and comparing the
CC expression level with that in the eosinophils of a healthy individual
CC (i.e. differential display). Also included are methods of screening for
CC candidate compounds which affect the expression level of the gene or the
CC activity of the protein encoded by the gene (including related proteins
CC and mutants), the use of probes based on the gene sequence in the
CC examination of allergic diseases, the use of reporter constructs in the
CC screening of candidate compounds, a vector containing a the transcription
CC -controlling region of the gene, cells transformed with the vector, an
CC antibody against the protein and a model animal for allergic diseases
CC which is a transgenic non-human vertebrate with lowering of expression
CC intensity of the gene in eosinophils. The method is examining allergic
CC diseases particularly atopic dermatitis which is also applicable in
CC screening candidate compounds for remedies. Such method can be performed
CC in high throughput, at low cost. The present sequence is a differential
CC display PCR primer for the cDNA encoding the human acetyltransferase-like
CC protein 20-90-05
XX
XX Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
SQ

Query Match 1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1480 TAAAAAATAAAAAAAAAA 1495
Db 17 TAAAAAATAAAAAAAAAA 2

RESULT 240
ABL59038/c
ID ABL59038 standard; DNA; 17 BP.
XX AC ABL59038;
XX
XX 20-AUG-2002 (first entry)
DE Nucleotide sequence of PCR primer GT15A.
XX Human; allergosis; eosinophil; PCR; primer; ss.
XX Homo sapiens.
XX JP2002095500-A.
XX
XX 02-APR-2002.
XX
XX 25-SEP-2000; 2000JP-00291316.
XX
XX 25-SEP-2000; 2000JP-00291316.
XX
XX (GENO-) GENOX SOYAKU KENKYUSHO KK.
XX (KOKU-) KOKURITSU SHONI BYOIN INCHO.
XX
XX WPI; 2002-439993/47.
XX
XX Examining allergosis, involves measuring the expression levels of a
PT specific gene, and comparing it to the levels in the eosinophils of a
PT healthy control.
XX
XX Example 1; Page 17; 20pp; Japanese.
PS
XX

CC The specification describes a method for examining allergosis. The method
CC comprises measuring the expression level of the gene given in ABL59037,
CC and comparing it with the expression level of the gene in the eosinophils
CC of a healthy person. The method is used for the examination of
CC allergosis. The present sequence represents a PCR primer, which is used
CC in the course of the invention
XX
XX Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
SQ

Query Match 1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1480 TAAAAAATAAAAAAAAAA 1495
Db 17 TAAAAAATAAAAAAAAAA 2

RESULT 241
ABN99829/c
ID ABN99829 standard; DNA; 17 BP.
XX AC ABN99829;
XX
XX 15-AUG-2002 (first entry)
DE Human allergic disease related PCR primer SEQ ID NO: 18.
XX
XX Human; allergy; atopic dermatitis; eosinophil; anti-allergic; PCR;
XX primer; ss.
XX Homo sapiens.
XX WO200233069-A1.
XX
XX 25-APR-2002.
XX
XX 28-SEP-2001; 2001WO-JP008574.
XX
XX 13-OCT-2000; 2000JP-00314093.
XX
XX (GENO-) GENOX RES INC.
XX (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX
XX Sugita Y, Hashida R, Ogawa K, Obayashi M, Nagasu T, Saito H;
XX WPI; 2002-372311/40.
XX
XX Method for examining allergic diseases by differential display of
PT seventeen genes showing different expression particularly significant
PT increase in eosinophils in patients with mild atopic dermatitis, also
PT applicable in screening compounds.
XX
XX Example 1; Page 109; 165pp; Japanese.
XX
XX The present invention relates to a method for examining allergic diseases
CC which involves determining the expression level of a gene, having one of
CC the 17 nucleotide sequences shown in ABN99812-ABN99828, in the
CC eosinophils in a patient and comparing the expression level with that in
CC the eosinophils of a healthy individual. The method can be used to
CC examine allergic diseases, particularly atopic dermatitis, and its early
CC diagnosis, which is also applicable in screening candidate compounds for
CC remedies. The present sequence is a PCR primer described in the
CC exemplification of the invention
XX
XX Sequence: 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
SQ

Query Match 1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1480 TAAAAAATAAAAAAAAAA 1495
Db 17 TAAAAAATAAAAAAAAAA 2

```

Db      17 TAAAAAAAAAAAAAAAAA 2

RESULT 242
AAL49948/C
ID      AAL49948 standard; DNA; 17 BP.
XX
XX      AAL49948;
AC
XX      10-DEC-2002 (first entry)
DT
XX      Human B1153 expression in allergic disease related PCR primer GT15A.
DE
XX      Human; allergy; B1153; differential expression; antiallergic; asthma;
KW      antiasthmatic; antiinflammatory; atopic skin inflammation; PCR; primer;
KW      ss.
XX
XX      Unidentified.
OS
XX
XX      WO200250269-A1.
PN
XX
XX      27-JUN-2002.
PD
XX
XX      21-DEC-2001; 2001WO-JP011286.
PF
XX
XX      21-DEC-2000; 2000JP-00389476.
PR
XX
XX      (GENO-) GENOX RES INC.
PA
XX      (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
PA
XX      Matsumoto Y, Imai Y, Oshida T, Sugita Y, Nagasu T, Tsujimoto G;
PI
XX      WPI; 2002-713252/77.
DR
XX
XX      Examination of allergic diseases comprises detecting gene B1153 over-
PT      expressed in T cells of allergy patients for diagnosis treatment and
PT      investigation of atopic skin inflammation and asthma.
PT
XX
XX      Example 6; Page 81; 102pp; Japanese.
PS
XX
XX      The present invention relates to a method of examining allergic diseases
CC      which comprises comparing the expression level of gene B1153 in allergy
CC      patients with the expression level in healthy subjects. The method is
CC      useful for the treatment, prevention, diagnosis and study of allergic
CC      diseases including atopic skin inflammation and asthma. The present
CC      sequence is a PCR primer described in the exemplification of the
CC      invention
CC
XX      Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
SQ      Query Match      1.1%; Score 16; DB 1; Length 17;
          Best Local Similarity 100.0%; Pred. No. 1.4e+02;
          Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1480 TAAAAAAAAAAAAAAAAA 1495
          |||||
Db      17 TAAAAAAAAAAAAAAAAA 2

RESULT 243
AAL47234/C
ID      AAL47234 standard; DNA; 17 BP.
XX
XX      AAL47234;
AC
XX      22-AUG-2002 (first entry)
DT
XX
XX      Allergic disease examination method related anchor primer SEQ ID NO: 2.
DE
XX      Allergic disease; allergy; antiallergic; intersectin 2; eosinophil;
KW      atopic dermatitis; human; PCR; primer; ss.
XX
XX      Unidentified.
OS

```

```

XX      WO200233122-A1.
PN
XX      25-APR-2002.
PD
XX      11-OCT-2001; 2001WO-JP008937.
PF
XX      13-OCT-2000; 2000JP-00314093.
PR
XX      (GENO-) GENOX RES INC.
PA      (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
PA      (EISA) EISAI CO LTD.
XX
XX      Sugita Y, Hashida R, Ogawa K, Obayashi M, Nagasu T, Saito H;
PI      Takahashi E;
XX
XX      WPI; 2002-372313/40.
DR
XX
XX      Method for examining allergic diseases by differential display of
PT      intersectin 2 gene showing different expression particularly significant
PT      increase in eosinophils in patients.
PT
XX
XX      Example 1; Page 52; 90pp; Japanese.
PS
XX
XX      The present invention relates to a method for examining allergic diseases
CC      with intersectin 2 gene or a gene with equivalent function of intersectin
CC      2 as an indicator gene, which comprises determining the expression level
CC      of the gene in the eosinophils in a patient, and comparing the expression
CC      level with that in the eosinophils of a healthy individual. The method is
CC      for examining allergic diseases, particularly atopic dermatitis, which is
CC      also applicable in screening candidate compounds for remedies. The
CC      present sequence is an anchor primer described in the exemplification of
CC      the invention
CC
XX      Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
SQ      Query Match      1.1%; Score 16; DB 1; Length 17;
          Best Local Similarity 100.0%; Pred. No. 1.4e+02;
          Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1480 TAAAAAAAAAAAAAAAAA 1495
          |||||
Db      17 TAAAAAAAAAAAAAAAAA 2

RESULT 244
ABK49756/C
ID      ABK49756 standard; DNA; 17 BP.
XX
XX      ABK49756;
AC
XX      15-JUL-2002 (first entry)
DT
XX
XX      Human atopic dermatitis cDNA related PCR primer GT15a.
DE
XX      Atopic dermatitis; ss; differential display; primer; PCR; eosinophil;
KW      allergic disease; antiallergic; dermatological; GT15a.
XX
XX      Synthetic.
OS
XX
XX      WO200226962-A1.
PN
XX
XX      04-APR-2002.
PD
XX
XX      21-SEP-2001; 2001WO-JP008247.
PF
XX      26-SEP-2000; 2000JP-00293021.
PR
XX
XX      (GENO-) GENOX RES INC.
PA      (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
PA
XX      Sugita Y, Hashida R, Ogawa K, Fujishima T, Nagasu T, Saito H;
PI
XX

```

DR WPI; 2002-330097/36.
 XX Examining allergic diseases by differential display of genes showing
 PT different expression particularly increase in remission stage in
 PT eosinophils in patients.
 XX Example 1; Page 54; 74pp; Japanese.
 XX This invention relates to gene sequences that are differentially
 CC expressed in eosinophils from patients with atopic dermatitis in the
 CC increment stage as compared with those in the remission stage. These
 CC sequences are used in a novel method for examining allergic diseases
 CC comprising determining the expression levels of these genes and comparing
 CC the expression level with that in the eosinophils of a healthy
 CC individual. The method of the invention may have antiallergic or
 CC dermatological activities. The method can be used to diagnose allergic
 CC diseases particularly atopic dermatitis, and may also be used to screen
 CC candidate compounds for remedies. The method of the invention can be
 CC performed in high throughput, at low cost. The present sequence
 CC represents the G15a PCR primer used to amplify the differentially
 CC amplified atopic dermatitis related cDNA sequences of the invention
 XX
 SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
 Query Match 1.1%; Score 16; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1480 TAAAAAATAAAAAA 1495
 Db |||||
 17 TAAAAAATAAAAAA 2
 RESULT 245
 ADB04271/c
 ID ADB04271 standard; DNA; 17 BP.
 XX ADB04271;
 AC
 XX 20-NOV-2003 (first entry)
 DT
 XX Human MD27 scanning oligonucleotide SEQ ID 5257.
 DE
 XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
 KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
 KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
 KW developmental disorder; ss.
 XX
 OS Homo sapiens.
 XX
 XX EP1281758-A2.
 FN
 XX 05-FEB-2003.
 PD
 XX 30-JUL-2002; 2002EP-00016874.
 PF
 XX 02-AUG-2001; 2001US-00922181.
 PR
 XX (AEOM-) AEOMICA INC.
 PA
 XX Shannon M, Gu Y, Nguyen C;
 PI
 XX WPI; 2003-423107/40.
 DR
 XX New zinc finger-containing proteins and nucleic acids, useful in
 PT manufacturing a medicament for treating or preventing a disorder
 PT associated with decreased or increased expression or activity of MD23,
 PT MD24, MD27 or MD212, e.g. cancer.
 XX
 XX Example 8; SEQ ID NO 5257; 103pp; English.
 XX The present invention relates to novel human zinc finger-containing
 CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is

CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
 CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
 CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
 CC or in manufacturing a medicament for treating or preventing a disorder
 CC associated with decreased or increased expression or activity of MD23.
 CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
 CC acids and proteins are also useful for diagnosing or monitoring a disease
 CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
 CC acids can also be used as probes to detect and characterize gross
 CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
 CC useful in constructing microarrays for measuring gene expression. The
 CC proteins are useful as therapeutic agents for gene therapy or as
 CC vaccines. The present sequence was used to illustrate the invention.
 XX
 SQ Sequence 17 BP; 0 A; 1 C; 0 G; 16 T; 0 U; 0 Other;
 Query Match 1.1%; Score 16; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1481 AAAAAAATAAAAAA 1496
 Db |||||
 17 AAAAAAATAAAAAA 2
 RESULT 246
 ADB04272/c
 ID ADB04272 standard; DNA; 17 BP.
 XX ADB04272;
 AC
 XX 20-NOV-2003 (first entry)
 DT
 XX Human MD27 scanning oligonucleotide SEQ ID 5258.
 DE
 XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
 KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
 KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
 KW developmental disorder; ss.
 XX
 OS Homo sapiens.
 XX
 XX EP1281758-A2.
 FN
 XX 05-FEB-2003.
 PD
 XX 30-JUL-2002; 2002EP-00016874.
 PF
 XX 02-AUG-2001; 2001US-00922181.
 PR
 XX (AEOM-) AEOMICA INC.
 PA
 XX Shannon M, Gu Y, Nguyen C;
 PI
 XX WPI; 2003-423107/40.
 DR
 XX New zinc finger-containing proteins and nucleic acids, useful in
 PT manufacturing a medicament for treating or preventing a disorder
 PT associated with decreased or increased expression or activity of MD23,
 PT MD24, MD27 or MD212, e.g. cancer.
 XX
 XX Example 8; SEQ ID NO 5258; 103pp; English.
 XX The present invention relates to novel human zinc finger-containing
 CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
 CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
 CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
 CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
 CC or in manufacturing a medicament for treating or preventing a disorder
 CC associated with decreased or increased expression or activity of MD23,
 CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
 CC acids and proteins are also useful for diagnosing or monitoring a disease
 CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic

CC acids can also be used as probes to detect and characterize gross
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 17 BP; 0 A; 0 C; 1 G; 16 T; 0 U; 0 Other;

Query Match 1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
Db 16 AAAAAAAAAAAAAA 1

RESULT 247
ID ABZ70578/c
XX ABZ70578 standard; DNA; 17 BP.
AC ABZ70578;
XX
DT 23-MAY-2003 (first entry)
XX
DE Primer.
XX
KW Aspergillus phenolics; oxalate decarboxylase; APOXD; transgenic plant;
KW crop protection; primer; ss.
XX
OS Synthetic.
XX
PN CA2350328-A1.
XX
PD 26-DEC-2002.
XX
PF 26-JUN-2001; 2001CA-02350328.
XX
PR 26-JUN-2001; 2001CA-02350328.
XX
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Scelonge C, Bidney D;
XX
DR WPI; 2003-248733/25.
XX
PT New isolated nucleic acid encoding oxalate decarboxylase from Aspergillus
PT phenolics, for degrading oxalic acid, identifying transformed plant
PT cells, and preventing pathogenic disease in plants.
XX
PS Disclosure; Page 50; 60pp; English.
XX
SQ The present sequence is that of a primer used in the invention. The
CC invention relates to a novel nucleic acid (see ABZ70560) encoding
CC Aspergillus phenolics oxalate decarboxylase (APOXD) (see ABP72475). The
CC gene and its encoded protein are useful in degrading oxalate, in
CC diagnostic assays, for protecting plants against disease, and as a
CC selectable marker
XX
SQ Sequence 17 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 1 Other;

Query Match 1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
Db 17 AAAAAAAAAAAAAA 2

RESULT 248
ID AAD56441/c
XX AAD56441 standard; DNA; 17 BP.

XX
AC AAD56441;
XX
DT 07-AUG-2003 (first entry)
XX
DE Antisense oligo #2, to elicit RNase H degradation of target RNA.
XX
KW Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
KW antisense; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT misc_feature 9..10
FT /tag= a
FT /note= "Bases 9 and 10 are linked by a butanediol linker
FT which is represented as B in page 49 and X in page 59,
FT Fig 9 and 10 of the specification"
XX
PN WC2003037909-A1.
XX
PD 08-MAY-2003.
XX
PF 29-OCT-2002; 2002WO-CA001628.
XX
PR 29-OCT-2001; 2001US-0330719P.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;
XX WPI; 2003-421516/39.
XX
PT Novel acyclic linker-containing oligonucleotide useful for preventing or
PT decreasing translation, reverse transcription and/or replication of a
PT target RNA in a system, comprises a modified deoxyribonucleotide.
XX
PS Example 2; Page 90; 104pp; English.
XX
SQ The invention relates to an acyclic linker-containing oligonucleotide
CC comprising at least one modified deoxyribonucleotide. Oligonucleotides of
CC the invention are useful for preventing or decreasing translation,
CC reverse transcription and/or replication of a target RNA in a system.
CC They are useful for selectively preventing gene expression in a sequence-
CC specific manner, for hybridising to complementary RNA such as cellular
CC mRNA or viral RNA, to hybridise to and induce cleavage of complementary
CC RNA. They are also useful therapeutically in formulations or medicaments
CC to prevent or treat a disease characterised by the expression of a
CC particular target RNA. The invention is used in gene therapy. The present
CC sequence is an antisense oligo used to elicit human RNase (ribonuclease)
CC H degradation of target RNA. This sequence is used in the exemplification
CC of the invention
XX
SQ Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
Db 17 AAAAAAAAAAAAAA 2

RESULT 249
ID AAD56448/c
XX AAD56448 standard; DNA; 17 BP.
AC AAD56448;
XX
DT 07-AUG-2003 (first entry)
XX
DE 2'F-ANA antisense oligo #3, to elicit RNase H degradation of target RNA.


```

XX Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
KW antisense; ss.
XX Unidentified.
XX Key Location/Qualifiers
XX modified_base 1..17
XX /tag= a
XX /mod_base= OTHER
XX /note= "2'-deoxy-2'-fluoroarabinothymidine"
XX misc_feature 9..10
XX /tag= b
XX /note= "Bases 9 and 10 are linked by a butanediol linker
XX which is represented as B in page 49 and Fig 5 and as X
XX in page 52, 55 and Fig 6 of the specification"
XX WO2003037909-A1.
XX 08-MAY-2003.
XX 29-OCT-2002; 2002WO-CA001628.
XX 29-OCT-2001; 2001US-0330719P.
XX (UYMC-) UNIV MCGILL.
XX Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;
XX WPI; 2003-421516/39.
XX Novel acyclic linker-containing oligonucleotide useful for preventing or
XX decreasing translation, reverse transcription and/or replication of a
XX target RNA in a system, comprises a modified deoxyribonucleotide.
XX Example 2; Fig 5; 104pp; English.
XX The invention relates to an acyclic linker-containing oligonucleotide
XX comprising at least one modified deoxyribonucleotide. Oligonucleotides of
XX the invention are useful for preventing or decreasing translation,
XX reverse transcription and/or replication of a target RNA in a system.
XX They are useful for selectively preventing gene expression in a sequence-
XX specific manner, for hybridising to complementary RNA such as cellular
XX mRNA or viral RNA, to hybridise to and induce cleavage of complementary
XX RNA. They are also useful therapeutically in formulations or medicaments
XX to prevent or treat a disease characterised by the expression of a
XX particular target RNA. The invention is used in gene therapy. The present
XX sequence is an antisense oligo used to elicit human RNase (ribonuclease)
XX H degradation of target RNA. This sequence is used in the exemplification
XX of the invention
XX SQ Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
XX
XX Query Match 1..17; Score 16; DB 1; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 1.4e+02;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1481 AAAAAAAAAAAAAA 1496
XX |||||
XX 17 AAAAAAAAAAAAAA 2
XX
XX Db
XX
XX RESULT 250
XX AAD56449/C
XX ID AAD56449 standard; DNA; 17 BP.
XX AC AAD56449;
XX 07-AUG-2003 (first entry)
XX 2' P-ANA antisense oligo #4, to elicit RNase H degradation of target RNA.
XX Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;

```

```

KW antisense; ss.
XX Unidentified.
XX Key Location/Qualifiers
XX modified_base 1..17
XX /tag= a
XX /mod_base= OTHER
XX /note= "2'-deoxy-2'-fluoroarabinothymidine"
XX misc_feature 12..13
XX /tag= b
XX /note= "Bases 12 and 13 are linked by a butanediol linker
XX which is represented as B in page 49 and Fig 5 and as X
XX in page 55 and Fig 6 of the specification"
XX WO2003037909-A1.
XX 08-MAY-2003.
XX 29-OCT-2002; 2002WO-CA001628.
XX 29-OCT-2001; 2001US-0330719P.
XX (UYMC-) UNIV MCGILL.
XX Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;
XX WPI; 2003-421516/39.
XX Novel acyclic linker-containing oligonucleotide useful for preventing or
XX decreasing translation, reverse transcription and/or replication of a
XX target RNA in a system, comprises a modified deoxyribonucleotide.
XX Example 2; Fig 5; 104pp; English.
XX The invention relates to an acyclic linker-containing oligonucleotide
XX comprising at least one modified deoxyribonucleotide. Oligonucleotides of
XX the invention are useful for preventing or decreasing translation,
XX reverse transcription and/or replication of a target RNA in a system.
XX They are useful for selectively preventing gene expression in a sequence-
XX specific manner, for hybridising to complementary RNA such as cellular
XX mRNA or viral RNA, to hybridise to and induce cleavage of complementary
XX RNA. They are also useful therapeutically in formulations or medicaments
XX to prevent or treat a disease characterised by the expression of a
XX particular target RNA. The invention is used in gene therapy. The present
XX sequence is an antisense oligo used to elicit human RNase (ribonuclease)
XX H degradation of target RNA. This sequence is used in the exemplification
XX of the invention
XX SQ Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
XX
XX Query Match 1..17; Score 16; DB 1; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 1.4e+02;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1481 AAAAAAAAAAAAAA 1496
XX |||||
XX 17 AAAAAAAAAAAAAA 2
XX
XX Db
XX
XX RESULT 251
XX AAD56447/C
XX ID AAD56447 standard; DNA; 17 BP.
XX AC AAD56447;
XX 07-AUG-2003 (first entry)
XX 2' P-ANA antisense oligo #2, to elicit RNase H degradation of target RNA.
XX Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
XX antisense; ss.

```

```

OS Unidentified.
XX
PH Key Location/Qualifiers
FT modified_base 1..17
FT /tag= a
FT /mod_base= OTHER
FT /note= "2'-deoxy-2'-fluoroarabinothymidine"
FT misc_feature 4..5
FT /tag= b
FT /note= "Bases 4 and 5 are linked by a butanediol linker
FT which is represented as B in page 49 and Fig 5 and as X
FT in page 55 and Fig 6 of the specification"
XX
XX WO2003037909-A1.
XX
XX 08-MAY-2003.
XX
XX 29-OCT-2002; 2002WO-CA001628.
XX
XX 29-OCT-2001; 2001US-0330719P.
XX
XX (UYMC-) UNIV MCGILL.
XX
XX Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;
XX WPI; 2003-421516/39.
XX
XX Novel acyclic linker-containing oligonucleotide useful for preventing or
XX decreasing translation, reverse transcription and/or replication of a
XX target RNA in a system, comprises a modified deoxyribonucleotide.
XX
XX Example 2; Fig 5; 104pp; English.
XX
XX The invention relates to an acyclic linker-containing oligonucleotide
XX comprising at least one modified deoxyribonucleotide. Oligonucleotides of
XX the invention are useful for preventing or decreasing translation,
XX reverse transcription and/or replication of a target RNA in a system.
XX They are useful for selectively preventing gene expression in a sequence-
XX specific manner, for hybridising to complementary RNA such as cellular
XX mRNA or viral RNA, to hybridise to and induce cleavage of complementary
XX RNA. They are also useful therapeutically in formulations or medicaments
XX to prevent or treat a disease characterised by the expression of a
XX particular target RNA. The invention is used in gene therapy. The present
XX sequence is an antisense oligo used to elicit human RNase (ribonuclease)
XX H degradation of target RNA. This sequence is used in the exemplification
XX of the invention
XX
XX Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 16; DB 1; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 1.4e+02;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1481 AAAAAAAAAAAAAA 1496
XX |||||
XX Db 17 AAAAAAAAAAAAAA 2
XX
XX RESULT 252
XX AAD56450/c
XX ID AAD56450 standard; DNA; 17 BP.
XX
XX AC AAD56450;
XX
XX 07-AUG-2003 (first entry)
XX
XX 2'-F-RNA antisense oligo #5, to elicit RNase H degradation of target RNA.
XX
XX Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
XX antisense; ss.
XX
XX Unidentified.
XX

```

```

FH Key Location/Qualifiers
FT modified_base 1..17
FT /tag= a
FT /mod_base= OTHER
FT /note= "2'-deoxy-2'-fluoroarabinothymidine"
FT misc_feature 9..10
FT /tag= b
FT /note= "Bases 9 and 10 are linked by a secouridine linker
FT which is represented as S in page 49 and X in page 57 and
FT Fig 1, 2, 7 and 8 of the specification"
XX
XX WO2003037909-A1.
XX
XX 08-MAY-2003.
XX
XX 29-OCT-2002; 2002WO-CA001628.
XX
XX 29-OCT-2001; 2001US-0330719P.
XX
XX (UYMC-) UNIV MCGILL.
XX
XX Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;
XX WPI; 2003-421516/39.
XX
XX Novel acyclic linker-containing oligonucleotide useful for preventing or
XX decreasing translation, reverse transcription and/or replication of a
XX target RNA in a system, comprises a modified deoxyribonucleotide.
XX
XX Example 2; Fig 7; 104pp; English.
XX
XX The invention relates to an acyclic linker-containing oligonucleotide
XX comprising at least one modified deoxyribonucleotide. Oligonucleotides of
XX the invention are useful for preventing or decreasing translation,
XX reverse transcription and/or replication of a target RNA in a system.
XX They are useful for selectively preventing gene expression in a sequence-
XX specific manner, for hybridising to complementary RNA such as cellular
XX mRNA or viral RNA, to hybridise to and induce cleavage of complementary
XX RNA. They are also useful therapeutically in formulations or medicaments
XX to prevent or treat a disease characterised by the expression of a
XX particular target RNA. The invention is used in gene therapy. The present
XX sequence is an antisense oligo used to elicit human RNase (ribonuclease)
XX H degradation of target RNA. This sequence is used in the exemplification
XX of the invention
XX
XX Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 16; DB 1; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 1.4e+02;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1481 AAAAAAAAAAAAAA 1496
XX |||||
XX Db 17 AAAAAAAAAAAAAA 2
XX
XX RESULT 253
XX ACF36345/c
XX ID ACF36345 standard; DNA; 17 BP.
XX
XX AC ACF36345;
XX
XX 04-DEC-2003 (first entry)
XX
XX Nucleotide sequence of a double stranded product DNA fragment.
XX
XX Gene variant identification; restriction enzyme; FokI; ds.
XX
XX Synthetic.
XX
XX WO2003064689-A2.
XX
XX 07-AUG-2003.
XX

```

XX PF 28-JAN-2003; 2003WO-IB000255.
 XX PR 29-JAN-2002; 2002US-0352245P.
 XX PA (GLOB-) GLOBAL GENOMICS AB.
 XX PI Lonnberg P, Oldin M, Linnarsson S, Ernfors P;
 XX WPI; 2003-627619/59.
 XX CC Determining polyadenylation sites within transcribed gene sequences
 XX PT present in a sample comprises assigning to gene fragments gene candidates
 XX PT within a database by comparing signals in the dataset with the database.
 XX PS Example; Fig 3; 81pp; English.
 XX CC The invention relates to determining the presence of and/or identifying a
 CC polyadenylation site within a sequence of a transcribed gene or variants
 CC present in a sample. The method involves assigning to gene fragments gene
 CC candidates within a database by comparing signals in the dataset with the
 CC database, the database comprising data representing mRNAs with known
 CC polyA sites and/or 'virtual genes' representing a possible
 CC polyadenylation site within an actual gene. The method is useful for
 CC determining the presence of and/or identifying a polyadenylation site or
 CC alternative polyadenylation sites within a sequence of a transcribed gene
 CC or sequences of transcribed gene variants present or potentially present
 CC in a sample, in identifying gene features, particularly in identifying
 CC differences between sequence variants that occur in a population of
 CC nucleic acid molecules, especially in identifying or discovering polyA
 CC site usage or determining polyA site usage in a nucleic acid sample, and
 CC gene variants arising from alternative polyA sites. The present sequence
 CC represents a double stranded product DNA fragment
 XX SQ Sequence 17 BP; 0 A; 1 C; 0 G; 16 T; 0 U; 0 Other;
 Query Match 1.1%; Score 16; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1481 AAAAAAAAAAAAAA 1496
 DB 16 AAAAAAAAAAAAAA 1
 RESULT 254
 ACF36370/C
 ID ACF36370 standard; DNA; 17 BP.
 XX AC ACF36370;
 XX DT 04-DEC-2003 (first entry)
 XX DE Nucleotide sequence of a double stranded product DNA.
 XX KW Nucleic acid manipulation; mRNA profiling; polymerase chain reaction;
 XX KW electrophoresis; type II restriction enzyme; FokI; ds.
 XX OS Synthetic.
 XX PN WO2003064691-A2.
 XX PD 07-AUG-2003.
 XX PF 28-JAN-2003; 2003WO-IB000843.
 XX PR 29-JAN-2002; 2002US-0352215P.
 XX PA (GLOB-) GLOBAL GENOMICS AB.
 XX PI Linnarsson S, Ernfors P, Bauren G, Metsis A, Pihlak A;
 XX PT Montellius A;

DR WPI; 2003-618365/S8.
 XX CC Producing a population of double-stranded product DNA molecules, useful
 XX PT for mRNA profiling, comprises amplification by nested polymerase chain
 XX PT reaction.
 XX PS Example; Fig 2; 105pp; English.
 XX CC The invention relates to producing a population of double-stranded
 CC product DNA molecules comprising amplification by a nested PCR method.
 CC The method is useful in profiling mRNA transcribed in a system under
 CC investigation. The oligonucleotides are used as size standards in
 CC electrophoresis, and as internal controls allowing for calculation of
 CC relative amounts of material present. The present sequence represents a
 CC double stranded product DNA, which aids in outlining an approach to
 CC production of a single pattern characteristic of a sample, employing a
 CC type II restriction enzyme (FokI)
 XX SQ Sequence 17 BP; 0 A; 1 C; 0 G; 16 T; 0 U; 0 Other;
 Query Match 1.1%; Score 16; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1481 AAAAAAAAAAAAAA 1496
 DB 16 AAAAAAAAAAAAAA 1
 RESULT 255
 ADC84468/C
 ID ADC84468 standard; DNA; 17 BP.
 XX AC ADC84468;
 XX DT 01-JAN-2004 (first entry)
 XX DE PCR primer for amplifying plant blastogenesis specific gene #SEQ ID 1.
 XX KW Plant blastogenesis; transformation; gene expression; tissue specific;
 XX KW PCR; primer; ss.
 XX OS Synthetic.
 XX PN JP2003159071-A.
 XX PD 03-JUN-2003.
 XX PF 22-NOV-2001; 2001JP-00358366.
 XX PR 22-NOV-2001; 2001JP-00358366.
 XX PA (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.
 XX WPI; 2003-818678/77.
 XX CC New naturally derived DNA specifically expressed during blastogenesis of
 XX PT a plant, useful for producing a transformed plant and for compulsive
 XX PT expression of a protein.
 XX PS Example 3; SEQ ID NO 1; 43pp; Japanese.
 XX CC The invention relates to naturally derived DNA specifically expressed
 CC during plant blastogenesis. The DNA of the invention is useful for
 CC producing a transformed plant. Methods of the invention are also useful
 CC for compulsive expression of this DNA. Methods of the invention are
 CC useful for plant tissue specific expression of genes. Also, the growth
 CC stage of a plant can be controlled specifically. The current sequence
 CC represents a PCR primer for amplifying a plant blastogenesis specific
 CC gene of the invention.
 XX SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

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Query Match      1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAAA 1495
DB 17 TAAAAAATAAAAAA 2

RESULT 256
AAQ34110
ID AAQ34110 standard; DNA; 18 BP.
XX
AC AAQ34110;
XX
DT 25-MAR-2003 (revised)
DT 02-FEB-1993 (first entry)
XX
XX
DE Sequence of a microsatellite from clone TGLA60B.
XX
KW PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KW genetic mapping; traits; amplification; ss.
XX
OS Bos taurus.
XX
PN WO9213102-A1.
XX
PD 06-AUG-1992.
XX
PF 15-JAN-1992; 92WO-US000340.
XX
PR 15-JAN-1991; 91US-00642342.
XX
XX (GENM-) GENMARK.
XX
XX Georges M, Massey JM;
XX WPI; 1992-284684/34.
XX
PT Polymorphic bovine DNA markers - used in genetic identification, gene
PT mapping, and selective breeding.
XX
PS Table 7; Page 375; 517pp; English.
XX
XX The sequence is that of a bovine microsatellite sequence obt'd. by
XX screening a library of bovine MboI DNA fragments of between 250 and 500
XX bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
XX clones cross-hybridised. Assuming independent distribution of
XX microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
XX in the bovine genome is estimated at >100, 000. The sequence information
XX for ca. 230 such bovine microsatellites is summarised in the
XX specification and indexed herein (see below). The sequences upstream and
XX downstream of the microsatellite sequence were used to generate the
XX required PCR primers for in vitro amplification of the corresp.
XX microsatellite (using the program OPTIPRIM). The microsatellites may be
XX used to identify individuals, for parentage testing, and in the genetic
XX mapping of economic trait loci, or genes involved in the determination of
XX economically important traits esp. in cattle, to allow selective
XX breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
XX field.)
XX
SQ Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match      1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAATAAAAAA 1496
DB 1 AAAAAAATAAAAAA 16

RESULT 257
AAQ34110
ID AAQ34110 standard; DNA; 18 BP.
XX
AC AAQ34110;
XX
DT 25-MAR-2003 (revised)
DT 02-FEB-1993 (first entry)
XX
XX
DE Sequence of a microsatellite from clone TGLA60B.
XX
KW PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KW genetic mapping; traits; amplification; ss.
XX
OS Bos taurus.
XX
PN WO9213102-A1.
XX
PD 06-AUG-1992.
XX
PF 15-JAN-1992; 92WO-US000340.
XX
PR 15-JAN-1991; 91US-00642342.
XX
XX (GENM-) GENMARK.
XX
XX Georges M, Massey JM;
XX WPI; 1992-284684/34.
XX
PT Polymorphic bovine DNA markers - used in genetic identification, gene
PT mapping, and selective breeding.
XX
PS Table 7; Page 375; 517pp; English.
XX
XX The sequence is that of a bovine microsatellite sequence obt'd. by
XX screening a library of bovine MboI DNA fragments of between 250 and 500
XX bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
XX clones cross-hybridised. Assuming independent distribution of
XX microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
XX in the bovine genome is estimated at >100, 000. The sequence information
XX for ca. 230 such bovine microsatellites is summarised in the
XX specification and indexed herein (see below). The sequences upstream and
XX downstream of the microsatellite sequence were used to generate the
XX required PCR primers for in vitro amplification of the corresp.
XX microsatellite (using the program OPTIPRIM). The microsatellites may be
XX used to identify individuals, for parentage testing, and in the genetic
XX mapping of economic trait loci, or genes involved in the determination of
XX economically important traits esp. in cattle, to allow selective
XX breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
XX field.)
XX
SQ Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

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AAQ75025/c
ID AAQ75025 standard; RNA; 18 BP.
XX
AC AAQ75025;
XX
DT 25-MAR-2003 (revised)
DT 03-AUG-1995 (first entry)
XX
DE PCR primer.
XX
KW Synthetic oligo; solid phase immunoassay; ss.
XX
OS Synthetic.
XX
PN WO9426932-A1.
XX
PD 24-NOV-1994.
XX
PF 13-MAY-1994; 94WO-US005407.
XX
PR 13-MAY-1993; 93US-00061694.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PA Fields HA, Khudyakov YE;
XX
PI WPI; 1995-006819/01.
XX
XX Solid phase immunoassay using oligo:nucleotide as label - also new
XX conjugates of oligo:nucleotide coupled to antigenic peptide, partic. for
XX diagnosing hepatitis C or E virus infection.
XX
XX Example; Page 12; 34pp; English.
XX
XX AAR62941 and AAR62942 are examples of synthetic immunoreactive peptides.
XX They are used in a method for detecting an antigen in a subject. The
XX method involves binding the antigen to a solid support and then reacting
XX it with an immunoreactive ligand (L) bound to an oligo; removing any
XX unreacted L, and then detecting the presence of the oligo. A similar
XX method can be used to detect Abs, in which case the ligand is an oligo-
XX labelled Ag. The use of an amplifiable oligo as the label allows Ag or Ab
XX to be detected at very low levels. An exemplary oligo is AAQ75024 which
XX can be covalently attached by the 5'- terminus to the N- or C-terminal of
XX a synthetic peptide. In the example, peptide AAR62941 was coupled to
XX oligo AAQ75024 using disuccinimidyl suberate. Serum samples suspected to
XX contain HEV Abs were immobilised on plastic tubes or wells, then
XX incubated for 30-60 mins with the peptide-oligo product. The vessels were
XX washed; bound oligo was released with 0.2M glycine and amplified in a
XX separate tube using as primers AAQ75025 and AAQ75026 in 30 cycles of PCR.
XX The amplification product - AAQ75031 - was treated with uracil DNA
XX glycosylase to remove the U18 fragment, and the product captured by
XX immobilised oligo-dT. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 0 T; 18 U; 0 Other;

Query Match      1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAATAAAAAA 1496
DB 18 AAAAAAATAAAAAA 3

RESULT 258
AAQ74668/c
ID AAQ74668 standard; DNA; 18 BP.
XX
AC AAQ74668;
XX
DT 27-MAR-1998 (first entry)
XX
XX Anchored poly(T) oligonucleotide polyT-AnchC.

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```

XX Flavonoid 3'-hydroxylase; pigmentation; flower colour; transgenic plant;
KW snapdragon; primer; ss.
XX Synthetic.
XX WO9732023-A1.
XX 04-SEP-1997.
XX 28-FEB-1997; 97WO-AU000124.
XX 01-MAR-1996; 96AU-00008386.
XX (FLOR-) FLORIGENE LTD.
XX Brugliera F, Holton TA, Michael MZ;
XX WPI; 1997-448691/41.
XX Novel flavonoid 3'-hydroxylase(s) from flowering plants - and
PT. corresponding DNA, used in the manipulation of pigmentation in plants.
XX Example 15; Page 59; 234pp; English.
XX Anchored poly(T) oligonucleotides polyT-ancha (AAT94667), polyT-anchC
CC (AAT94668) and polyT-anchG (AAT94669) are complementary to the upstream
CC region of a polyadenylation sequence. They were used to prime cDNA
CC synthesis from snapdragon (Antirrhinum majus) petal and leaf RNA, and
CC were also utilised in the PCR amplification of plant cytochrome P450
CC sequences (see also AAT94670-73). A cDNA clone (see AAT94657) encoding
CC flavonoid 3'-hydroxylase (see AAW35704) was isolated using a differential
CC display approach. This can be used to manipulate the pigmentation of
CC transgenic plants
XX SQ Sequence 18 BP; 0 A; 1 C; 0 G; 17 T; 0 U; 0 Other;
Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1496
DB 17 AAAAAAAAAAAAAA 2
RESULT 259
AAV54173/C
ID AAV54173 standard; cDNA; 18 BP.
AC AAV54173;
XX 21-DEC-1998 (first entry)
XX Nucleotide sequence PCR primer 10.
DE PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KW immunohistological staining.
XX Synthetic.
XX WO9839437-A1.
XX 11-SEP-1998.
XX 05-MAR-1998; 98WO-JP000905.
XX 05-MAR-1997; 97JP-00050302.
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX Sakaki Y;
XX WPI; 1998-495844/42.
XX Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
PT treating diseases associated with apoptosis.
XX Example 1; Page 47; 70pp; Japanese.
XX This is the nucleotide sequence of a PCR primer used in the method of the
CC invention, involving the use of novel apoptosis-related DNAs and
CC proteins. The inventions can be used as diagnostic reagents for apoptosis
CC e.g. (monoclonal) antibodies for the protein, as a reagent in
CC immunohistological staining, as apoptosis inhibitors. It can also be used
CC for treatment of apoptosis-related diseases
XX SQ Sequence 18 BP; 2 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1480 TAAAAAAAAAAAAA 1495
DB 17 TAAAAAAAAAAAAA 2
RESULT 260
AAV54164/C
ID AAV54164 standard; cDNA; 18 BP.
XX AAV54164;
XX 21-DEC-1998 (first entry)
XX Nucleotide sequence PCR primer 1.
DE PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KW immunohistological staining.
XX Synthetic.
XX WO9839437-A1.
XX 11-SEP-1998.
XX 05-MAR-1998; 98WO-JP000905.
XX 05-MAR-1997; 97JP-00050302.
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX Sakaki Y;
XX WPI; 1998-495844/42.
XX Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
PT treating diseases associated with apoptosis.
XX Example 1; Page 47; 70pp; Japanese.
XX This is the nucleotide sequence of a PCR primer used in the method of the
CC invention, involving the use of novel apoptosis-related DNAs and
CC proteins. The inventions can be used as diagnostic reagents for apoptosis
CC e.g. (monoclonal) antibodies for the protein, as a reagent in
CC immunohistological staining, as apoptosis inhibitors. It can also be used
CC for treatment of apoptosis-related diseases
XX SQ Sequence 18 BP; 2 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1480 TAAAAAAAAAAAAA 1495
DB 17 TAAAAAAAAAAAAA 2

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```

Db      17 TAAAAAAAAAAAAAAAAA 2
|||||
RESULT 261
AAV54167/c
ID   AAV54167 standard; cDNA; 18 BP.
XX
XX
AC   AAV54167;
XX
XX  21-DEC-1998 (first entry)
DE
DE  Nucleotide sequence PCR primer 4.
XX
XX  PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
XX  immunohistological staining.
XX
XX  Synthetic.
XX
XX  WO9839437-A1.
PN
XX
XX  11-SEP-1998.
PD
XX
XX  05-MAR-1998; 98WO-JP000905.
XX
XX  05-MAR-1997; 97JP-00050302.
XX
XX  (KYOW ) KYOWA HAKKO KOGYO KK.
PA
XX
XX  Sakaki Y;
PI
XX
XX  WPI; 1998-495844/42.
DR
XX
XX  Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
PT  treating diseases associated with apoptosis.
XX
XX  Example 1; Page 48; 70pp; Japanese.
XX
XX  This is the nucleotide sequence of a PCR primer used in the method of the
CC  invention, involving the use of novel apoptosis-related DNAs and
CC  proteins. The inventions can be used as diagnostic reagents for apoptosis
CC  e.g. (monoclonal) antibodies for the protein, as a reagent in
CC  immunohistological staining, as apoptosis inhibitors. It can also be used
CC  for treatment of apoptosis-related diseases
XX
XX  Sequence 18 BP; 1 A; 0 C; 1 G; 16 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAAAAAAA 1495
Db 17 TAAAAAAAAAAAAAAAAA 2
|||||
RESULT 262
AAV37712
ID   AAV37712 standard; cDNA; 18 BP.
XX
XX
AC   AAV37712;
XX
XX  25-MAR-2003 (revised)
DT
DT  07-SEP-1998 (first entry)
XX
XX  Human protein AQ2_li 3'-portion and polyA tail.
DE
XX
XX  Human; secreted protein; murine adult spleen; human foetal kidney; ovary;
XX  bone marrow; thymus; AE648_11; AE693_11; AK438_11; AK609_11; AM1060_11;
XX  AQ2_li; K433_11; L256_11; prevent; treat; ameliorate; medical; ds.
XX
XX  Homo sapiens.
OS
XX
PN WO9820130-A2.
XX
XX  14-MAY-1998.
XX
XX  31-OCT-1997; 97WO-US019857.
PF
XX
XX  01-NOV-1996; 96US-00742973.
PR
XX
XX  29-OCT-1997; 97US-00960024.
XX
XX  (GEMY ) GENETICS INST INC.
PA
XX
XX  Jacobs K, McCooy JM, Lavallie ER, Racie LA, Merberg D, Treacy M;
PI  Spaulding V, Agostino MJ;
XX
XX  WPI; 1998-286946/25.
DR
XX
XX  New secreted proteins and associated polynucleotides - obtained from
PT  murine adult spleen, human foetal kidney, human ovary, murine bone marrow
PT  and murine adult thymus.
XX
XX  Disclosure; Page 58; 75pp; English.
XX
XX  The present invention describes novel proteins isolated from cDNA clones:
CC  AE648_11; AE693_11; AK438_11; AK609_11; AM1060_11; AQ2_li; K433_11; or
CC  L256_11, deposited as ATCC 98237. The present sequence represents the 3'-
CC  portion of AQ2_li isolated from a human ovary cDNA library. The proteins
CC  from the present invention may be administered in a composition to
CC  prevent, treat or ameliorate a medical condition. The proteins may
CC  exhibit biological activities such as nutritional activity, cytokine and
CC  cell proliferation/differentiation activity, immune stimulating or
CC  suppressing activity, haematopoiesis regulating activity, tissue growth
CC  activity, activin/inhibin activity, chemotactic/chemokinetic activity,
CC  haemostatic and thrombotic activity, receptor/ligand activity, anti-
CC  inflammatory activity, cadherin/tumour invasion suppressor activity,
CC  tumour inhibition activity and other activities. (Updated on 25-MAR-2003
XX  to correct PR field.)
XX
XX  Sequence 18 BP; 17 A; 0 C; 1 G; 0 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAAAAAA 1496
Db 2 AAAAAAAAAAAAAAAAAA 17
|||||
RESULT 263
AAV07750
ID   AAV07750 standard; DNA; 18 BP.
XX
XX
AC   AAV07750;
XX
XX  02-DEC-1998 (first entry)
DT
XX
XX  Phosphorothioate oligodeoxynucleotide.
DE
XX
XX  phosphorothioate; electrospray ionisation-Fourier transform;
XX  mass spectrometry; off-resonance excitation; ss.
XX
XX  Synthetic.
OS
XX
XX  Key Location/Qualifiers
FH misc_difference 1..18 /*tag= a
FT
FT /note= "phosphorothioate internucleotide linkages"
XX
XX  WO9840520-A1.
PN
XX
XX  17-SEP-1998.
PD
XX
XX  12-MAR-1998; 98WO-US004919.
PF

```

XX 14-MAR-1997; 97US-0040717P.
 XX (HYBR-) HYBRIDON INC.
 XX Wang BH;
 XX WPI; 1998-520830/44.
 XX Determining the nucleotide sequence of a nucleic acid analyte - using
 XX electro-spray ionisation.
 XX Example 1; Fig 3A; 25pp; English.
 XX The invention relates to an analytical method for determining the
 XX nucleotide sequence of nucleic acid analytes, including chemically
 XX modified oligonucleotides. This new method utilises electrospray
 XX ionisation-Fourier transform mass spectrometry. The ions are excited by
 XX sustained off-resonance excitation with single shot excitation, and the
 XX target fragmented by collisionally activated dissociation by a neutral
 XX gas, e.g. carbon dioxide. Alternatively, the excitation and dissociation
 XX can be nozzle skimmer dissociations. The method is used in molecular
 XX biology and biomedical applications. The method, utilising electrospray
 XX ionisation-Fourier transform ion cyclotron resonance mass spectrometry,
 XX is extremely rapid and acts directly on the oligonucleotide. The method
 XX is effective for a variety of nucleic acid analytes, particularly
 XX chemically modified oligonucleotides which have not previously been
 XX successfully sequenced. The present sequence represents a
 XX phosphorothioate oligodeoxynucleotide
 XX Sequence 18 BP; 17 A; 0 C; 0 G; 1 T; 0 U; 0 Other;
 XX
 XX Query Match 1.1%; Score 16; DB 1; Length 18;
 XX Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1481 AAAAAAAAAAAAAA 1496
 XX Db 1 AAAAAAAAAAAAAA 16
 XX
 XX RESULT 264
 XX AAV21970/C
 XX ID AAV21970 standard; DNA; 18 BP.
 XX AC AAV21970;
 XX DT 14-JUL-1998 (first entry)
 XX DE Nuclease resistant antisense oligo NBT 13 targeted against (T)18.
 XX KW Nuclease resistant; bacterial infection; antibiotic; target;
 XX KW veterinary medicine; treatment; human; industrial process;
 XX KW bacterial control; ss.
 XX OS Synthetic.
 XX PN WO9803533-A1.
 XX PD 29-JAN-1998.
 XX PF 23-JUL-1997; 97WO-US012961.
 XX PR 24-JUL-1996; 96US-00685575.
 XX PA (OLIG-) OLIGOS ETC & OLIGOS THERAPEUTICS INC.
 XX PI Arrow A, Dale RMK, Thompson TL;
 XX DR WPI; 1998-120687/11.
 XX PT Treating bacterial infections in humans or animals with
 XX oligo:nucleotide(s) - resistant to nuclease and targetted to bacterial

PT nucleic acid or proteins, also conjugates of these oligo:nucleotide(s)
 XX with antibiotics.
 XX Claim 49; Page 87; 163pp; English.
 XX This antisense oligonucleotide is nuclease resistant and can be used in
 XX the treatment of animals, including humans, having a bacterial infection.
 XX The treatment comprises administration of such nuclease resistant
 XX oligonucleotides, targeted to a nucleic acid or protein of the bacterium,
 XX and formulated with a carrier. A compound comprising this nuclease
 XX resistant oligonucleotide can be covalently linked to an antibiotic. The
 XX method is used to treat infections by a wide variety of Gram-positive and
 XX Gram-negative, or acid-fast, bacteria, in human and veterinary medicine.
 XX The methods are particularly used in immuno-compromised individuals (e.g.
 XX patients with acquired immunodeficiency syndrome or those receiving
 XX chemotherapy or radiation therapy). Optionally in combination with, or
 XX fused to, antiviral or other antimicrobial oligonucleotides. Apart from
 XX therapeutic use, the oligonucleotides can be used to control bacteria in
 XX laboratory cultures, foods, beverages and industrial processes. The
 XX oligonucleotides are specific for bacteria, without affecting metabolism
 XX in mammalian cells. They may also activate RNase H and have a general,
 XX non-specific immune-stimulating effect. The oligonucleotides can be
 XX administered orally, intranasally, rectally, topically or by injection,
 XX optionally coupled to an agent (e.g. carbohydrate or polyamine) that
 XX enhances cellular uptake
 XX Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
 XX
 XX Query Match 1.1%; Score 16; DB 1; Length 18;
 XX Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1481 AAAAAAAAAAAAAA 1496
 XX Db 18 AAAAAAAAAAAAAA 3
 XX
 XX RESULT 265
 XX AAX19943/C
 XX ID AAX19943 standard; DNA; 18 BP.
 XX AC AAX19943;
 XX DT 14-JUN-1999 (first entry)
 XX DE Primer SEQ ID NO:3 from JP11075880.
 XX KW Primer; oligonucleotide; labelling; detection; self-priming; PCR; ss.
 XX OS Synthetic.
 XX PN JP11075880-A.
 XX PD 23-MAR-1999.
 XX PF 10-JUL-1998; 98JP-00195719.
 XX PR 14-JUL-1997; 97JP-00205378.
 XX PA (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
 XX DR WPI; 1999-257710/22.
 XX PT Labelling of an oligonucleotide - useful for detecting genes.
 XX PS Example 1; Page 7; 10pp; Japanese.
 XX A method has been developed for labelling an oligonucleotide having a
 XX repeated sequence of (XY)n (where X and Y consists of a combination of
 XX adenine and thymine or uracil or guanine and cytosine, and n is an
 XX integer of 1 or more) at the 3'-terminal side in which the repeated
 XX sequence is added and extended using a labelled body of the nucleotide
 XX constituting the repeated sequence and a DNA polymerase lacked in 5' to

CC 3' exonuclease activity. The method can be used for detecting a gene. The
CC method can detect a gene in a sensitivity up to ten times higher than
CC prior art methods. The present sequence represents a primer used in an
CC example from the present invention

XX SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
DB 18 AAAAAAAAAAAAAA 3

RESULT 266
AAAX19942
ID AAX19942 standard; DNA; 18 BP.
XX
AC AAX19942;
XX
DT 14-JUN-1999 (First entry)
DE Primer SEQ ID NO:2 from JP11075880.
KW Primer; oligonucleotide; labelling; detection; self-priming; PCR; ss.
XX
OS Synthetic.
XX
PN JP11075880-A.
XX
PD 23-MAR-1999.
XX
PF 10-JUL-1998; 98JP-00195719.
PR
PR 14-JUL-1997; 97JP-00205378.
XX
PA (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
XX
DR WPI; 1999-257710/22.
XX
PT Labelling of an oligonucleotide - useful for detecting genes.
XX
PS Example 1; Page 7; 10pp; Japanese.
XX
CC A method has been developed for labelling an oligonucleotide having a
CC repeated sequence of (XY)_n (where X and Y consists of a combination of
CC adenine and thymine or uracil or guanine and cytosine, and n is an
CC integer of 1 or more) at the 3'-terminal side in which the repeated
CC sequence is added and extended using a labelled body of the nucleotide
CC constituting the repeated sequence and a DNA polymerase lacked in 5' to
CC 3' exonuclease activity. The method can be used for detecting a gene. The
CC method can detect a gene in a sensitivity up to ten times higher than
CC prior art methods. The present sequence represents a primer used in an
CC example from the present invention

XX SQ Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
DB 1 AAAAAAAAAAAAAA 16

RESULT 267
AAA40563
ID AAA40563 standard; cDNA; 18 BP.
XX
AC AAA40563;

XX
DT
XX
DE
XX
KW Secreted protein; cytostatic; immunostimulatory; antimicrobial;
KW antiviral; immunosuppressive; antiinflammatory; vulnerrary; cytokine;
KW cell proliferation; differentiation; regulator; treatment; tumor;
KW autoimmune disease; inflammatory disorder; wound; microbial infection;
KW viral disease; graft versus host reaction suppression; ss.
XX
OS Homo sapiens.
XX
PN WO200037630-A1.
XX
PD 29-JUN-2000.
XX
PF 22-DEC-1999; 99WO-US011005.
XX
PR 23-DEC-1998; 98US-00220876.
XX
PA (GEMY) GENETICS INST INC.
XX
PI Jacobs K, McCooy JM, Lavallie ER, Collins-Racie LA, Evans C;
PI Merberg D, Treacy M, Bowman MR;
XX
DR WPI; 2000-442661/38.
DR P-PSDB; AAB10274.
XX
PT Secreted human proteins AS296-li and AS34-li, useful for treating tumors,
PT autoimmune diseases, inflammatory disorders, wounds, microbial infections
PT and viral diseases.
XX
PS Disclosure; Page 269; 293pp; English.
XX
CC This invention describes novel secreted human proteins (I) which have
CC cytostatic, immunostimulatory, antimicrobial, antiviral,
CC immunosuppressive, antiinflammatory and vulnerrary activity and which act
CC as cytokine, cell proliferation or differentiation regulators. (I) is
CC useful for treating tumors, autoimmune diseases, inflammatory disorders,
CC wounds, microbial infections and viral diseases. (I) is also useful for
CC suppressing graft versus host reaction. AAA40490-A40580 represent cDNA
CC fragments that encode the secreted proteins AAB10226-B10288 described in
CC the method of the invention

XX SQ Sequence 18 BP; 17 A; 0 C; 1 G; 0 T; 0 U; 0 Other;
Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
DB 2 AAAAAAAAAAAAAA 17

RESULT 268
AAZ90649/C
ID AAZ90649 standard; DNA; 18 BP.
XX
AC AAZ90649;
XX
DT 13-JUN-2000 (first entry)
XX
DE Human adipose tissue gene amplifying primer #10.
XX
KW Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
KW arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN JP2000037190-A.
XX


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PD 08-FEB-2000.
PF 23-JUL-1998; 98JP-00225228.
PR 23-JUL-1998; 98JP-00225228.
XX (NISB ) JAPAN TOBACCO INC.
PA WPI; 2000-306578/27.
DR
XX
XX A physiologically active protein specifically derived from mammal tissue.
PT
XX Example 2; Page 18; 50pp; Japanese.
PS
XX The invention relates to identification of genes and proteins of adipose
CC tissue relating to obesity, particularly complications of visceral
CC obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
CC hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
CC proteins (AAV67598-Y67600) are used in the genetic diagnosis, prevention
CC and treatment of adipose tissue related diseases. Sequences AAZ90640-51
CC represent PCR primers amplifying the human adipose tissue genes
XX
XX Sequence 18 BP; 1 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1480 TAAAAA
DB 17 TAAAAA
RESULT 269
AAZ90646/C
ID AAZ90646 standard; DNA; 18 BP.
XX
XX AAZ90646;
AC
XX 13-JUN-2000 (first entry)
DT
XX Human adipose tissue gene amplifying primer #7.
DE
XX Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
XX arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX Homo sapiens.
OS
XX JF2000037190-A.
PN
XX 08-FEB-2000.
PD
XX 23-JUL-1998; 98JP-00225228.
PF
XX 23-JUL-1998; 98JP-00225228.
PR
XX (NISB ) JAPAN TOBACCO INC.
PA WPI; 2000-306578/27.
DR
XX A physiologically active protein specifically derived from mammal tissue.
PT
XX Example 2; Page 18; 50pp; Japanese.
PS
XX The invention relates to identification of genes and proteins of adipose
CC tissue relating to obesity, particularly complications of visceral
CC obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
CC hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
CC proteins (AAV67598-Y67600) are used in the genetic diagnosis, prevention
CC and treatment of adipose tissue related diseases. Sequences AAZ90640-51
CC represent PCR primers amplifying the human adipose tissue genes
XX
XX Sequence 18 BP; 2 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1480 TAAAAA
DB 17 TAAAAA
RESULT 269
AAZ90646/C
ID AAZ90646 standard; DNA; 18 BP.
XX
XX AAZ90646;
AC
XX 13-JUN-2000 (first entry)
DT
XX Human adipose tissue gene amplifying primer #7.
DE
XX Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
XX arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX Homo sapiens.
OS
XX JF2000037190-A.
PN
XX 08-FEB-2000.
PD
XX 23-JUL-1998; 98JP-00225228.
PF
XX 23-JUL-1998; 98JP-00225228.
PR
XX (NISB ) JAPAN TOBACCO INC.
PA WPI; 2000-306578/27.
DR
XX A physiologically active protein specifically derived from mammal tissue.
PT
XX Example 2; Page 18; 50pp; Japanese.
PS
XX The invention relates to identification of genes and proteins of adipose
CC tissue relating to obesity, particularly complications of visceral
CC obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
CC hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
CC proteins (AAV67598-Y67600) are used in the genetic diagnosis, prevention
CC and treatment of adipose tissue related diseases. Sequences AAZ90640-51
CC represent PCR primers amplifying the human adipose tissue genes
XX
XX Sequence 18 BP; 2 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
SQ

```

```

Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1480 TAAAAA
DB 17 TAAAAA
RESULT 270
AAZ90643/C
ID AAZ90643 standard; DNA; 18 BP.
XX
XX AAZ90643;
AC
XX 13-JUN-2000 (first entry)
DT
XX Human adipose tissue gene amplifying primer #4.
DE
XX Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
XX arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX Homo sapiens.
OS
XX JF2000037190-A.
PN
XX 08-FEB-2000.
PD
XX 23-JUL-1998; 98JP-00225228.
PF
XX 23-JUL-1998; 98JP-00225228.
PR
XX (NISB ) JAPAN TOBACCO INC.
PA WPI; 2000-306578/27.
DR
XX A physiologically active protein specifically derived from mammal tissue.
PT
XX Example 2; Page 18; 50pp; Japanese.
PS
XX The invention relates to identification of genes and proteins of adipose
CC tissue relating to obesity, particularly complications of visceral
CC obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
CC hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
CC proteins (AAV67598-Y67600) are used in the genetic diagnosis, prevention
CC and treatment of adipose tissue related diseases. Sequences AAZ90640-51
CC represent PCR primers amplifying the human adipose tissue genes
XX
XX Sequence 18 BP; 1 A; 0 C; 1 G; 16 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1480 TAAAAA
DB 17 TAAAAA
RESULT 271
AAZ87161
ID AAZ87161 standard; RNA; 18 BP.
XX
XX AAZ87161;
AC
XX 08-MAY-2000 (first entry)
DT
XX Oligoarabinonucleotide SEQ ID NO:2.
DE
XX Beta-D-arabinose; antisense; inhibition; transcription; expression;
XX reverse transcription; viral replication; RNase H cleavage;
XX triple helix formation; ss.

```

```
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT modified_base 1..18
FT /*tag= a
FT /*note= "Ribose moiety replaced by beta-D-arabinose"
XX PN WO967378-A1.
XX PD 29-DEC-1999.
XX PF 17-JUN-1999; 99WO-CA000571.
XX PR 19-JUN-1998; 98CA-02241361.
XX PA (UYMC-) UNIV MCGILL.
XX PI Damha MJ, Parniak MA, Noronha AM, Wilds C, Borkow G, Arion D;
XX DR WPI; 2000-160584/14.
XX PT Therapeutic composition containing antisense oligonucleotides that
XX PT include arabinose sugars, particularly for inhibiting viral replication.
XX PS Example 1; Page 29; 91pp; English.
XX CC The invention relates to a new composition for selective, sequence-
XX CC specific inhibition of gene transcription and expression in a host. The
XX CC composition comprises oligonucleotides containing arabinose sugars that
XX CC can hybridise to either a single-stranded (ss) RNA to induce RNase H
XX CC cleavage activity, or to a DNA/DNA or DNA/RNA duplex to form a triple
XX CC helix, thereby inhibiting DNA replication and/or transcription. The
XX CC oligoarabinonucleotides are used for antisense inhibition of gene
XX CC expression or to prevent DNA replication, or reverse transcription of RNA
XX CC by retroviruses. The compositions are therefore particularly used to
XX CC inhibit retroviral replication. The oligoarabinonucleotides can also be
XX CC used, in combination with RNase H, as reagents for sequence-specific
XX CC cleavage or RNA mapping, and additionally for the study and control of
XX CC gene expression in cells. The oligoarabinonucleotides have excellent
XX CC affinity for RNA, increased resistance to nucleases and show little if
XX CC any non-specific binding to cellular or serum proteins. They target ss
XX CC RNA, but not complementary ss DNA, so may be useful for targeting
XX CC retroviral genomic RNA to inhibit the early stages of viral replication.
XX CC Oligoarabinonucleotides containing pyrimidine bases form triple helices
XX CC with significantly higher thermal stability than those produced by normal
XX CC oligonucleotides. Sequences AAZ87160-287164 represent
XX CC oligoarabinonucleotides containing beta-D-arabinose used in an
XX CC exemplification of the present invention
XX SQ Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
Db 1 AAAAAAAAAAAAAA 16

RESULT 272
AAZ87162/c
ID AAZ87162 standard; RNA; 18 BP.
XX AC AAZ87162;
XX DT 08-MAY-2000 (first entry)
XX DE Oligoarabinonucleotide SEQ ID NO:3.
XX KW Beta-D-arabinose; antisense; inhibition; transcription; expression;
XX KW reverse transcription; viral replication; RNase H cleavage;
```

```
KW triple helix formation; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT modified_base 1..18
FT /*tag= a
FT /*note= "Ribose moiety replaced by beta-D-arabinose"
XX PN WO967378-A1.
XX PD 29-DEC-1999.
XX PF 17-JUN-1999; 99WO-CA000571.
XX PR 19-JUN-1998; 98CA-02241361.
XX PA (UYMC-) UNIV MCGILL.
XX PI Damha MJ, Parniak MA, Noronha AM, Wilds C, Borkow G, Arion D;
XX DR WPI; 2000-160584/14.
XX PT Therapeutic composition containing antisense oligonucleotides that
XX PT include arabinose sugars, particularly for inhibiting viral replication.
XX PS Example 1; Page 29; 91pp; English.
XX CC The invention relates to a new composition for selective, sequence-
XX CC specific inhibition of gene transcription and expression in a host. The
XX CC composition comprises oligonucleotides containing arabinose sugars that
XX CC can hybridise to either a single-stranded (ss) RNA to induce RNase H
XX CC cleavage activity, or to a DNA/DNA or DNA/RNA duplex to form a triple
XX CC helix, thereby inhibiting DNA replication and/or transcription. The
XX CC oligoarabinonucleotides are used for antisense inhibition of gene
XX CC expression or to prevent DNA replication, or reverse transcription of RNA
XX CC by retroviruses. The compositions are therefore particularly used to
XX CC inhibit retroviral replication. The oligoarabinonucleotides can also be
XX CC used, in combination with RNase H, as reagents for sequence-specific
XX CC cleavage or RNA mapping, and additionally for the study and control of
XX CC gene expression in cells. The oligoarabinonucleotides have excellent
XX CC affinity for RNA, increased resistance to nucleases and show little if
XX CC any non-specific binding to cellular or serum proteins. They target ss
XX CC RNA, but not complementary ss DNA, so may be useful for targeting
XX CC retroviral genomic RNA to inhibit the early stages of viral replication.
XX CC Oligoarabinonucleotides containing pyrimidine bases form triple helices
XX CC with significantly higher thermal stability than those produced by normal
XX CC oligonucleotides. Sequences AAZ87160-287164 represent
XX CC oligoarabinonucleotides containing beta-D-arabinose used in an
XX CC exemplification of the present invention
XX SQ Sequence 18 BP; 0 A; 0 C; 0 G; 0 T; 18 U; 0 Other;

Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
Db 18 AAAAAAAAAAAAAA 3

RESULT 273
AAZ87166/c
ID AAZ87166 standard; DNA; 18 BP.
XX AC AAZ87166;
XX DT 08-MAY-2000 (first entry)
XX DE Deoxyarabinonucleotide SEQ ID NO:7.
XX KW 2'-deoxy-2'-fluoro-beta-D-arabinose; antisense; inhibition;
```

PR TAKESHI NAGASU, YUJI SUGITA, TOMOKO KASHIWABARA, TADAHIRO OSHIDA,
PI MASAYA OBAYASHI, SHIGEMICHI GUNJI, IZUMI OBAYASHI, YUKIHO IMAI,
PI NING NO,
PI KAOKU OGAWA
PC C12N15/09,A61K31/00,A61K39/36,A61K45/00,C12Q1/68,C12N15/00 CC

FH Key Location/Qualifiers
FT source 1..17
PT /organism='Artificial Sequence'

FEATURES
source
1..17
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 1..1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAA1496
Db 17 TAAAAA1496

RESULT 58
AR187062/c
LOCUS AR187062 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 2550 from patent US 6346398.
ACCESSION AR187062
VERSION AR187062.1 GI:20233027
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 2550 12-FEB-2002;
FEATURES
source 1..17
Location/Qualifiers
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1..1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAA1496
Db 17 AAAAAA1496

RESULT 59
AR187063/c
LOCUS AR187063 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 2551 from patent US 6346398.
ACCESSION AR187063
VERSION AR187063.1 GI:20233028
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 2551 12-FEB-2002;
FEATURES
source 1..17
Location/Qualifiers
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1..1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAA1496
Db 16 AAAAAA1496

RESULT 60
AR222463
LOCUS AR222463 17 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 23 from patent US 6429300.
ACCESSION AR222463
VERSION AR222463.1 GI:23329994
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Kurz, M., Lohse, P. and Wagner, R.
TITLE Peptide acceptor ligation methods
JOURNAL Patent: US 6429300-A 23 06-AUG-2002;
FEATURES
source 1..17
Location/Qualifiers
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1..1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAA1496
Db 1 AAAAAA1496

RESULT 61
AR236087/c
LOCUS AR236087 17 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 5 from patent US 6462184.
ACCESSION AR236087
VERSION AR236087.1 GI:27279786
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Manoharan, M. and Maier, M.A.
TITLE Compounds, processes and intermediates for synthesis of mixed backbone oligomeric compounds
JOURNAL Patent: US 6462184-A 5 08-OCT-2002;
FEATURES
source 1..17
Location/Qualifiers
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1..1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAA1496
Db 17 AAAAAA1496

RESULT 62
AR266625/c
LOCUS AR266625 17 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 63 from patent US 6495319.
ACCESSION AR266625
VERSION AR266625.1 GI:29695689

```

KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 17)
AUTHORS     McClelland,M., Welsh,J. and Trenkle,T.
TITLE       Reduced complexity nucleic acid targets and methods of using same
JOURNAL     Patent: US 6495319-A 63 17-DEC-2002;
FEATURES    Location/Qualifiers
            source
            1..17
                /organism="unknown"
                /mol_type="genomic DNA"

Query Match      1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1480 TAAAAA
Db      17 TAAAAA

RESULT 63
AR323672/c
LOCUS      AR323672      17 bp      RNA      linear      PAT 17-AUG-2003
DEFINITION Sequence 1074 from patent US 6566127.
ACCESSION  AR323672
VERSION     AR323672.1 GI:33709480
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Favco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE       Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
JOURNAL     Patent: US 6566127-A 1074 20-MAY-2003;
FEATURES    Location/Qualifiers
            source
            1..17
                /organism="unknown"
                /mol_type="unassigned RNA"

Query Match      1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAA
Db      17 AAAAAA

RESULT 64
AR323673/c
LOCUS      AR323673      17 bp      RNA      linear      PAT 17-AUG-2003
DEFINITION Sequence 1075 from patent US 6566127.
ACCESSION  AR323673
VERSION     AR323673.1 GI:33709481
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Favco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE       Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
JOURNAL     Patent: US 6566127-A 1075 20-MAY-2003;
FEATURES    Location/Qualifiers
            source
            1..17
                /organism="unknown"
                /mol_type="unassigned RNA"

Query Match      1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAA
Db      17 AAAAAA

KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 17)
AUTHORS     McClelland,M., Welsh,J. and Trenkle,T.
TITLE       Reduced complexity nucleic acid targets and methods of using same
JOURNAL     Patent: US 6495319-A 63 17-DEC-2002;
FEATURES    Location/Qualifiers
            source
            1..17
                /organism="unknown"
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Query Match      1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAA
Db      17 AAAAAA

RESULT 65
AX361606/c
LOCUS      AX361606      17 bp      DNA      linear      PAT 15-FEB-2002
DEFINITION Sequence 24 from Patent WO0208461.
ACCESSION  AX361606
VERSION     AX361606.1 GI:18694225
KEYWORDS    .
SOURCE      synthetic construct
            synthetic construct
            artificial sequences.
ORGANISM    .
REFERENCE   1
AUTHORS     Linnarsson,S.G., Ernfors,P.G. and Bauren,G.G.
TITLE       A method and an algorithm for mrna expression analysis
JOURNAL     Patent: WO 0208461-A 24 31-JAN-2002;
            Global Genomics AB (SE)
FEATURES    Location/Qualifiers
            source
            1..17
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Double-stranded product DNA"

Query Match      1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAA
Db      16 AAAAAA

RESULT 66
AX692525/c
LOCUS      AX692525      17 bp      DNA      linear      PAT 31-MAR-2003
DEFINITION Sequence 5257 from Patent EP1281758.
ACCESSION  AX692525
VERSION     AX692525.1 GI:29415483
KEYWORDS    .
SOURCE      Homo sapiens (human)
            Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ORGANISM    .
REFERENCE   1
AUTHORS     Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE       Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
JOURNAL     Patent: EP 1281758-A 5257 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES    Location/Qualifiers
            source
            1..17
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
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Query Match      1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAA
Db      17 AAAAAA

RESULT 67
AX692526/c
LOCUS      AX692526      17 bp      DNA      linear      PAT 31-MAR-2003

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DEFINITION Sequence 5258 from Patent EP1281758.
ACCESSION AX692526
VERSION AX692526.1 GI:29415484
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 5258 05-FEB-2003;
Acomica, Inc. (US)
FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1..17; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1496
Db 16 AAAAAAAAAAAAAA 1

RESULT 68
AX814938/c
LOCUS AX814938
DEFINITION Sequence 24 from Patent WO03064691.
ACCESSION AX814938
VERSION AX814938.1 GI:39104076
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Linnarsson,S., Ernfors,P., Bauren,G., Metsis,A., Pihlak,A. and Montelius,A.
TITLE Methods and means for manipulating nucleic acid
JOURNAL Patent: WO 03064691-A 24 07-AUG-2003;
Global Genomics AB (SE)
FEATURES
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/db_xref="taxon:32630"
/note="Description of Artificial Sequence: Double-stranded product DNA"

Query Match 1..17; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1496
Db 16 AAAAAAAAAAAAAA 1

RESULT 69
BD011730/c
LOCUS BD011730
DEFINITION 795, a novel gene related to pollen allergy.
ACCESSION BD011730
VERSION BD011730.1 GI:22091919
KEYWORDS WO 0065050-A/2.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 17)

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AUTHORS Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
Takahashi,E. and Yokoi,A.
TITLE 795, a novel gene related to pollen allergy
JOURNAL Patent: WO 0065050-A 2 02-NOV-2000;
GENOX RESEARCH INC.TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
TADAHIRO OSHIDA,MASAYA OBAAYASHI,SHIGEMICHI GUNJI,IZUMI OBAAYASHI,
YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI
TAKAHASHI,AKIRA YOKOI
COMMENT OS Artificial Sequence
PN WO 0065050-A/2
PD 02-NOV-2000
PF 26-APR-2000 WO 2000JP002734
PR 27-APR-1999 JP 99P 120494
PI TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
PI MASAYA OBAAYASHI,SHIGEMICHI GUNJI,IZUMI OBAAYASHI,YUKIHO IMAI,
PI NEI YOSHIDA,
PI KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI PC
C12N15/12,C07K14/47,C07K16/18,C12Q1/68,G01N33/50//A61K31/00, PC
A61P37/00
CC Description of Artificial Sequence:Artificially Synthesized CC
Primer Sequence
FH Key Location/Qualifiers
source
1..17
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 1..17; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1480 TAAAAAAAAAAAAA 1495
Db 17 TAAAAAAAAAAAAA 2

RESULT 70
BD091742/c
LOCUS BD091742
DEFINITION 441, a novel gene related to pollen allergy.
ACCESSION BD091742
VERSION BD091742.1 GI:22637353
KEYWORDS WO 0073435-A/2.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 17)
AUTHORS Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K. and Matsui,K.
TITLE 441, a novel gene related to pollen allergy
JOURNAL Patent: WO 0073435-A 2 07-DEC-2000;
GENOX RESEARCH INC.TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
TADAHIRO OSHIDA,MASAYA OBAAYASHI,SHIGEMICHI GUNJI,IZUMI OBAAYASHI,
YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI
COMMENT OS Artificial Sequence
PN WO 0073435-A/2
PD 07-DEC-2000
PF 18-MAY-2000 WO 2000JP003190
PR 27-MAY-1999 JP 99P 148783
PI TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
PI MASAYA OBAAYASHI,SHIGEMICHI GUNJI,IZUMI OBAAYASHI,YUKIHO IMAI,
PI NEI YOSHIDA,
PI KAORU OGAWA,KEIKO MATSUI
PI C12N15/10,C12Q1/68,G01N33/15,G01N33/50
PC Description of Artificial Sequence:Artificially Synthesized CC
Primer Sequence
FH Key Location/Qualifiers
source
1..17
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/mol_type="genomic DNA"

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/db_xref="taxon:32630"

Query Match      1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAA 1495
DB 17 TAAAAA 2

RESULT 71
BD091750/c
LOCUS      17 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION
465, a novel gene related to pollen allergy.
ACCESSION      BD091750
VERSION      BD091750.1 GI:22637361
KEYWORDS      synthetic construct
SOURCE      synthetic construct
ORGANISM      artificial sequences.
REFERENCE      1 (bases 1 to 17)
AUTHORS      Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
Takahashi,E. and Yokoi,A.
TITLE      465, a novel gene related to pollen allergy
JOURNAL      Patent: WO 0073439-A 2 07-DEC-2000;
GENOX RESEARCH INC, TAKESHI NAGASU, YUJI SUGITA, TOMOKO KASHIWABARA,
TADAHIRO OSHIDA, MASAYA ODAYASHI, SHIGEMICHI GUNJI, IZUMI ODAYASHI,
YUKIHO IMAI, NEI YOSHIDA, KAORU OGAWA, KEIKO MATSUI, EIKI
TAKAHASHI, AKIRA YOKOI
COMMENT      OS Artificial Sequence
PN WO 0073439-A/2
PF 07-DEC-2000
PR 18-MAY-2000 WO 2000JP003191
PI 27-MAY-1999 JP 99P 148784
PT TAKESHI NAGASU, YUJI SUGITA, TOMOKO KASHIWABARA, TADAHIRO OSHIDA,
MASAYA ODAYASHI, SHIGEMICHI GUNJI, IZUMI ODAYASHI, YUKIHO IMAI,
NEI YOSHIDA, KAORU OGAWA, KEIKO MATSUI, EIKI TAKAHASHI, AKIRA YOKOI PC
C12N15/12, C12Q1/68, A61K39/36, A61K45/00 CC Description
of Artificial Sequence:Artificially Synthesized CC Primer
Sequence
FH Key Location/Qualifiers
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match      1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAA 1495
DB 17 TAAAAA 2

RESULT 73
BD097334/c
LOCUS      17 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION
Method for examination for allergosis.
ACCESSION      BD097334
VERSION      BD097334.1 GI:23642908
KEYWORDS      WO 0165259-A/5.
SOURCE      synthetic construct
ORGANISM      artificial sequences.
REFERENCE      1 (bases 1 to 17)
AUTHORS      Nagasu,T., Oshida,T., Obayashi,I., Matsui,K. and Sait,H.
TITLE      Method for examination for allergosis
JOURNAL      Patent: WO 0165259-A 5 07-SEP-2001;
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
NATIONAL CHILDREN'S HOSPITAL, HIROMITSU NAKAUCHI, YUTAKA
FUJIKI, KAZUO FUKAWA, OSAMU KUDO TAKESHI NAGASU, TADAHIRO OSHIDA, IZUMI
OBAYASHI, KEIKO MATSUI, HIROHISA SAITO
COMMENT      OS Artificial Sequence
PN WO 0165259-A/5
PD 07-SEP-2001
PF 23-FEB-2001 WO 2001JP001372
PR 02-MAR-2000 JP 00P 61832
PT TAKESHI NAGASU, TADAHIRO OSHIDA, IZUMI OBAYASHI, KEIKO MATSUI, PI
HIROHISA SAITO
PC GOIN33/53, C12Q1/68, C12N15/12, G01N33/15, A01K67/027, A61K39/395,
A61P37/08
CC Description of Artificial Sequence:Artificially Synthesized CC
Primer Sequence
FH Key Location/Qualifiers
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/db_xref="taxon:32630"

Query Match      1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAA 1495
DB 17 TAAAAA 2

RESULT 72
BD091773/c
LOCUS      17 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION
787, a novel gene related to pollen allergy.
ACCESSION      BD091773
VERSION      BD091773.1 GI:22637384
KEYWORDS      synthetic construct
SOURCE      synthetic construct
ORGANISM      artificial sequences.
REFERENCE      1 (bases 1 to 17)
AUTHORS      Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
Takahashi,E. and Yokoi,A.
TITLE      787, a novel gene related to pollen allergy.
JOURNAL      Patent: WO 0073440-A 2 07-DEC-2000;
GENOX RESEARCH INC, TAKESHI NAGASU, YUJI SUGITA, TOMOKO KASHIWABARA,
TADAHIRO OSHIDA, MASAYA ODAYASHI, SHIGEMICHI GUNJI, IZUMI ODAYASHI,
YUKIHO IMAI, NEI YOSHIDA, KAORU OGAWA, KEIKO MATSUI, EIKI
TAKAHASHI, AKIRA YOKOI
COMMENT      OS Artificial Sequence
PN WO 0073440-A/2
PF 07-DEC-2000
PR 18-MAY-2000 WO 2000JP003192
PI 27-MAY-1999 JP 99P 148785
PT TAKESHI NAGASU, YUJI SUGITA, TOMOKO KASHIWABARA, TADAHIRO OSHIDA,
MASAYA ODAYASHI, SHIGEMICHI GUNJI, IZUMI ODAYASHI, YUKIHO IMAI,
NEI YOSHIDA, KAORU OGAWA, KEIKO MATSUI, EIKI TAKAHASHI, AKIRA YOKOI PC
C12N15/12, C12Q1/68, C12N5/08, C12N5/06, C07K14/415 CC Description
of Artificial Sequence:Artificially Synthesized CC Primer
Sequence
FH Key Location/Qualifiers
1..17
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/mol_type="genomic DNA"
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Query Match      1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAA 1495
DB 17 TAAAAA 2

RESULT 72
BD091773/c
LOCUS      17 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION
787, a novel gene related to pollen allergy.
ACCESSION      BD091773
VERSION      BD091773.1 GI:22637384
KEYWORDS      synthetic construct
SOURCE      synthetic construct
ORGANISM      artificial sequences.
REFERENCE      1 (bases 1 to 17)
AUTHORS      Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
Takahashi,E. and Yokoi,A.
TITLE      787, a novel gene related to pollen allergy.
JOURNAL      Patent: WO 0073440-A 2 07-DEC-2000;
GENOX RESEARCH INC, TAKESHI NAGASU, YUJI SUGITA, TOMOKO KASHIWABARA,
TADAHIRO OSHIDA, MASAYA ODAYASHI, SHIGEMICHI GUNJI, IZUMI ODAYASHI,
YUKIHO IMAI, NEI YOSHIDA, KAORU OGAWA, KEIKO MATSUI, EIKI
TAKAHASHI, AKIRA YOKOI
COMMENT      OS Artificial Sequence
PN WO 0073440-A/2
PF 07-DEC-2000
PR 18-MAY-2000 WO 2000JP003192
PI 27-MAY-1999 JP 99P 148785
PT TAKESHI NAGASU, YUJI SUGITA, TOMOKO KASHIWABARA, TADAHIRO OSHIDA,
MASAYA ODAYASHI, SHIGEMICHI GUNJI, IZUMI ODAYASHI, YUKIHO IMAI,
NEI YOSHIDA, KAORU OGAWA, KEIKO MATSUI, EIKI TAKAHASHI, AKIRA YOKOI PC
C12N15/12, C12Q1/68, C12N5/08, C12N5/06, C07K14/415 CC Description
of Artificial Sequence:Artificially Synthesized CC Primer
Sequence
FH Key Location/Qualifiers
1..17
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match      1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAA 1495
DB 17 TAAAAA 2

RESULT 72
BD091773/c
LOCUS      17 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION
787, a novel gene related to pollen allergy.
ACCESSION      BD091773
VERSION      BD091773.1 GI:22637384
KEYWORDS      synthetic construct
SOURCE      synthetic construct
ORGANISM      artificial sequences.
REFERENCE      1 (bases 1 to 17)
AUTHORS      Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
Takahashi,E. and Yokoi,A.
TITLE      787, a novel gene related to pollen allergy.
JOURNAL      Patent: WO 0073440-A 2 07-DEC-2000;
GENOX RESEARCH INC, TAKESHI NAGASU, YUJI SUGITA, TOMOKO KASHIWABARA,
TADAHIRO OSHIDA, MASAYA ODAYASHI, SHIGEMICHI GUNJI, IZUMI ODAYASHI,
YUKIHO IMAI, NEI YOSHIDA, KAORU OGAWA, KEIKO MATSUI, EIKI
TAKAHASHI, AKIRA YOKOI
COMMENT      OS Artificial Sequence
PN WO 0073440-A/2
PF 07-DEC-2000
PR 18-MAY-2000 WO 2000JP003192
PI 27-MAY-1999 JP 99P 148785
PT TAKESHI NAGASU, YUJI SUGITA, TOMOKO KASHIWABARA, TADAHIRO OSHIDA,
MASAYA ODAYASHI, SHIGEMICHI GUNJI, IZUMI ODAYASHI, YUKIHO IMAI,
NEI YOSHIDA, KAORU OGAWA, KEIKO MATSUI, EIKI TAKAHASHI, AKIRA YOKOI PC
C12N15/12, C12Q1/68, C12N5/08, C12N5/06, C07K14/415 CC Description
of Artificial Sequence:Artificially Synthesized CC Primer
Sequence
FH Key Location/Qualifiers
1..17
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match      1.1%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAA 1495
DB 17 TAAAAA 2

RESULT 72
BD091773/c
LOCUS      17 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION
787, a novel gene related to pollen allergy.
ACCESSION      BD091773
VERSION      BD091773.1 GI:22637384
KEYWORDS      synthetic construct
SOURCE      synthetic construct
ORGANISM      artificial sequences.
REFERENCE      1 (bases 1 to 17)
AUTHORS      Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
Takahashi,E. and Yokoi,A.
TITLE      787, a novel gene related to pollen allergy.
JOURNAL      Patent: WO 0073440-A 2 07-DEC-2000;
GENOX RESEARCH INC, TAKESHI NAGASU, YUJI SUGITA, TOMOKO KASHIWABARA,
TADAHIRO OSHIDA, MASAYA ODAYASHI, SHIGEMICHI GUNJI, IZUMI ODAYASHI,
YUKIHO IMAI, NEI YOSHIDA, KAORU OGAWA, KEIKO MATSUI, EIKI
TAKAHASHI, AKIRA YOKOI
COMMENT      OS Artificial Sequence
PN WO 0073440-A/2
PF 07-DEC-2000
PR 18-MAY-2000 WO 2000JP003192
PI 27-MAY-1999 JP 99P 148
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Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAA1495
Db 17 TAAAAA1495

RESULT 74
BD142808/c
LOCUS
DEFINITION Method of examining allergic disease.
ACCESSION BD142808
VERSION BD142808.1 GI:23237753
KEYWORDS WO 0224903-A/2.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 17)
AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T., Nagasu,T.,
Tsujimoto,G. and Takahashi,E.
TITLE Method of examining allergic disease
JOURNAL Patent: WO 0224903-A 2 28-MAR-2002;
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
NATIONAL CHILDREN'S HOSPITAL, YUJI SUGITA, RYOICHI HASHIDA, KAORU
OGAWA, TOMOKO FUJISHIMA, TAKESHI NAGASU, GOZO TSUJIMOTO, EIKI
TAKAHASHI
OS Artificial Sequence
PN WO 0224903-A/2
PD 28-MAR-2002
PE 21-SEP-2001 WO 2001JP008246
PR 25-SEP-2000 JP 00P 291318
PI YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, TOMOKO FUJISHIMA,
TAKESHI NAGASU,
PC GOZO TSUJIMOTO, EIKI TAKAHASHI
PC C12N15/09, C12N5/10, C07K14/47, C07K16/18, C12P21/02, C12Q1/02, PC
C12Q1/68, A01K67/027, A61K31/713, A61K45/00, A61P17/00, A61P37/08,
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CC Description of Artificial Sequence:an artificially synthesized

CC sequence primer
FH Key Location/Qualifiers
FT source 1..17
/organism='Artificial Sequence'.

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Query Match 1..1; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAA1495
Db 17 TAAAAA1495

RESULT 75
BD143834/c
LOCUS
DEFINITION Method of examining allergic disease.
ACCESSION BD143834
VERSION BD143834.1 GI:27849592
KEYWORDS JP 2002095500-A/2.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 17)
AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T. and
Tsujimoto,K.
TITLE Method of examining allergic disease
JOURNAL Patent: JP 2002095500-A 2 02-APR-2002;
GENOX RESEARCH INC, THE DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL
OS Artificial Sequence
PN JP 2002095500-A/2
PD 02-APR-2002
PE 25-SEP-2000 JP 2000291316
PR 13-OCT-2000 JP 00P 314093
PI YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, MASAYA OBAYASHI, PI
TAKESHI NAGASU,
PC YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, MASAYA OBAYASHI, PI
PC C12Q1/68, A01K67/027, A61K31/7088, A61K31/711, A61K45/00, A61P37/08, PC
C07K14/47,
PC C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N5/10 PC
C12N15/09, C12P21/02,
PC C12Q1/02, G01N33/15, G01N33/50//C12P21/08, C12N5/00, C12N5/00, PC
C12N15/00
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CC sequence primer
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QY 1480 TAAAAA1495
Db 17 TAAAAA1495

RESULT 76
BD167835/c
LOCUS
DEFINITION Method for examination of allergosis.
ACCESSION BD167835
VERSION BD167835.1 GI:27873647
KEYWORDS WO 0233122-A/2.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 17)
AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T., Saito,H.
and Takahashi,E.
TITLE Method for examination of allergosis
JOURNAL Patent: WO 0233122-A 2 25-APR-2002;
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
NATIONAL CHILDREN'S HOSPITAL, RINAKO NAKAGAWA YUJI SUGITA, RYOICHI
HASHIDA, KAORU OGAWA, MASAYA OBAYASHI, TAKESHI NAGASU, HIROHISA
SAITO, EIKI TAKAHASHI
OS Artificial Sequence
PN WO 0233122-A/2
PD 25-APR-2002
PE 11-OCT-2001 WO 2001JP008937
PR 13-OCT-2000 JP 00P 314093
PI YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, MASAYA OBAYASHI, PI
TAKESHI NAGASU,
PC YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, MASAYA OBAYASHI, PI
PC C12Q1/68, C12N15/09, G01N33/53, G01N33/50, C12Q1/02, A61K48/00, PC
A61K39/395,
PC A01K67/027//C07K16/18, C12N5/10
CC Description of Artificial Sequence:an artificially synthesized

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TITLE
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OS Artificial Sequence
PN JP 2002095500-A/2
PD 02-APR-2002
PE 25-SEP-2000 JP 2000291316
PR 13-OCT-2000 JP 00P 314093
PI YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, MASAYA OBAYASHI, PI
TAKESHI NAGASU,
PC YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, MASAYA OBAYASHI, PI
PC C12Q1/68, A01K67/027, A61K31/7088, A61K31/711, A61K45/00, A61P37/08, PC
C07K14/47,
PC C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N5/10 PC
C12N15/09, C12P21/02,
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CC sequence primer
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Best Local Similarity 100.0%; Pred. No. 74;
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QY 1480 TAAAAA1495
Db 17 TAAAAA1495

RESULT 76
BD167835/c
LOCUS
DEFINITION Method for examination of allergosis.
ACCESSION BD167835
VERSION BD167835.1 GI:27873647
KEYWORDS WO 0233122-A/2.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 17)
AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T., Saito,H.
and Takahashi,E.
TITLE Method for examination of allergosis
JOURNAL Patent: WO 0233122-A 2 25-APR-2002;
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
NATIONAL CHILDREN'S HOSPITAL, RINAKO NAKAGAWA YUJI SUGITA, RYOICHI
HASHIDA, KAORU OGAWA, MASAYA OBAYASHI, TAKESHI NAGASU, HIROHISA
SAITO, EIKI TAKAHASHI
OS Artificial Sequence
PN WO 0233122-A/2
PD 25-APR-2002
PE 11-OCT-2001 WO 2001JP008937
PR 13-OCT-2000 JP 00P 314093
PI YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, MASAYA OBAYASHI, PI
TAKESHI NAGASU,
PC YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, MASAYA OBAYASHI, PI
PC C12Q1/68, C12N15/09, G01N33/53, G01N33/50, C12Q1/02, A61K48/00, PC
A61K39/395,
PC A01K67/027//C07K16/18, C12N5/10
CC Description of Artificial Sequence:an artificially synthesized

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CC primer sequence      Location/Qualifiers
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FT source               /organism='Artificial Sequence'.

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Query Match
Best Local Similarity 100.0%; DB 1; Length 17;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAAA 1495
Db 17 TAAAAAAAAAAAAA 2

RESULT 77
BD167907/c
LOCUS BD167907 17 bp DNA linear PAT 17-JAN-2003
DEFINITION Method of examining allergic disease.
ACCESSION BD167907
VERSION BD167907.1 GI:27873719
KEYWORDS WO 0226962-A/6.
SOURCE synthetic construct
ORGANISM artificial construct
REFERENCE 1 (bases 1 to 17)
AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T., Nagasu,T. and Saito,H.
TITLE Method of examining allergic disease
JOURNAL Patent: WO 0226962-A 6 04-APR-2002;
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
NATIONAL CHILDREN'S HOSPITAL, MASAKAZU ADACHI, KAZUO MIYANAGA YUJI
SUGITA, RYOICHI HASHIDA, KAORU OGAWA, TOMOKO FUJISHIMA, TAKESHI
NAGASU, HIROHISA SAITO
OS Artificial Sequence
PN WO 0226962-A/6
PD 04-APR-2002
PF 21-SEP-2001 WO 2001JP008247
PR 26-SEP-2000 JP OOP 293021
PI YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, TOMOKO FUJISHIMA, PI
TAKESHI NAGASU,
PI HIROHISA SAITO
PC C12N15/09, C12N5/10, C07K14/47, C07K16/18, C12P21/02, C12Q1/02, PC
A01K67/027, A61K31/713, A61K45/00, A61K48/00, A61P17/00, A61P37/08,
PC GOIN33/15,
PC GOIN33/50//C12P21/08, (C12N5/10, C12R1:91), (C12P21/02, C12R1:91)
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CC sequence primer
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Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAAA 1495
Db 17 TAAAAAAAAAAAAA 2

RESULT 78
BD168111/c
LOCUS BD168111 17 bp DNA linear PAT 17-JAN-2003
DEFINITION Method for examination for allergies.
ACCESSION BD168111
VERSION BD168111.1 GI:27873923
KEYWORDS WO 0233069-A/18.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 17)
AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T. and Saito,H.
TITLE Method for examination for allergies
JOURNAL Patent: WO 0233069-A 18 25-APR-2002;
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
NATIONAL CHILDREN'S HOSPITAL, TOMOYUKI FUKASAWA, CHUHEI NOJIRI, NOBUO
MATSUHASHI, KOJI NISHIZAWA, YUJI SUGITA, RYOICHI HASHIDA, KAORU
OGAWA, MASAYA OBAYASHI, TAKESHI NAGASU, HIROHISA SAITO
OS Artificial Sequence
PN WO 0233069-A/18
PD 25-APR-2002
PF 28-SEP-2001 WO 2001JP008574
PR 13-OCT-2000 JP OOP 314093
PI YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, MASAYA OBAYASHI, PI
TAKESHI NAGASU,
PI HIROHISA SAITO
PC C12N15/09, C12N15/63, C12Q1/68, C12Q1/02, G01N33/53, C12N5/10, PC
A61K39/395,
PC C07K14/47, C07K16/18//C12P21/02, C12P21/08
CC Description of Artificial Sequence:an artificially synthesized

CC anchor
CC primer sequence
FH Key Location/Qualifiers
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Query Match
Best Local Similarity 100.0%; DB 1; Length 17;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAAA 1495
Db 17 TAAAAAAAAAAAAA 2

RESULT 79
BD171177/c
LOCUS BD171177 17 bp DNA linear PAT 17-JAN-2003
DEFINITION Method of examining allergic disease.
ACCESSION BD171177
VERSION BD171177.1 GI:27876989
KEYWORDS WO 0250269-A/2.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 17)
AUTHORS Matsumoto,Y., Imai,Y., Oshida,T., Sugita,Y., Nagasu,T. and Tsujimoto,G.
TITLE Method of examining allergic disease
JOURNAL Patent: WO 0250269-A 2 27-JUN-2002;
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
NATIONAL CHILDREN'S HOSPITAL, MASAMICHI TAKAGI, AKINORI OTA YOSHIKO
MATSUMOTO, YUKIHO IMAI, TADAHIRO OSHIDA, YUJI SUGITA, TAKESHI NAGASU,
GOZO TSUJIMOTO
OS Artificial Sequence
PN WO 0250269-A/2

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PD 27-JUN-2002
PF 21-DEC-2001 WO 2001JP011286
PI 21-DEC-2000 JP 00P 389476
PI YOSHIKO MATSUMOTO, YUKIHO IMAI, TADAHIRO OSHIDA, YUJI SUGITA, PI
TAKESHI NAGASU,
PI GOZO TSUJIMOTO
PC C12N15/11.C07K16/18.A61K67/027.A61K31/711.A61K45/00.A61K48/00,
PC A61P37/08,
PC C12Q1/68.G01N33/50
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CC primer sequence
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Best Local Similarity 100.0%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1480 TAAAAA1495
Db 17 TAAAAA1495
RESULT 80
AR034896/c
LOCUS AR034896 18 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 12 from patent US 5869643.
ACCESSION AR034896
VERSION AR034896.1 GI:5950501
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Chatelain,F. and Kumarev,V.
TITLE Process for preparing polynucleotides on a solid support in a
tightly packed bed
JOURNAL Patent: US 5869643-A 12 09-FEB-1999;
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source Location/Qualifiers
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Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAA1496
Db 18 AAAAAA1496
RESULT 81
AR034899
LOCUS AR034899 18 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 18 from patent US 5869643.
ACCESSION AR034899
VERSION AR034899.1 GI:5950504
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Chatelain,F. and Kumarev,V.
TITLE Process for preparing polynucleotides on a solid support in a
tightly packed bed

JOURNAL Patent: US 5869643-A 18 09-FEB-1999;
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/mol_type="unassigned DNA"
Query Match 1..1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAA1496
Db 1 AAAAAA1496
RESULT 82
AR058305
LOCUS AR058305 18 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 3 from patent US 5837820.
ACCESSION AR058305
VERSION AR058305.1 GI:5983882
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS De Rose,R., Douce,R., Duval,M., Job,C. and Job,D.
TITLE Seed specific biotinylated protein, SBP65, from leguminous plants
JOURNAL Patent: US 5837820-A 3 17-NOV-1998;
FEATURES
source Location/Qualifiers
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Query Match 1..1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAA1496
Db 1 AAAAAA1496
RESULT 83
AR097579/c
LOCUS AR097579 18 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 9 from patent US 6071745.
ACCESSION AR097579
VERSION AR097579.1 GI:12806309
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Lin,C.-I.Patsy., Wallace,R.Bruce., Cossman,J. and French,C.
TITLE Method and formulation for lyophilizing cultured human cells to
preserve RNA and DNA contained in cells for use in molecular
biology experiments
JOURNAL Patent: US 6071745-A 9 06-JUN-2000;
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Query Match 1..1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 18 AAAAAA1496

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RESULT 84
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DEFINITION
ACCESSION
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KEYWORDS
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ORGANISM
REFERENCE
AUTHORS
TITLE
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QY 1481 AAAAAAAAAAAAAA 1496
Db 1 AAAAAAAAAAAAAA 16

RESULT 85
E28535
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
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    PN JP 1999075880-A/2
    PD 23-MAR-1999
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    PI KENICHI HANAKI, HIROSHI YOSHIKURA, MASAHIDE NOZAKI PC
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    CC Topology: Linear;
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RESULT 86
E28536/c
LOCUS
DEFINITION
ACCESSION
VERSION
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REFERENCE
AUTHORS
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COMMENT
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    PN JP 1999075880-A/3
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    PF 10-JUL-1998 JP 1998195719
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QY 1481 AAAAAAAAAAAAAA 1496
Db 1 AAAAAAAAAAAAAA 16

RESULT 87
E32453/c
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DEFINITION
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VERSION
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SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
    OS Artificial Sequence
    PN JP 2000037190-A/13
    PD 08-FEB-2000
    PF 23-JUL-1998 JP 1998225228
    PR
    PI JUN NISHI, YUSUKE NAKAMURA, TOSHIHIRO TANAKA
    C12N15/09, C07K14/47, C07K16/18, C12N1/19, C12N1/21, C12N5/10, PC
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DEFINITION
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RESULT 87
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REFERENCE
AUTHORS
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    PN JP 2000037190-A/13
    PD 08-FEB-2000
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    C12N15/02
    PC C12P21/02, C12P21/08, C12N5/10, C12R1/91, (C12P21/08, C12R1/91),
    PC C12N15/00,
    PC C12N5/00, C12N15/00, (C12N5/00, C12R1/91)
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Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Gaps 0;

QY 1480 TAAAAAATAAAAA 1495
DB 17 TAAAAAATAAAAA 2

RESULT 88
E32456/c
LOCUS      18 bp      DNA      linear      PAT 18-JUN-2001
DEFINITION Mammal-derived tissue specific physiologically active protein.
ACCESSION  E32456
VERSION    E32456.1 GI:13018692
KEYWORDS  JP 2000037190-A/16.
SOURCE    synthetic construct
ORGANISM  artificial sequences.
REFERENCE  1 (bases 1 to 18)
AUTHORS  Jun,N., Yusuken,N. and Toshihiro,T.
TITLE    Mammal-derived tissue specific physiologically active protein
JOURNAL  Patent: JP 2000037190-A 16 08-FEB-2000,
        JAPAN TOBACCO INC
COMMENT   OS Artificial Sequence
        PN JP 2000037190-A/16
        PD 08-FEB-2000
        PF 23-JUL-1998 JP 1998225228
PR JUN NISHIU, YUSUKE NAKAMURA, TOSHIHIRO TANAKA
PC C12N15/09, C07K14/47, C07K16/18, C12N1/19, C12N1/21, C12N5/10, PC
C12N15/02,
PC C12P21/02, C12P21/08// (C12N5/10, C12R1:91), (C12P21/08, C12R1:91),
PC C12N15/00,
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FH Key      Location/Qualifiers
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Query Match      1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Gaps 0;

QY 1480 TAAAAAATAAAAA 1495
DB 17 TAAAAAATAAAAA 2

RESULT 89
E32459/c
LOCUS      18 bp      DNA      linear      PAT 18-JUN-2001
DEFINITION Mammal-derived tissue specific physiologically active protein.
ACCESSION  E32459
VERSION    E32459.1 GI:13018695
KEYWORDS  JP 2000037190-A/19.
SOURCE    synthetic construct
ORGANISM  artificial sequences.
REFERENCE  1 (bases 1 to 18)
AUTHORS  Jun,N., Yusuken,N. and Toshihiro,T.
TITLE    Mammal-derived tissue specific physiologically active protein
JOURNAL  Patent: JP 2000037190-A 19 08-FEB-2000,
        JAPAN TOBACCO INC
COMMENT   OS Artificial Sequence
        PN JP 2000037190-A/19
        PD 08-FEB-2000
        PF 23-JUL-1998 JP 1998225228
PR JUN NISHIU, YUSUKE NAKAMURA, TOSHIHIRO TANAKA
PC C12N15/09, C07K14/47, C07K16/18, C12N1/19, C12N1/21, C12N5/10, PC
C12N15/02,
PC C12P21/02, C12P21/08// (C12N5/10, C12R1:91), (C12P21/08, C12R1:91),
PC C12N15/00,
PC C12N5/00, C12N15/00, (C12N5/00, C12R1:91)
CC
FH Key      Location/Qualifiers
FT primer_bind (1)..(18).
   1..18
   /organism="synthetic construct"
   /mol_type="genomic DNA"
   /db_xref="taxon:32630"

Query Match      1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Gaps 0;

QY 1480 TAAAAAATAAAAA 1495
DB 17 TAAAAAATAAAAA 2

RESULT 90
E32459/c
LOCUS      18 bp      DNA      linear      PAT 10-JUN-1998
DEFINITION Sequence 16 from patent US 5707807.
ACCESSION  I79509
VERSION    I79509.1 GI:3207799
KEYWORDS  Unknown.
SOURCE    Unclassified.
ORGANISM  Kato,K.
REFERENCE  1 (bases 1 to 18)
AUTHORS  Kato,K.
TITLE    Molecular indexing for expressed gene analysis
JOURNAL  Patent: US 5707807-A 16 13-JAN-1998;
FEATURES  Location/Qualifiers
   source      1..18
               /organism="unknown"
               /mol_type="unassigned DNA"

Query Match      1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Gaps 0;

QY 1481 AAAAAAATAAAAA 1496
DB 18 AAAAAAATAAAAA 3

RESULT 91
AR208426/c
LOCUS      18 bp      DNA      linear      PAT 20-JUN-2002
DEFINITION Sequence 6 from patent US 6383754.
ACCESSION  AR208426
VERSION    AR208426.1 GI:21509577
KEYWORDS  Unknown.
SOURCE    Unclassified.
ORGANISM  Kaufman,J.C., Roth,M.E., Lizardi,P.M., Feng,L. and Latimer,D.R.
REFERENCE  1 (bases 1 to 18)
AUTHORS  Kaufman,J.C., Roth,M.E., Lizardi,P.M., Feng,L. and Latimer,D.R.
TITLE    Binary encoded sequence tags
JOURNAL  Patent: US 6383754-A 6 07-MAY-2002;
FEATURES  Location/Qualifiers
   source      1..18
               /organism="unknown"
               /mol_type="unassigned DNA"

Query Match      1.1%; Score 16; DB 1; Length 18;
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PR JUN NISHIU, YUSUKE NAKAMURA, TOSHIHIRO TANAKA
PC C12N15/09, C07K14/47, C07K16/18, C12N1/19, C12N1/21, C12N5/10, PC
C12N15/02,
PC C12P21/02, C12P21/08// (C12N5/10, C12R1:91), (C12P21/08, C12R1:91),
PC C12N15/00,
PC C12N5/00, C12N15/00, (C12N5/00, C12R1:91)
CC
FH Key      Location/Qualifiers
FT primer_bind (1)..(18).
   1..18
   /organism="synthetic construct"
   /mol_type="genomic DNA"
   /db_xref="taxon:32630"

Query Match      1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Gaps 0;

QY 1480 TAAAAAATAAAAA 1495
DB 17 TAAAAAATAAAAA 2

RESULT 90
E32459/c
LOCUS      18 bp      DNA      linear      PAT 10-JUN-1998
DEFINITION Sequence 16 from patent US 5707807.
ACCESSION  I79509
VERSION    I79509.1 GI:3207799
KEYWORDS  Unknown.
SOURCE    Unclassified.
ORGANISM  Kato,K.
REFERENCE  1 (bases 1 to 18)
AUTHORS  Kato,K.
TITLE    Molecular indexing for expressed gene analysis
JOURNAL  Patent: US 5707807-A 16 13-JAN-1998;
FEATURES  Location/Qualifiers
   source      1..18
               /organism="unknown"
               /mol_type="unassigned DNA"

Query Match      1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Gaps 0;

QY 1481 AAAAAAATAAAAA 1496
DB 18 AAAAAAATAAAAA 3

RESULT 91
AR208426/c
LOCUS      18 bp      DNA      linear      PAT 20-JUN-2002
DEFINITION Sequence 6 from patent US 6383754.
ACCESSION  AR208426
VERSION    AR208426.1 GI:21509577
KEYWORDS  Unknown.
SOURCE    Unclassified.
ORGANISM  Kaufman,J.C., Roth,M.E., Lizardi,P.M., Feng,L. and Latimer,D.R.
REFERENCE  1 (bases 1 to 18)
AUTHORS  Kaufman,J.C., Roth,M.E., Lizardi,P.M., Feng,L. and Latimer,D.R.
TITLE    Binary encoded sequence tags
JOURNAL  Patent: US 6383754-A 6 07-MAY-2002;
FEATURES  Location/Qualifiers
   source      1..18
               /organism="unknown"
               /mol_type="unassigned DNA"

Query Match      1.1%; Score 16; DB 1; Length 18;
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Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
Db 16 AAAAAAAAAAAAAA 1

RESULT 92
AR208427/c AR208427 18 bp DNA linear PAT 20-JUN-2002
LOCUS Sequence 7 from patent US 6383754.
DEFINITION AR208427
ACCESSION AR208427
VERSION AR208427.1 GI:21509578
KEYWORDS
SOURCE
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kaufman,J.C., Roth,M.E., Lizardi,P.M., Feng,L. and Latimer,D.R.
TITLE Binary encoded sequence tags
JOURNAL Patent: US 6383754-A 7 07-MAY-2002;
FEATURES
    source
        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
Db 16 AAAAAAAAAAAAAA 1

RESULT 93
AR215435/c AR215435 18 bp DNA linear PAT 25-SEP-2002
LOCUS Sequence 9 from patent US 6410321.
DEFINITION AR215435
ACCESSION AR215435
VERSION AR215435.1 GI:23313691
KEYWORDS
SOURCE
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Lin,C.-I.P., Wallace,R.B., Cossman,J. and French,C.
TITLE Method and formulation for lyophilizing cultured human cells to
    preserve RNA and DNA contained in cells for use in molecular
    biology experiments
JOURNAL Patent: US 6410321-A 9 25-JUN-2002;
FEATURES
    source
        /organism="unknown"
        /mol_type="genomic DNA"

Query Match
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
Db 18 AAAAAAAAAAAAAA 3

RESULT 94
AR222464 AR222464 18 bp DNA linear PAT 26-SEP-2002
LOCUS Sequence 24 from patent US 6429300.
DEFINITION AR222464
ACCESSION AR222464
VERSION AR222464.1 GI:23329995
KEYWORDS

Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
Db 18 AAAAAAAAAAAAAA 3

RESULT 96
AX004875/c AX004875 18 bp DNA linear PAT 24-AUG-2000
LOCUS Sequence 4 from Patent WO9910527.
DEFINITION AX004875
ACCESSION AX004875
VERSION AX004875.1 GI:9928275
KEYWORDS
SOURCE
ORGANISM synthetic construct
    synthetic construct
    artificial sequences.
REFERENCE 1
AUTHORS Bayer,E. and Schewitz,J.
TITLE Method for isolating anionic organic substances from aqueous
    systems using cationic polymer nanoparticles
JOURNAL Patent: WO 9910527-A 4 04-MAR-1999;
    SUEDEDEUTSCHE KALKSTICKSTOFF (DE); BAYER ERNST (DE)
FEATURES
    source
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="3' palmityl oligonucleotide"
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Query Match      1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
Db 18 AAAAAAAAAAAAAA 3

RESULT 97
LOCUS AX004879/c 18 bp RNA linear PAT 24-AUG-2000
DEFINITION Sequence 8 from Patent WO9910527.
ACCESSION AX004879
VERSION AX004879.1 GI:9928279
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE 1
AUTHORS Bayer, E. and Schewitz, J.
TITLE Method for isolating anionic organic substances from aqueous
        systems using cationic polymer nanoparticles
JOURNAL Patent: WO 9910527-A 8 04-MAR-1999;
        SUEDEDEUTSCHE KALKSTICKSTOFF (DE); BAYER ERNST (DE)
FEATURES
    source
        Location/Qualifiers
            1..18
                /organism="synthetic construct"
                /mol_type="unassigned RNA"
                /db_xref="taxon:32630"
                /note="2, methyl-modified oligonucleotide"
    modified_base 1..18
        /mod_base=um

Query Match      1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
Db 18 AAAAAAAAAAAAAA 3

RESULT 98
LOCUS AX008117 18 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 2 from Patent WO9967378.
ACCESSION AX008117
VERSION AX008117.1 GI:9995742
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE 1
AUTHORS Damha, M.J., Parniak, M.A., Wilds, C., Arion, D., Noronha, A.M. and
        Borkow, G.
TITLE Antisense oligonucleotide constructs based on beta -arabinofuranose
        and its analogues
JOURNAL Patent: WO 9967378-A 2 29-DEC-1999;
        DAMHA MASSAD JOSE (CA); PARNIAK MICHAEL A (CA); WILDS CHRISTOPHER
        (CA); UNIV MCGILL (CA); ARION DOMINIQUE (CA); NORONHA ANNE M (CA);
        BORKOW GADI (IL)
FEATURES
    source
        Location/Qualifiers
            1..18
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Use as an oligomer"

Query Match      1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
Db 18 AAAAAAAAAAAAAA 3

RESULT 99
LOCUS AX008118/c 18 bp RNA linear PAT 06-SEP-2000
DEFINITION Sequence 3 from Patent WO9967378.
ACCESSION AX008118
VERSION AX008118.1 GI:9995743
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE 1
AUTHORS Damha, M.J., Parniak, M.A., Wilds, C., Arion, D., Noronha, A.M. and
        Borkow, G.
TITLE Antisense oligonucleotide constructs based on beta -arabinofuranose
        and its analogues
JOURNAL Patent: WO 9967378-A 3 29-DEC-1999;
        DAMHA MASSAD JOSE (CA); PARNIAK MICHAEL A (CA); WILDS CHRISTOPHER
        (CA); UNIV MCGILL (CA); ARION DOMINIQUE (CA); NORONHA ANNE M (CA);
        BORKOW GADI (IL)
FEATURES
    source
        Location/Qualifiers
            1..18
                /organism="synthetic construct"
                /mol_type="unassigned RNA"
                /db_xref="taxon:32630"
                /note="Use as an oligomer"

Query Match      1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
Db 18 AAAAAAAAAAAAAA 3

RESULT 100
LOCUS AX008122/c 18 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 7 from Patent WO9967378.
ACCESSION AX008122
VERSION AX008122.1 GI:9995747
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE 1
AUTHORS Damha, M.J., Parniak, M.A., Wilds, C., Arion, D., Noronha, A.M. and
        Borkow, G.
TITLE Antisense oligonucleotide constructs based on beta -arabinofuranose
        and its analogues
JOURNAL Patent: WO 9967378-A 7 29-DEC-1999;
        DAMHA MASSAD JOSE (CA); PARNIAK MICHAEL A (CA); WILDS CHRISTOPHER
        (CA); UNIV MCGILL (CA); ARION DOMINIQUE (CA); NORONHA ANNE M (CA);
        BORKOW GADI (IL)
FEATURES
    source
        Location/Qualifiers
            1..18
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Use as an oligomer"

Query Match      1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
Db 18 AAAAAAAAAAAAAA 3

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RESULT 101
AX008123
LOCUS AX008123 18 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 8 from Patent WO9967378.
ACCESSION AX008123
VERSION AX008123.1 GI:9995748
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Damha,M.J., Parniak,M.A., Wilds,C., Arion,D., Noronha,A.M. and
Borkow,G.
TITLE Antisense oligonucleotide constructs based on beta -arabinofuranose
and its analogues
JOURNAL Patent: WO 9967378-A 8 29-DEC-1999;
DAMHA MASSAD JOSE (CA); PARNIAK MICHAEL A (CA); WILDS CHRISTOPHER
(CA); UNIV MCGILL (CA); ARION DOMINIQUE (CA); NORONHA ANNE M (CA);
BORKOW GADI (IL)
FEATURES
source Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Use as an oligomer"

Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
Db 1 AAAAAAAAAAAAAA 16

RESULT 102
AX028644/c
LOCUS AX028644 18 bp DNA linear PAT 24-NOV-2000
DEFINITION Sequence 28 from Patent WO9732023.
ACCESSION AX028644
VERSION AX028644.1 GI:10189947
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Brugliera,F., Holton,T.A. and Michael,M.Z.
TITLE Genetic sequences encoding flavonoid pathway enzymes and uses
therefor
JOURNAL Patent: WO 9732023-A 28 04-SEP-1997;
FLORIGENE LIMITED (AU); BRUGLIERA FILIPPA (AU); HOLTON TIMOTHY
ALBERT (AU); MICHAEL MICHAEL ZENON (AU)
FEATURES
source Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide"

Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
Db 17 AAAAAAAAAAAAAA 2

RESULT 103
AX047271
LOCUS AX047271 18 bp DNA linear PAT 15-DEC-2000
DEFINITION Sequence 21 from Patent WO0068422.
ACCESSION AX047271
VERSION AX047271.1 GI:11876551
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Muehleger,K., Angerer,B., Seela,F., Ankenbauer,W., Augustin,M.,
Gumbiowski,K. and Zulauf,M.
TITLE High density labeling of dna with modified or chromophore carrying
nucleotides and dna polymerases used
JOURNAL Patent: WO 0068422-A 21 16-NOV-2000;
Roche Diagnostics GmbH (DE)
FEATURES
source Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="second fragment of SEQ ID NO: 6"

Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
Db 1 AAAAAAAAAAAAAA 16

RESULT 104
AX047273/c
LOCUS AX047273 18 bp DNA linear PAT 15-DEC-2000
DEFINITION Sequence 23 from Patent WO0068422.
ACCESSION AX047273
VERSION AX047273.1 GI:11876553
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Muehleger,K., Angerer,B., Seela,F., Ankenbauer,W., Augustin,M.,
Gumbiowski,K. and Zulauf,M.
TITLE High density labeling of dna with modified or chromophore carrying
nucleotides and dna polymerases used
JOURNAL Patent: WO 0068422-A 23 16-NOV-2000;
Roche Diagnostics GmbH (DE)
FEATURES
source Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="second fragment of SEQ ID NO: 6"

Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
Db 18 AAAAAAAAAAAAAA 3

RESULT 105
AX085252/c
LOCUS AX085252 18 bp DNA linear PAT 09-MAR-2001
DEFINITION Sequence 6 from Patent WO0112855.
ACCESSION AX085252
VERSION AX085252.1 GI:13275310
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Muehleger,K., Angerer,B., Seela,F., Ankenbauer,W., Augustin,M.,
Gumbiowski,K. and Zulauf,M.
TITLE High density labeling of dna with modified or chromophore carrying
nucleotides and dna polymerases used
JOURNAL Patent: WO 0068422-A 23 16-NOV-2000;
Roche Diagnostics GmbH (DE)
FEATURES
source Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="second fragment of SEQ ID NO: 6"

Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
Db 18 AAAAAAAAAAAAAA 3

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REFERENCE
1
AUTHORS Kaufman,J.C., Roth,M.E., Lizardi,P.M., Feng,L. and Latimer,D.R.
TITLE Binary encoded sequence tags
JOURNAL Patent: WO 0112855-A 6 22-FEB-2001;
YALE UNIVERSITY (US)
FEATURES
source
Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match
Best Local Similarity 1.1%; Score 16; DB 1; Length 18;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
|||||
Db 16 AAAAAAAAAAAAAA 1

RESULT 106
AX085253/c
LOCUS AX085253 18 bp DNA linear PAT 09-MAR-2001
DEFINITION Sequence 7 from Patent WO0112855.
ACCESSION AX085253
VERSION AX085253.1 GI:13275311
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS Kaufman,J.C., Roth,M.E., Lizardi,P.M., Feng,L. and Latimer,D.R.
TITLE Binary encoded sequence tags
JOURNAL Patent: WO 0112855-A 7 22-FEB-2001;
YALE UNIVERSITY (US)
FEATURES
source
Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match
Best Local Similarity 1.1%; Score 16; DB 1; Length 18;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
|||||
Db 16 AAAAAAAAAAAAAA 1

RESULT 107
AX104721/c
LOCUS AX104721 18 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 913 from Patent WO0122972.
ACCESSION AX104721
VERSION AX104721.1 GI:13920918
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 913 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
FEATURES
source
Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"
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Query Match
Best Local Similarity 1.1%; Score 16; DB 1; Length 18;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
|||||
Db 18 AAAAAAAAAAAAAA 3

RESULT 108
AX104747/c
LOCUS AX104747 18 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 939 from Patent WO0122972.
ACCESSION AX104747
VERSION AX104747.1 GI:13920944
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 939 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
FEATURES
source
Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match
Best Local Similarity 1.1%; Score 16; DB 1; Length 18;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
|||||
Db 18 AAAAAAAAAAAAAA 3

RESULT 109
AX105651/c
LOCUS AX105651 18 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 10 from Patent WO0123564.
ACCESSION AX105651
VERSION AX105651.1 GI:13921674
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS Stanton,L.W. and Kapoun,A.M.
TITLE Secreted factors
JOURNAL Patent: WO 0123564-A 10 05-APR-2001;
Scios Inc. (US)
FEATURES
source
Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic"

Query Match
Best Local Similarity 1.1%; Score 16; DB 1; Length 18;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
|||||
Db 18 AAAAAAAAAAAAAA 3

RESULT 110
AX105651/c
LOCUS AX105651 18 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 10 from Patent WO0123564.
ACCESSION AX105651
VERSION AX105651.1 GI:13921674
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS Stanton,L.W. and Kapoun,A.M.
TITLE Secreted factors
JOURNAL Patent: WO 0123564-A 10 05-APR-2001;
Scios Inc. (US)
FEATURES
source
Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic"
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AX108642/c
LOCUS AX108642 18 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 10 from Patent WO0123419.
ACCESSION AX108642
VERSION AX108642.1 GI:13923875
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Stanton,L.W. and Kapoun,A.M.
TITLE Differentially expressed genes
JOURNAL Patent: WO 0123419-A 10 05-APR-2001;
SCIOS INC. (US)
FEATURES
source Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic"

Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAAA 1496
|||||
Db 18 AAAAAAAAAAAAAAA 3

RESULT 111
AX268883/c
LOCUS AX268883 18 bp DNA linear PAT 29-OCT-2001
DEFINITION Sequence 84 from Patent WO0174901.
ACCESSION AX268883
VERSION AX268883.1 GI:16541910
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Stanton,L.W. and White,R.T.
TITLE Secreted factors
JOURNAL Patent: WO 0174901-A 84 11-OCT-2001;
Scios Inc. (US)
FEATURES
source Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligos corresponding to polylinker sequence."

Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAAA 1496
|||||
Db 18 AAAAAAAAAAAAAAA 3

RESULT 112
AX355809/c
LOCUS AX355809 18 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 837 from Patent WO0197843.
ACCESSION AX355809
VERSION AX355809.1 GI:18620477
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Weiner,G. and Hartmann,G.

TITLE Methods for enhancing antibody-induced cell lysis and treating cancer
JOURNAL Patent: WO 0157843-A 837 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES
source Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide-phosphorothioate backbone"

Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAAA 1496
|||||
Db 18 AAAAAAAAAAAAAAA 3

RESULT 113
AX547774/c
LOCUS AX547774 18 bp DNA linear PAT 01-MAR-2003
DEFINITION Sequence 913 from Patent WO02053141.
ACCESSION AX547774
VERSION AX547774.1 GI:25812918
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Bratzler,R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 913 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
FEATURES
source Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Sequence"

Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAAA 1496
|||||
Db 18 AAAAAAAAAAAAAAA 3

RESULT 114
AX547800/c
LOCUS AX547800 18 bp DNA linear PAT 01-MAR-2003
DEFINITION Sequence 939 from Patent WO02053141.
ACCESSION AX547800
VERSION AX547800.1 GI:25812944
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Bratzler,R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 939 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
FEATURES
source Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Sequence"


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Query Match      1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1496
Db 18 AAAAAAAAAAAAAA 3

RESULT 115
AX814716/c
LOCUS      AX814716      18 bp      DNA      linear      PAT 05-DEC-2003
DEFINITION Sequence 1 from Patent WO03064441.
ACCESSION  AX814716
VERSION     AX814716.1 GI:39103916
KEYWORDS    .
SOURCE      synthetic construct
ORGANISM    synthetic construct
            artificial sequences.
REFERENCE 1
AUTHORS     Damha, M.J. and Parniak, M.A.
TITLE       Oligonucleotides comprising alternating segments and uses thereof
JOURNAL     Patent: WO 03064441-A 1 07-AUG-2003;
            MCGILL UNIVERSITY (CA)
FEATURES    Location/Qualifiers
            source
              1..18
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Oligonucleotide"
            misc_feature
              1..17
                /note="Residues 1, 3, 5, 7, 9, 11, 13, 15 and 17 are
                2'-O-methyl-D-uridine"

Query Match      1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1496
Db 18 AAAAAAAAAAAAAA 3

RESULT 116
AX814723/c
LOCUS      AX814723      18 bp      DNA      linear      PAT 05-DEC-2003
DEFINITION Sequence 8 from Patent WO03064441.
ACCESSION  AX814723
VERSION     AX814723.1 GI:39103922
KEYWORDS    .
SOURCE      synthetic construct
ORGANISM    synthetic construct
            artificial sequences.
REFERENCE 1
AUTHORS     Damha, M.J. and Parniak, M.A.
TITLE       Oligonucleotides comprising alternating segments and uses thereof
JOURNAL     Patent: WO 03064441-A 8 07-AUG-2003;
            MCGILL UNIVERSITY (CA)
FEATURES    Location/Qualifiers
            source
              1..18
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Oligonucleotide"
            misc_feature
              1..17
                /note="Residues 1, 3, 5, 7, 9, 11, 13, 15 and 17 are
                2'-O-methyl-D-uridine"

Query Match      1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1496
Db 18 AAAAAAAAAAAAAA 3

RESULT 117
AX814724/c
LOCUS      AX814724      18 bp      DNA      linear      PAT 05-DEC-2003
DEFINITION Sequence 9 from Patent WO03064441.
ACCESSION  AX814724
VERSION     AX814724.1 GI:39103923
KEYWORDS    .
SOURCE      synthetic construct
ORGANISM    synthetic construct
            artificial sequences.
REFERENCE 1
AUTHORS     Damha, M.J. and Parniak, M.A.
TITLE       Oligonucleotides comprising alternating segments and uses thereof
JOURNAL     Patent: WO 03064441-A 9 07-AUG-2003;
            MCGILL UNIVERSITY (CA)
FEATURES    Location/Qualifiers
            source
              1..18
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Oligonucleotide"
            misc_feature
              1..15
                /note="Residues 1-3, 7-9, and 13-15 are
                2'-O-methyl-D-uridine"

Query Match      1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1496
Db 18 AAAAAAAAAAAAAA 3

RESULT 118
AX814725/c
LOCUS      AX814725      18 bp      DNA      linear      PAT 05-DEC-2003
DEFINITION Sequence 10 from Patent WO03064441.
ACCESSION  AX814725
VERSION     AX814725.1 GI:39103924
KEYWORDS    .
SOURCE      synthetic construct
ORGANISM    synthetic construct
            artificial sequences.
REFERENCE 1
AUTHORS     Damha, M.J. and Parniak, M.A.
TITLE       Oligonucleotides comprising alternating segments and uses thereof
JOURNAL     Patent: WO 03064441-A 10 07-AUG-2003;
            MCGILL UNIVERSITY (CA)
FEATURES    Location/Qualifiers
            source
              1..18
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Oligonucleotide"
            misc_feature
              1..18
                /note="Residues 1-6 and 13-18 are 2'-O-methyl-D-uridine"

Query Match      1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1496
Db 18 AAAAAAAAAAAAAA 3

RESULT 119
AX814736
LOCUS      AX814736      18 bp      RNA      linear      PAT 05-DEC-2003
DEFINITION Sequence 21 from Patent WO03064441.

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ACCESSION AX814736
VERSION AX814736.1 GI:39103935
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE 1
AUTHORS Damha,M.J. and Patniak,M.A.
TITLE Oligonucleotides comprising alternating segments and uses thereof
JOURNAL Patent: WO 03064441-A 21 07-AUG-2003;
        MCGILL UNIVERSITY (CA)
FEATURES
    source
        Location/Qualifiers
            1..18
            /organism="synthetic construct"
            /mol_type="unassigned RNA"
            /db_xref="taxon:32830"
            /note="Target RNA oligonucleotide"

Query Match
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAAAAAA 1496
Db 1 AAAAAAAAAAAAAAAAAA 16

RESULT 120
LOCUS BD085545/c
DEFINITION Method of comparison and detection of RNA amount and DNA amount.
ACCESSION BD085545
VERSION BD085545.1 GI:22631155
KEYWORDS JP 2001333800-A/2.
ORGANISM Homo sapiens (human)
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 18)
AUTHORS Shimada,K.
TITLE Method of comparison and detection of RNA amount and DNA amount
JOURNAL Patent: JP 2001333800-A 2 04-DEC-2001;
        UNITECH CO LTD
COMMENT OS Homo sapiens (human)
        PN JP 2001333800-A/2
        PD 04-DEC-2001
        PF 30-MAY-2000 JP 2000160324
        PI KAORI SHIMADA
        PC C12Q1/68,C12N15/09,G01N33/50,C12N15/00
        CC Method of comparison and detection of RNA amount and DNA CC
        FH Key Location/Qualifiers
        FT source 1..18
        FT /organism="Homo sapiens"
        FT /mol_type="genomic RNA"
        FT /db_xref="taxon:9606"

FEATURES
    source
        Location/Qualifiers
            1..18
            /organism="Homo sapiens"
            /mol_type="genomic RNA"
            /db_xref="taxon:9606"

Query Match
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAAAAAA 1496
Db 18 AAAAAAAAAAAAAAAAAA 3

RESULT 121
LOCUS BD190553
DEFINITION Secretory proteins and polynucleotides encoding the same.

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ACCESSION BD190553
VERSION BD190553.1 GI:33000292
KEYWORDS JP 2002515753-A/12.
SOURCE Rattus
ORGANISM Rattus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae.
REFERENCE 1 (bases 1 to 18)
AUTHORS Jacobs,K., McCoy,J.M., Lavallie,E.R., Racie,L.A., Merberg,D.,
        Treacy,M., Spaulding,V. and Agostino,M.J.
TITLE Secretory proteins and polynucleotides encoding the same
JOURNAL Patent: JP 2002515753-A 12 28-MAY-2002;
        GENETICS INSTITUTE INC
COMMENT PN JP 2002515753-A/12
        PD 28-MAY-2002
        PF 31-OCT-1997 JP 1998521609
        PR 01-NOV-1996 US 08/724973
        PI KENNETH JACOBS,JOHN M MCCOY,EDWARD R LAVALLE,LISA A RACIE, PI
          DAVID MERBERG,
        PI MAURICE TREACY,VIKKI SPAULDING,MICHAEL J AGOSTINO PC
        C12N15/12,C12N5/10,C07K14/47,C12Q1/68,A61K38/17 CC Strandedness:
        Double;
        CC Topology: Linear;
        FH Key Location/Qualifiers
        FT source 1..18
        FT /organism="Rattus"
        FT /mol_type="genomic DNA"
        FT /db_xref="taxon:10114"

Query Match
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAAAAAA 1496
Db 2 AAAAAAAAAAAAAAAAAA 17

RESULT 122
LOCUS BD222596/c
DEFINITION Aminoxy-modified nucleoside compound and oligomer compound
          produced therefrom.
ACCESSION BD222596
VERSION BD222596.1 GI:33032366
KEYWORDS JP 2002522447-A/14.
SOURCE synthetic construct
ORGANISM artificial sequences.
          1 (bases 1 to 18)
REFERENCE Manoharan,M., Cook,P.D., Prakash,T.P. and Kawasaki,A.M.
AUTHORS Aminoxy-modified nucleoside compound and oligomer compound
TITLE produced therefrom
JOURNAL Patent: JP 2002522447-A 14 23-JUL-2002;
        ISIS PHARMACEUTICALS INC
COMMENT OS Artificial Sequence
        PN JP 2002522447-A/14
        PD 23-JUL-2002
        PF 09-AUG-1999 JP 2000563675
        PR 07-AUG-1998 US 09/130973
        PI MUTHIAH MANOHARAN,PHILIP DAN COOK,THAZHA P PRAKASH,ANDREW M
        PI KAWASAKI
        PC C07H19/167,C07H19/067,C07H19/10,C07H19/20,C07H21/02,C12N15/00,
        PC C12N15/00
        CC Description of Artificial Sequence: antisense sequence FH
        CC Key Location/Qualifiers
        FT source 1..18
        FT /organism="Artificial Sequence".
        FT /organism="synthetic construct"
        FT /mol_type="genomic DNA"

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/db_xref="taxon:32630"

Query Match      1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
    |||||
Db 18 AAAAAAAAAAAAAA 3

RESULT 123
BD233654/c
LOCUS BD233654 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Two-color differential display as a method for detecting regulated
genes.
ACCESSION BD233654
VERSION BD233654.1 GI:33043424
KEYWORDS JP 2002524088-A/2.
SOURCE unclassified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Kozian, D. and Reuner, B.
TITLE Two-color differential display as a method for detecting regulated
JOURNAL Patent: JP 2002524088-A 2 06-AUG-2002;
COMMENT AVENTIS PHARMA DEUTSCHLAND GMBH
PN JP 2002524088-A/2
PD 06-AUG-2002
PF 26-AUG-1999 JP 2000569015
PR 07-SEP-1998 DE 198 40 731.9
PC DETLEF KOZIAN, BIRGIT REUNER
PC C12Q1/68, G01N33/58//A61K45/00, C12N15/09, C12N15/09, C12N15/00,
PC C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
CC /note= 'M = A, C, G, N = A, C, G, T'
FH Key Location/Qualifiers
FT exon 1..17.
FEATURES
    source
    1..17
        /organism="unidentified"
        /mol_type="genomic DNA"
        /db_xref="taxon:32644"

Query Match      1.0%; Score 15.6; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 89;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAATAAAAAAAAAAAAA 1495
    :|||||
Db 17 SNAAAAAAAAAAAAAA 1

RESULT 125
AX423222
LOCUS AX423222 17 bp RNA linear PAT 18-JUN-2002
DEFINITION Sequence 1558 from Patent WO018124.
ACCESSION AX423222
VERSION AX423222.1 GI:21526604
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Jarvis, T., von Carlwitz, I., Mcswiggen, J.A., McLaughlin, F.G. and
Randi, A.M.
TITLE Method and reagent for the inhibition of erg
JOURNAL Patent: WO 018124-A 1558 22-NOV-2001;
FEATURES RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
    source
    1..17
        /organism="Homo sapiens"
        /mol_type="unassigned RNA"
        /db_xref="taxon:9606"

Query Match      1.0%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 97;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 25 CGCGCGCGCGCGCGCG 41
    |||||
Db 1 CGCGCGCGCGCGCGCG 17

RESULT 126
AX691936
LOCUS AX691936 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 4668 from Patent EP1281758.
ACCESSION AX691936
VERSION AX691936.1 GI:29414877
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Umaneky, S. and Melkonyan, H.
TITLE Gene family encoding apoptosis-associated peptides, peptides
JOURNAL Patent: JP 2002516564-A 6 04-JUN-2002;
COMMENT TANOX INC
OS Unidentified

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REFERENCE
AUTHORS      Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE        Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
              mdz12
JOURNAL      Patent: EP 1281758-A 4668 05-FEB-2003;
              Aeomica, Inc. (US)
FEATURES
source
  1. .17
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

Query Match      1.0%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 97;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      946 CTGAGGCCCGCAGCTC 962
Db      1 CTGAGGCCCGCAGCTC 17

RESULT 127
AX692527/c
LOCUS      AX692527      17 bp      DNA      linear      PAT 31-MAR-2003
DEFINITION Sequence 5259 from Patent EPI281758.
ACCESSION  AX692527
VERSION     AX692527.1 GI:29415485
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS      Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE        Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
              mdz12
JOURNAL      Patent: EP 1281758-A 5259 05-FEB-2003;
              Aeomica, Inc. (US)
FEATURES
source
  1. .17
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

Query Match      1.0%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 97;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1480 TAAAAAATAAAAAAAAAA 1496
Db      17 TCAAAAAAAAAAAAAAAAAA 1

RESULT 128
AX692528/c
LOCUS      AX692528      17 bp      DNA      linear      PAT 31-MAR-2003
DEFINITION Sequence 5260 from Patent EPI281758.
ACCESSION  AX692528
VERSION     AX692528.1 GI:29415486
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS      Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE        Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
              mdz12
JOURNAL      Patent: EP 1281758-A 5260 05-FEB-2003;
              Aeomica, Inc. (US)
FEATURES
source
  1. .17
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

Query Match      1.0%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 97;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1480 TAAAAAATAAAAAAAAAA 1496
Db      17 TCAAAAAAAAAAAAAAAAAA 1

RESULT 129
E32451/c
LOCUS      E32451      18 bp      DNA      linear      PAT 18-JUN-2001
DEFINITION Mammal-derived tissue specific physiologically active protein.
ACCESSION  E32451
VERSION     E32451.1 GI:13018687
KEYWORDS    JP 2000037190-A/11.
SOURCE      synthetic construct
ORGANISM    artificial sequences.
            Jun,N., Yusuke,N. and Toshihiro,T.
            Mammal-derived tissue specific physiologically active protein
            Patent: JP 2000037190-A 11 08-FEB-2000;
            JAPAN TOBACCO INC
            OS Artificial Sequence
            PN JP 2000037190-A/11
            PD 08-FEB-2000
            PF 23-JUL-1998 JP 1998225228
            PR JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
            PC C12N15/00,C07K14/47,C12N1/19,C12N1/21,C12N5/10, PC
            C12N15/02,
            PC C12P21/02,C12P21/08/(C12N5/10,C12R1:91), (C12P21/08,C12R1:91),
            PC C12N15/00,
            PC C12N5/00,C12N15/00, (C12N5/00,C12R1:91)
            CC CC
            FH Key
            FT primer bind (1)..(18).
FEATURES
source
  1..18
    /organism="synthetic construct"
    /mol_type="genomic DNA"
    /db_xref="taxon:32630"

Query Match      1.0%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 11e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1479 CTAAAAAATAAAAAAAAA 1495
Db      18 CCAAAAAAAAAAAAAAAAAA 2

RESULT 130
E32452/c
LOCUS      E32452      18 bp      DNA      linear      PAT 18-JUN-2001
DEFINITION Mammal-derived tissue specific physiologically active protein.
ACCESSION  E32452
VERSION     E32452.1 GI:13018688
KEYWORDS    JP 2000037190-A/12.
SOURCE      synthetic construct
ORGANISM    artificial sequences.
            Jun,N., Yusuke,N. and Toshihiro,T.
            Mammal-derived tissue specific physiologically active protein
            Patent: JP 2000037190-A 12 08-FEB-2000;
            JAPAN TOBACCO INC
            OS Artificial Sequence
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RESULT 132

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source          1. .18
                /organism="synthetic construct"
                /mol_type="genomic DNA"
                /db_xref="taxon:32630"

Query Match
Best Local Similarity 1.0%; Score 15.4; DB 1; Length 18;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1478 GCTAAAAA 1494
Db 18 GCAAAAAA 2

RESULT 134
AX838308
LOCUS AX838308 18 bp DNA linear PAT 15-DEC-2003
DEFINITION Sequence 5432 from Patent EPI347046.
ACCESSION AX838308
VERSION AX838308.1 GI:39922000
KEYWORDS .
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1
AUTHORS Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S.,
Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R.,
Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and
Masuho,Y.
TITLE Full-length cDNA sequences
JOURNAL Patent: EP 1347046-A 5432 24-SEP-2003;
RESEARCH Association for Biotechnology (JP)
FEATURES
source
1. .18
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
/ncfe="Description of Artificial Sequence: an artificially
synthesized primer se q"

Query Match
Best Local Similarity 1.0%; Score 15.4; DB 1; Length 18;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1459 AGAAGGACATCAGGC 1475
Db 1 AAGAGGACATCAGGC 17

RESULT 135
E52143/c
LOCUS E52143 16 bp DNA linear PAT 31-JAN-2002
DEFINITION TSA7005 gene.
ACCESSION E52143
VERSION E52143.1 GI:18629626
KEYWORDS JP 2001025389-A/3.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Ogawara,T., Suzuki,M. and Ozaki,K.
TITLE TSA7005 Gene
JOURNAL Patent: JP 2001025389-A 3 30-JAN-2001;
OTSUKA PHARMACEUT CO LTD
COMMENT OS Unknown
PN JP 2001025389-A/3
PD 30-JAN-2001
PE 15-JUL-1999 JP 1999201279
PR TSUYOSHI OGAWARA,MIKIO SUZUKI,KOICHI OZAKI
PI C12N15/09,C07K14/47,C12N1/15,C12N1/19,C12N1/21, PC
C12N5/10//A61K31/00,
PC A61K38/00,A61K48/00,C12P21/02,C12N15/00,C12N5/00,A61K37/02 CC

source          1. .18
                /organism="synthetic construct"
                /mol_type="genomic DNA"
                /db_xref="taxon:32630"

Query Match
Best Local Similarity 1.0%; Score 15.2; DB 1; Length 16;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAA 1495
Db 16 TAAAAA 1

RESULT 136
AR183909/c
LOCUS AR183909 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 2 from patent US 6342376.
ACCESSION AR183909
VERSION AR183909.1 GI:20227878
KEYWORDS .
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Kozian,D. and Reuner,B.
TITLE Two-color differential display as a method for detecting regulated
genes
JOURNAL Patent: US 6342376-A 2 29-JAN-2002;
FEATURES
source
1. .17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.0%; Score 15.2; DB 1; Length 17;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAA 1495
Db 16 BAAAAA 1

RESULT 137
AR429726/c
LOCUS AR429726 17 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 2 from patent US 6645741.
ACCESSION AR429726
VERSION AR429726.1 GI:40190064
KEYWORDS .
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Kozian,D. and Reuner,B.
TITLE Two-color differential display as a method for detecting regulated
genes
JOURNAL Patent: US 6645741-A 2 11-NOV-2003;
FEATURES
source
1. .17
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 1.0%; Score 15.2; DB 1; Length 17;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAA 1495
Db 16 BAAAAA 1

RESULT 138
AR429726/c
LOCUS AR429726 17 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 2 from patent US 6645741.
ACCESSION AR429726
VERSION AR429726.1 GI:40190064
KEYWORDS .
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Kozian,D. and Reuner,B.
TITLE Two-color differential display as a method for detecting regulated
genes
JOURNAL Patent: US 6645741-A 2 11-NOV-2003;
FEATURES
source
1. .17
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 1.0%; Score 15.2; DB 1; Length 17;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAA 1495
Db 16 BAAAAA 1
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Db      :|||||
16 BAAAAAAAAAAAAA 1

RESULT 138
LOCUS   AR029402/c          15 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION   Sequence 3 from patent US 5859233.
ACCESSION   AR029402
VERSION     AR029402.1 GI:5941375
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 15)
AUTHORS     Hirschbein,B.L., Fearon,K.L., Gryaznov,S.M., McCurdy,S.N.,
            Nelson,J.S. and Schultz,R.G.
TITLE       Synthons for synthesis of oligonucleotide N3-P5 phosphoramidates
JOURNAL     Patent: US 5859233-A 3 12-JAN-1999;
FEATURES
source      Location/Qualifiers
            1..15
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAA 1495
Db      :|||||
15 AAAAAAAAAAAAAA 1

RESULT 139
LOCUS   AR029403          15 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION   Sequence 4 from patent US 5859233.
ACCESSION   AR029403
VERSION     AR029403.1 GI:5941376
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 15)
AUTHORS     Hirschbein,B.L., Fearon,K.L., Gryaznov,S.M., McCurdy,S.N.,
            Nelson,J.S. and Schultz,R.G.
TITLE       Synthons for synthesis of oligonucleotide N3-P5 phosphoramidates
JOURNAL     Patent: US 5859233-A 4 12-JAN-1999;
FEATURES
source      Location/Qualifiers
            1..15
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAA 1495
Db      :|||||
15 AAAAAAAAAAAAAA 1

RESULT 140
LOCUS   AR034895/c          15 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION   Sequence 10 from patent US 5869643.
ACCESSION   AR034895
VERSION     AR034895.1 GI:5950500
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 15)

AUTHORS
TITLE       Radiolabeled DNA oligonucleotide and method of preparation
JOURNAL     Patent: US 5821354-A 2 13-OCT-1998;
FEATURES
source      Location/Qualifiers
            1..15
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAA 1495
Db      :|||||
1 AAAAAAAAAAAAAA 15

RESULT 141
LOCUS   AR034898          15 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION   Sequence 16 from patent US 5869643.
ACCESSION   AR034898
VERSION     AR034898.1 GI:5950503
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 15)
AUTHORS     Chatelain,F. and Kumarev,V.
TITLE       Process for preparing polynucleotides on a solid support in a
            tightly packed bed
JOURNAL     Patent: US 5869643-A 16 09-FEB-1999;
FEATURES
source      Location/Qualifiers
            1..15
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAA 1495
Db      :|||||
15 AAAAAAAAAAAAAA 1

RESULT 142
LOCUS   AR048768          15 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION   Sequence 2 from patent US 5821354.
ACCESSION   AR048768
VERSION     AR048768.1 GI:5971111
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 15)
AUTHORS     Leclerc,G. and Martel,R.
TITLE       Radiolabeled DNA oligonucleotide and method of preparation
JOURNAL     Patent: US 5821354-A 2 13-OCT-1998;
FEATURES
source      Location/Qualifiers
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            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAA 1495
Db      :|||||
1 AAAAAAAAAAAAAA 15

AUTHORS
TITLE       Process for preparing polynucleotides on a solid support in a
            tightly packed bed
JOURNAL     Patent: US 5869643-A 16 09-FEB-1999;
FEATURES
source      Location/Qualifiers
            1..15
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481 AAAAAAAAAAAAAA 1495
Db      :|||||
1 AAAAAAAAAAAAAA 15
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RESULT 143
AR049970/c
LOCUS AR049970 15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 3 from patent US 5824793.
ACCESSION AR049970
VERSION AR049970.1 GI:5971962
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Hirschbein,B.L., Fearon,K.L., Gryaznov,S.M., McCurdy,S.N.,
Nelson,J.S. and Schultz,R.G.
TITLE Solid phase synthesis of oligonucleotide N3'-P5' phosphoramidates
JOURNAL Patent: US 5824793-A 3 20-OCT-1998;
FEATURES
source Location/Qualifiers
1..15
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1
RESULT 144
AR049971
LOCUS AR049971 15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 4 from patent US 5824793.
ACCESSION AR049971
VERSION AR049971.1 GI:5971963
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Hirschbein,B.L., Fearon,K.L., Gryaznov,S.M., McCurdy,S.N.,
Nelson,J.S. and Schultz,R.G.
TITLE Solid phase synthesis of oligonucleotide N3'-P5' phosphoramidates
JOURNAL Patent: US 5824793-A 4 20-OCT-1998;
FEATURES
source Location/Qualifiers
1..15
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1
RESULT 145
AR056157/c
LOCUS AR056157 15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 361 from patent US 5837542.
ACCESSION AR056157
VERSION AR056157.1 GI:5981734
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
Draper,K.G.
TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes
JOURNAL Patent: US 5837542-A 361 17-NOV-1998;
FEATURES
source Location/Qualifiers
1..15
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 146
AR056158/c
LOCUS AR056158 15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 362 from patent US 5837542.
ACCESSION AR056158
VERSION AR056158.1 GI:5981735
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
Draper,K.G.
TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes
JOURNAL Patent: US 5837542-A 362 17-NOV-1998;
FEATURES
source Location/Qualifiers
1..15
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1
RESULT 147
AR080676/c
LOCUS AR080676 15 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 5 from patent US 5968822.
ACCESSION AR080676
VERSION AR080676.1 GI:10007406
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Pecker,I., Vlodavsky,I. and Feinstein,E.
TITLE Polynucleotide encoding a polypeptide having heparanase activity
and expression of same in transduced cells
JOURNAL Patent: US 5968822-A 5 19-OCT-1999;
FEATURES
source Location/Qualifiers
1..15
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 153

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ARI170375
LOCUS       ARI170375               15 bp    DNA          linear      PAT 17-DEC-2001
DEFINITION   Sequence 1 from patent US 6291438.
ACCESSION   ARI170375
VERSION     ARI170375.1 GI:17908334
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 15)
AUTHORS    Wang,J.H.
TITLE       Antiviral anticancer poly-substituted phenyl derivatized
            oligoribonucleotides and methods for their use
JOURNAL    Patent: US 6291438-A 1 18-SEP-2001;
FEATURES    Location/Qualifiers
            source          1..15
                        /organism="unknown"
                        /mol_type="unassigned DNA"
Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1481 AAAAAAAAAAAAAA 1495
Db      1 AAAAAAAAAAAAAA 15

RESULT 154
E08522/c
LOCUS       E08522               15 bp    DNA          linear      PAT 29-SEP-1997
DEFINITION   PCR primer.
ACCESSION   E08522
VERSION     E08522.1 GI:2176637
KEYWORDS    .
SOURCE      unidentified
ORGANISM    unclassified.
REFERENCE   1 (bases 1 to 15)
AUTHORS    Tei,I., Nakada,K., Ito,T., Horiuchi,H., Ota,A., Takagi,M.,
            Tsubura,H., Tanaka,H. and Ishiguro,Y.
TITLE       S-RIBONUCLEASE SPECIFIC TO STYLE AND DNA SEQUENCE CODING THEREFOR
JOURNAL    Patent: JP 1994335389-A 7 06-DEC-1994;
            KAGOME CO LTD
COMMENT     OS None
            OC Artificial sequences.
            PN JP 1994335389-A/7
            PD 06-DEC-1994
            PF 27-MAY-1993 JP 1993126286
            PI TEI ITSUIRU, NAKADA KENGO, ITO TORU, HORIUCHI HIROYUKI, PI
            OTA AKINORI,
            PI TAKAGI MASAMICHI, TSUBURA HIROKAZU, TANAKA HIROSHI, PI
            ISHIGURO YUKIO
            PC C12N9/22,C12N15/52;
            CC strandedness: Single;
            CC topology: Linear;
            FH Key      Location/Qualifiers
            FT source          1..15
                        /organism='Artificial sequences'.
FEATURES    source          1..15
                        /organism="unidentified"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:32644"
Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1481 AAAAAAAAAAAAAA 1495
Db      15 AAAAAAAAAAAAAA 1

ARI170375
LOCUS       ARI170375               15 bp    DNA          linear      PAT 17-DEC-2001
DEFINITION   Sequence 1 from patent US 6291438.
ACCESSION   ARI170375
VERSION     ARI170375.1 GI:17908334
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 15)
AUTHORS    Wang,J.H.
TITLE       Antiviral anticancer poly-substituted phenyl derivatized
            oligoribonucleotides and methods for their use
JOURNAL    Patent: US 6291438-A 1 18-SEP-2001;
FEATURES    Location/Qualifiers
            source          1..15
                        /organism="unknown"
                        /mol_type="unassigned DNA"
Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1481 AAAAAAAAAAAAAA 1495
Db      1 AAAAAAAAAAAAAA 15

RESULT 155
E12591/c
LOCUS       E12591               15 bp    DNA          linear      PAT 27-APR-1998
DEFINITION   PRIMER.
ACCESSION   E12591
VERSION     E12591.1 GI:3251423
KEYWORDS    .
SOURCE      JP 1997028381-A/8.
ORGANISM    unidentified
            unclassified.
REFERENCE   1 (bases 1 to 15)
AUTHORS    Tei,I., Minami,K. and Takagi,M.
TITLE       S- RIBONUCLEASE GENE AND PROMOTER SEQUENCE
JOURNAL    Patent: JP 1997028381-A 8 04-FEB-1997;
            TEI ITSUKIYON, MINAMI KOUKICHI, TAKAGI MASAMICHI
COMMENT     OS None
            OC Artificial sequences.
            PN JP 1997028381-A/8
            PD 04-FEB-1997
            PF 24-JUL-1995 JP 1995187557
            PI TEI ITSUKIYON, MINAMI KOUKICHI, TAKAGI MASAMICHI PC
            C12N15/09,C07H21/04,C12N1/21//A01H1/00,C12N5/10,C12N9/22, PC
            (C12N1/21,
            PC C12R1.19);
            CC strandedness: Single;
            CC topology: Linear;
            CC hypothetical: No;
            FH Key      Location/Qualifiers
            FT source          1..15
                        /organism='Artificial sequences'.
FEATURES    source          1..15
                        /organism="unidentified"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:32644"
Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1481 AAAAAAAAAAAAAA 1495
Db      15 AAAAAAAAAAAAAA 1

RESULT 156
I29068
LOCUS       I29068               15 bp    DNA          linear      PAT 06-FEB-1997
DEFINITION   Sequence 6 from patent US 5576427.
ACCESSION   I29068
VERSION     I29068.1 GI:1819859
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 15)
AUTHORS    Cook,P.D., Delecki,D.J. and Guinosso,C.
TITLE       Acyclic nucleoside analogs and oligonucleotide sequences containing
            them
JOURNAL    Patent: US 5576427-A 6 19-NOV-1996;
FEATURES    Location/Qualifiers
            source          1..15
                        /organism="unknown"
                        /mol_type="unassigned DNA"
Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1481 AAAAAAAAAAAAAA 1495
Db      15 AAAAAAAAAAAAAA 1
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TITLE	Gene expression profiles in normal and cancer cells
JOURNAL	Patent: US 633152-A 594 25-DEC-2001;
FEATURES	Location/Qualifiers
source	1..15
	/organism="unknown"
	/mol_type="unassigned DNA"
Query Match	1.0%; Score 15; DB 1; Length 15;
Best Local Similarity	100.0%; Pred. No. 86;
Matches 15; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1390 CATGCACCTGTCCTT 1404
Db	1 CATGCACCTGTCCTT 15
RESULT 160	
AR180723	
LOCUS	AR180723 15 bp DNA linear PAT 20-APR-2002
DEFINITION	Sequence 791 from patent US 633152.
ACCESSION	AR180723
VERSION	AR180723.1 GI:20222756
KEYWORDS	
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 15)
TITLE	Vogelstein,B., Kinzler,K.W., Zhang,L. and Zhou,W.
JOURNAL	Gene expression profiles in normal and cancer cells
FEATURES	Patent: US 633152-A 791 25-DEC-2001;
source	Location/Qualifiers
	1..15
	/organism="unknown"
	/mol_type="unassigned DNA"
Query Match	1.0%; Score 15; DB 1; Length 15;
Best Local Similarity	100.0%; Pred. No. 86;
Matches 15; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1475 CATGCTAAAAAAA 1489
Db	1 CATGCTAAAAAAA 15
RESULT 161	
AR200476/c	
LOCUS	AR200476 15 bp DNA linear PAT 20-APR-2002
DEFINITION	Sequence 19 from patent US 6357163.
ACCESSION	AR200476
VERSION	AR200476.1 GI:20251364
KEYWORDS	
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 15)
TITLE	Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
JOURNAL	Use of nucleic acid analogues in diagnostics and analytical procedures
FEATURES	Patent: US 6357163-A 19 19-MAR-2002;
source	Location/Qualifiers
	1..15
	/organism="unknown"
	/mol_type="unassigned DNA"
Query Match	1.0%; Score 15; DB 1; Length 15;
Best Local Similarity	100.0%; Pred. No. 86;
Matches 15; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1481 AAAAAAAAAAAAAA 1495
Db	15 AAAAAAAAAAAAAA 1

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RESULT 162
LOCUS AR200477 15 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 20 from patent US 6357163.
ACCESSION AR200477
VERSION AR200477.1 GI:20251365
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
TITLE Use of nucleic acid analogues in diagnostics and analytical
JOURNAL procedures
FEATURES Patent: US 6357163-A 20 19-MAR-2002;
Location/Qualifiers
source
1. .15
/mol_type="unassigned DNA"

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 1 AAAAAAAAAAAAAA 15

RESULT 163
LOCUS AR222461 15 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 21 from patent US 6429300.
ACCESSION AR222461
VERSION AR222461.1 GI:23329992
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Kurz,M., Lohse,P. and Wagner,R.
TITLE Peptide acceptor ligation methods
JOURNAL Patent: US 6429300-A 21 06-AUG-2002;
FEATURES Location/Qualifiers
source
1. .15
/mol_type="unassigned DNA"

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 1 AAAAAAAAAAAAAA 15

RESULT 164
LOCUS AR266630 15 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 68 from patent US 6495319.
ACCESSION AR266630
VERSION AR266630.1 GI:29695694
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS McClelland,M., Welsh,J. and Trenkle,T.
TITLE Reduced complexity nucleic acid targets and methods of using same
JOURNAL Patent: US 6495319-A 68 17-DEC-2002;
FEATURES Location/Qualifiers
source
1. .15
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/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 165
LOCUS AR371280 15 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 17 from patent US 6395474.
ACCESSION AR371280
VERSION AR371280.1 GI:34608212
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
TITLE Peptide nucleic acids
JOURNAL Patent: US 6395474-A 17 28-MAY-2002;
FEATURES Location/Qualifiers
source
1. .15
/mol_type="unassigned DNA"

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 166
LOCUS AR371281 15 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 18 from patent US 6395474.
ACCESSION AR371281
VERSION AR371281.1 GI:34608213
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
TITLE Peptide nucleic acids
JOURNAL Patent: US 6395474-A 18 28-MAY-2002;
FEATURES Location/Qualifiers
source
1. .15
/mol_type="unassigned DNA"

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 1 AAAAAAAAAAAAAA 15

RESULT 167
LOCUS AR410213 15 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 9 from patent US 6635452.
ACCESSION AR410213
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VERSION AR410213.1 GI:40161460
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 15)
TITLE Monforte,J.A., Becker,C.H., Pollart,D.J. and Shaler,T.A.
JOURNAL Releasable nonvolatile mass label molecules
FEATURES Patent: US 6635452-A 9 21-OCT-2003;
Location/Qualifiers
1. .15
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 168
AX004877/c
LOCUS AX004877 15 bp DNA linear PAT 24-AUG-2000
DEFINITION Sequence 6 from Patent WO9910527.
ACCESSION AX004877
VERSION AX004877.1 GI:9928277
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Bayer,E. and Schewitz,J.
TITLE Method for isolating anionic organic substances from aqueous
JOURNAL systems using cationic polymer nanoparticles
FEATURES Patent: WO 9910527-A 6 04-MAR-1999;
SUEDEDEUTSCHE KALKSTICKSTOFF (DE); BAYER ERNST (DE)
Location/Qualifiers
1. .15
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="3' palmityl modified oligonucleotide"

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 169
AX026066/c
LOCUS AX026066 15 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 4 from Patent WO0028046.
ACCESSION AX026066
VERSION AX026066.1 GI:10187502
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Marraccini,P. and Rogers,J.
TITLE Coffee arabica mannanase
JOURNAL Patent: WO 0028046-A 4 18-MAY-2000;
FEATURES NESTLE SA (CH); MARRACCINI PIERRE (FR); ROGERS JOHN (FR)
Location/Qualifiers
1. .15
/organism="synthetic construct"

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 170
AX048407/c
LOCUS AX048407 15 bp DNA linear PAT 12-JAN-2001
DEFINITION Sequence 6 from Patent WO0071747.
ACCESSION AX048407
VERSION AX048407.1 GI:12225571
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp,D., Hoppe,H.U. and Bургstaller,P.
TITLE Detection system for separating constituents of a sample and
JOURNAL production and use of the same
FEATURES Patent: WO 0071747-A 6 30-NOV-2000;
Aventis Research & Technologies GmbH & Co. KG (DE)
Location/Qualifiers
1. .15
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Region A"

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 171
AX106973
LOCUS AX106973 15 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 26 from Patent WO0125442.
ACCESSION AX106973
VERSION AX106973.1 GI:13922522
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Blanco,D.L., bernad Miana,A., dominguez Lopez,O. and garcia Diaz,M.
TITLE Dna polymerase lambda and uses thereof
JOURNAL Patent: WO 0125442-A 26 12-APR-2001;
FEATURES CONSEJO SUPERIOR DE INVESTIGACIONES CIENTIFICAS (ES)
Location/Qualifiers
1. .15
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligo dA"

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1
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Db      1  AAAAAAAAAAAAAA 15

RESULT 172
AX127272/c
LOCUS      AX127272      15 bp      DNA      linear      PAT 30-MAY-2001
DEFINITION Sequence 3 from Patent EP1111068.
ACCESSION  AX127272
VERSION     AX127272.1 GI:14133346
KEYWORDS    .
SOURCE      synthetic construct
ORGANISM    synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS     Schmidt,W., Hiller,R., Huber,M. and Mueller,M.
TITLE       Branched compound for use in nucleic acid detection and analysis
            reactions
JOURNAL     Patent: EP 1111068-A 3 27-JUN-2001;
            LION Bioscience AG (DE) ; VBC Genomics GmbH (AT)
FEATURES    Location/Qualifiers
            source
            1..15
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            misc_structure 1
            /note=" (NH2-C6-ttt)2-branch-"
            misc_feature 15
            /note="NH2
            kunstliche"

Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481  AAAAAAAAAAAAAA 1495
Db      15  AAAAAAAAAAAAAA 1

RESULT 173
AX127273/c
LOCUS      AX127273      15 bp      DNA      linear      PAT 30-MAY-2001
DEFINITION Sequence 4 from Patent EP1111068.
ACCESSION  AX127273
VERSION     AX127273.1 GI:14133347
KEYWORDS    .
SOURCE      synthetic construct
ORGANISM    synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS     Schmidt,W., Hiller,R., Huber,M. and Mueller,M.
TITLE       Branched compound for use in nucleic acid detection and analysis
            reactions
JOURNAL     Patent: EP 1111068-A 4 27-JUN-2001;
            LION Bioscience AG (DE) ; VBC Genomics GmbH (AT)
FEATURES    Location/Qualifiers
            source
            1..15
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            misc_structure 1
            /note=" (dt-COOH)2-branch-"
            misc_feature 15
            /note="NH2
            kunstliche"

Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481  AAAAAAAAAAAAAA 1495
Db      15  AAAAAAAAAAAAAA 1

RESULT 174
AX180140/c
LOCUS      AX180140      15 bp      DNA      linear      PAT 06-AUG-2001
DEFINITION Sequence 3 from Patent WO0146464.
ACCESSION  AX180140
VERSION     AX180140.1 GI:15132181
KEYWORDS    .
SOURCE      synthetic construct
ORGANISM    synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS     Huber,M., Schmidt,W., Mueller,M. and Hiller,R.
TITLE       Branched compound for use in nucleic acid detection and analysis
            reactions
JOURNAL     Patent: WO 0146464-A 3 28-JUN-2001;
            LION Bioscience AG (DE)
FEATURES    Location/Qualifiers
            source
            1..15
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="stem of branched oligonucleotide - base 1
            modified-Modification is (NH2-C6-TTT)2-branch-"

Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481  AAAAAAAAAAAAAA 1495
Db      15  AAAAAAAAAAAAAA 1

RESULT 175
AX180141/c
LOCUS      AX180141      15 bp      DNA      linear      PAT 06-AUG-2001
DEFINITION Sequence 4 from Patent WO0146464.
ACCESSION  AX180141
VERSION     AX180141.1 GI:15132182
KEYWORDS    .
SOURCE      synthetic construct
ORGANISM    synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS     Huber,M., Schmidt,W., Mueller,M. and Hiller,R.
TITLE       Branched compound for use in nucleic acid detection and analysis
            reactions
JOURNAL     Patent: WO 0146464-A 4 28-JUN-2001;
            LION Bioscience AG (DE)
FEATURES    Location/Qualifiers
            source
            1..15
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="stem of branched oligonucleotide - base 1
            modified-Modification is (dt-COOH)2-branch-"

Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1481  AAAAAAAAAAAAAA 1495
Db      15  AAAAAAAAAAAAAA 1

RESULT 176
AX429224/c
LOCUS      AX429224      15 bp      DNA      linear      PAT 21-JUN-2002
DEFINITION Sequence 1 from Patent EP1201765.
ACCESSION  AX429224
```

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VERSION AX429224.1 GI:21540537
SOURCE   synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Schubart,D., Habenberger,P., Stein-Cerlach,M. and Bevec,D.
TITLE    Cellular kinases involved in cytomagalovirus infection and their
          inhibition
JOURNAL  Patent: EP 1201765-A 1 02-MAY-2002;
          Axxima Pharmaceuticals Aktiengesellschaft (DE)
FEATURES Location/Qualifiers
          source
            1..15
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="N/A"

Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 177
AX525141
LOCUS      AX525141          15 bp      DNA      linear      PAT 21-NOV-2002
DEFINITION Sequence 1 from Patent WO02066675.
ACCESSION  AX525141
VERSION     AX525141.1  GI:25170126
KEYWORDS   synthetic construct
           synthetic construct
           artificial sequences.
ORGANISM
REFERENCE  1
AUTHORS    Kahmann,S. and Mueller,O.
TITLE      Methods for detecting mutations
JOURNAL    Patent: WO 02066675-A 1 29-AUG-2002;
           Max-Planck-Gesellschaft zur Foerderung der Wissenschaften e.V. (DE)
FEATURES   Location/Qualifiers
           source
             1..15
             /organism="synthetic construct"
             /mol_type="unassigned DNA"
             /db_xref="taxon:32630"
             /note="lys-Biotin"

Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 15

RESULT 178
AX525143
LOCUS      AX525143          15 bp      DNA      linear      PAT 21-NOV-2002
DEFINITION Sequence 3 from Patent WO02066675.
ACCESSION  AX525143
VERSION     AX525143.1  GI:25170128
KEYWORDS   synthetic construct
           synthetic construct
           artificial sequences.
ORGANISM
REFERENCE  1
AUTHORS    Kahmann,S. and Mueller,O.
TITLE      Methods for detecting mutations
JOURNAL    Patent: WO 02066675-A 3 29-AUG-2002;
           Max-Planck-Gesellschaft zur Foerderung der Wissenschaften e.V. (DE)

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FEATURES   Location/Qualifiers
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             /organism="synthetic construct"
             /mol_type="unassigned DNA"
             /db_xref="taxon:32630"
             /note="lys-Digoxigenin"

Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 15

RESULT 179
AX633197/c
LOCUS      AX633197          15 bp      RNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 336 from Patent EP1260586.
ACCESSION  AX633197
VERSION     AX633197.1  GI:28468811
KEYWORDS   unidentified
           unidentified
           unclassified.
ORGANISM
REFERENCE  1
AUTHORS    Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
           Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
           Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
           Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
           Woolf,T.
TITLE      Method and reagent for inhibiting the expression of disease related
           genes
JOURNAL    Patent: EP 1260586-A 336 27-NOV-2002;
           RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES   Location/Qualifiers
           source
             1..15
             /organism="unidentified"
             /mol_type="unassigned RNA"
             /db_xref="taxon:32644"

Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 180
AX633199/c
LOCUS      AX633199          15 bp      RNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 338 from Patent EP1260586.
ACCESSION  AX633199
VERSION     AX633199.1  GI:28468813
KEYWORDS   unidentified
           unidentified
           unclassified.
ORGANISM
REFERENCE  1
AUTHORS    Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
           Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
           Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
           Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
           Woolf,T.
TITLE      Method and reagent for inhibiting the expression of disease related
           genes
JOURNAL    Patent: EP 1260586-A 338 27-NOV-2002;
           RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES   Location/Qualifiers
           source
             1..15

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/organism="unidentified"
/mol_type="unassigned RNA"
/db_xref="taxon:32644"

Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 181
AX696087/c
LOCUS          AX696087              15 bp      DNA          linear      PAT 31-MAR-2003
DEFINITION     Sequence 6 from Patent WO03008643.
ACCESSION      AX696087
VERSION        AX696087.1 GI:29419249
KEYWORDS       .
SOURCE         synthetic construct
ORGANISM       synthetic construct
               artificial sequences.
REFERENCE      1
AUTHORS        Hammonds,T.R.
TITLE          Method and polynukleotides for assaying the activity of a dna
               modifying enzyme
JOURNAL        Patent: WO 03008643-A 6 30-JAN-2003;
               Cancer Research Technology Limited (GB)
FEATURES       Location/Qualifiers
               source
               1..15
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="Polynucleotide 6"

Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 182
AX711176
LOCUS          AX711176              15 bp      RNA          linear      PAT 11-APR-2003
DEFINITION     Sequence 476 from Patent EP1288296.
ACCESSION      AX711176
VERSION        AX711176.1 GI:29787557
KEYWORDS       .
SOURCE         synthetic construct
ORGANISM       synthetic construct
               artificial sequences.
REFERENCE      1
AUTHORS        Draper,K.G., Mcswiggen,J.A., Holecsek,J.J., Dudycz,L.W.,
               Macejak,D.G. and Mamone,J.A.
TITLE          Method and reagent for inhibiting HBV viral replication
JOURNAL        Patent: EP 1288296-A 476 05-MAR-2003;
               RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES       Location/Qualifiers
               source
               1..15
               /organism="synthetic construct"
               /mol_type="unassigned RNA"
               /db_xref="taxon:32630"
               /note="Polyadenylation region"

Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
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Db 1 AAAAAAAAAAAAAA 15
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BD074424      15 bp      DNA          linear      PAT 27-AUG-2002
DEFINITION     Polynucleotide encoding polypeptide having heparanase activity and
               expression of the polypeptide in induced cell.
ACCESSION      BD074424
VERSION        BD074424.1 GI:22620027
KEYWORDS       .
SOURCE         unidentified
ORGANISM       unidentified.
REFERENCE      1 (bases 1 to 15)
AUTHORS        Pecker,I., Vlodavsky,I. and Elena,F.
TITLE          Polynucleotide encoding polypeptide having heparanase activity and
               expression of the polypeptide in induced cell
JOURNAL        Patent: JP 2001514855-A 5 18-SEP-2001;
               INSIGHT STRATEGY & MARKETING LTD, HADASIT MEDICAL RESEARCH SERVICES
               & DEVELOPMENT LTD
COMMENT        OS Nucleic acid
               PN JP 2001514855-A/5
               PD 18-SEP-2001
               PF 31-AUG-1998 JP 2000508806
               PR 02-SEP-1997 US 08/922170,02-JUL-1998 US 09/109386 PI
               IRIS PECKER,ISRAEL VLODAVSKY,FEINSTEIN ELENA
               PC C12N15/09,A61K38/00,A61P9/10,A61P17/00,A61P29/00,A61P35/00, PC
               A61P37/00,
               PC A61P43/00,C12N5/10,C12N9/24,C12Q1/68,G01N33/15,G01N33/50// PC
               A61K39/395,
               PC A61K39/395,C12N15/00,A61K37/02,C12N5/00
               CC Polynucleotide encoding polypeptide having
               heparanase activity
               CC and
               CC expression of the polypeptide in induced cell FH Key
               FT source
               1..15
               /organism='Nucleic acid'.
               FT Location/Qualifiers
               1..15
               /organism="unidentified"
               /mol_type="genomic DNA"
               /db_xref="taxon:32644"

Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1
|||||
BD084687      15 bp      DNA          linear      PAT 27-AUG-2002
DEFINITION     Releasable nonvolatile mass-label molecules.
ACCESSION      BD084687
VERSION        BD084687.1 GI:22630297
KEYWORDS       .
SOURCE         synthetic construct
ORGANISM       synthetic construct
               artificial sequences.
REFERENCE      1 (bases 1 to 15)
AUTHORS        Montforte,J.A., Becker,C.H., Pollart,D.J. and Shaler,T.A.
TITLE          Releasable nonvolatile mass-label molecules
JOURNAL        Patent: JP 2001524808-A 5 04-DEC-2001;
               GENETRACE SYSTEMS INC
               OS Artificial Sequence
               PN JP 2001524808-A/5
               PD 04-DEC-2001
```



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PF 10-DEC-1997 JP 1998526924
PR 10-DEC-1996 US 60/033037,16-MAY-1997 US 60/046719 PI
JOSEPH A MONTFORT,CHRISTOPHER H BECKER,DANIEL J POLLART, PI
THOMAS A SHALER
PC C12Q1/68,G01N15/06,G01N33/53,G01N33/542,C12P19/34,C12M1/00, PC
B01D59/44,
PC H01J49/00,C07K15/26,C07K15/28
CC Description of Artificial Sequence: oligo dT15 primer FH Key
FT source 1..15
FT Location/Qualifiers
FEATURES
source
1..15
/organism='Artificial Sequence'.
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
|||||
Db 15 AAAAAAAAAAAAAA 1

RESULT 185
BD184668/c
LOCUS
DEFINITION
Method and detector for identifying subtypes of human papilloma
viruses.
ACCESSION
BD184668.1 GI:31876868
VERSION
JP 2002360271-A/647.
KEYWORDS
synthetic construct
SOURCE
synthetic construct
ORGANISM
artificial sequences.
REFERENCE
1 (bases 1 to 15)
AUTHORS
Ling,C., Lin,R., Yoo,Z., Huang,X., Lee,B., Lee,S., Lin,Y.,
Huang,C., Hau,H., Shi,C., Yeh,C., Cao,Y. and Pan,C.
TITLE
Method and detector for identifying subtypes of human papilloma
JOURNAL
Patent: JP 2002360271-A 647 17-DEC-2002;
COMMENT
KING CAR FOOD INDUSTRIAL CO LTD
OS Artificial Sequence
PN JP 2002360271-A/647
PD 17-DEC-2002
PF 28-NOV-2001 JP 2001362595
PR 04-MAY-2001 TW 90110785
PI CHING-FEE LING,RUEY-WEN LIN,ZHOU-MENG YOO,XIN-HSUAN HUANG,BOW-
PI HAENG LEE,
PI SHENG-HSIUNG LEE,YI-JU LIN,CI-CHUNG HUANG,HAN-CHANG HSU,CHA-
PI WEN SHI,
PI CHIH-XIN YEH,YI-PENG CAO,CHIH-LONG PAN
PC C12N15/09,C12N15/09,C12M1/34,C12Q1/04,C12Q1/42,C12Q1/68 PC
,C12Q1/70,G01N21/64,
PC G01N33/53,G01N33/574,G01N33/58,G01N37/00/(C12M1/34,C12R1:93),
PC C12Q1/70,C12R1:93,C12N15/00,C12N15/00
CC Added sequence for 3' end labeling of oligonucleic acid. FH
Key
Location/Qualifiers
FT source 1..15
FT Location/Qualifiers
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source
1..15
/organism='Artificial Sequence'.
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
|||||
Db 15 AAAAAAAAAAAAAA 1

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Db 15 AAAAAAAAAAAAAA 1

RESULT 186
BD206432/c
LOCUS
DEFINITION
Enzymatic nucleic acid treatment of diseases or conditions related
to hepatitis C virus infection.
ACCESSION
BD206432.1 GI:33016202
VERSION
JP 2002512791-A/22.
KEYWORDS
unidentified
SOURCE
unidentified
ORGANISM
unclassified.
REFERENCE
1 (bases 1 to 15)
AUTHORS
Blatt,L., McSwiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.
TITLE
Enzymatic nucleic acid treatment of diseases or conditions related
to hepatitis C virus infection
JOURNAL
Patent: JP 2002512791-A 22 08-MAY-2002;
COMMENT
RIBOZYME PHARMACEUTICALS INC
OS Hepatitis virus (hepatitis C virus)
PN JP 2002512791-A/22
PD 08-MAY-2002
PF 26-APR-1999 JP 2000545991
PR 27-APR-1998 US 60/083217,18-SEP-1998 US 60/100842 PR
25-FEB-1999 US 09/257608,23-MAR-1999 US 09/274553 PI
LAWRENCE BLATT,JAMES A MCSWIGGEN,ELISABETH ROBERTS,PAMELA A PI
PAVCO,
PI DENNIS MACEJAK
PC C12N9/00,A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,
PC A61K37/66,
PC C12N15/00
CC Enzymatic nucleic acid treatment of diseases or conditions CC
related to
hepatitis C virus infection.
FT key Location/Qualifiers
FT source 1..15
FT Location/Qualifiers
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source
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/organism='unidentified'
/db_xref='taxon:32644'

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
|||||
Db 15 AAAAAAAAAAAAAA 1

RESULT 187
BD209488/c
LOCUS
DEFINITION
Enzymatic nucleic acid treatment of diseases or conditions related
to hepatitis C virus infection.
ACCESSION
BD209488.1 GI:33019258
VERSION
JP 2002512791-A/3078.
KEYWORDS
unidentified
SOURCE
unidentified
ORGANISM
unclassified.
REFERENCE
1 (bases 1 to 15)
AUTHORS
Blatt,L., McSwiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.
TITLE
Enzymatic nucleic acid treatment of diseases or conditions related
to hepatitis C virus infection
JOURNAL
Patent: JP 2002512791-A 3078 08-MAY-2002;
COMMENT
RIBOZYME PHARMACEUTICALS INC
OS Hepatitis virus (hepatitis C virus)
PN JP 2002512791-A/3078

```

PD 08-MAY-2002
PF 26-APR-1999 JP 2000545991
PR 27-APR-1998 US 60/083217,18-SEP-1998 US 60/100842 PR
25-FEB-1999 US 09/257608,23-MAR-1999 US 09/274553 PI
LAWRENCE BLATT, JAMES A MCSWIGGEN, ELISABETH ROBERTS, PAMELA A PI
PAVCO,
PI DENNIS MACEJAK
PC C12N9/00,A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,
PC A61K37/66,
PC C12N15/00
CC Enzymatic nucleic acid treatment of diseases or conditions CC
related to
CC hepatitis C virus infection.
FH Key Location/Qualifiers
FT source 1..15
FT /organism='Hepatitis virus (hepatitis C FT
virus)'
FEATURES
source Location/Qualifiers
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/organism='unidentified'
/mol_type='genomic RNA'
/db_xref='taxon:32644'
Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1
|||||
RESULT 188
AR221693/c
LOCUS AR221693 16 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 3 from patent US 6426408.
ACCESSION AR221693
VERSION AR221693.1 GI:23328765
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL Patent: US 6426408-A 3 30-JUL-2002;
FEATURES
source Location/Qualifiers
1..16
/organism='unknown'
/mol_type='genomic DNA'
Query Match 1.0%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1
|||||
RESULT 189
AR221694/c
LOCUS AR221694 16 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 4 from patent US 6426408.
ACCESSION AR221694
VERSION AR221694.1 GI:23328766
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE Covalently linked oligonucleotide minor groove binder conjugates

JOURNAL Patent: US 6426408-A 4 30-JUL-2002;
FEATURES
source Location/Qualifiers
1..16
/organism='unknown'
/mol_type='genomic DNA'
Query Match 1.0%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1
|||||
RESULT 190
AR221695/c
LOCUS AR221695 16 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 5 from patent US 6426408.
ACCESSION AR221695
VERSION AR221695.1 GI:23328767
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL Patent: US 6426408-A 5 30-JUL-2002;
FEATURES
source Location/Qualifiers
1..16
/organism='unknown'
/mol_type='genomic DNA'
Query Match 1.0%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1
|||||
RESULT 191
AR221696/c
LOCUS AR221696 16 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 6 from patent US 6426408.
ACCESSION AR221696
VERSION AR221696.1 GI:23328768
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL Patent: US 6426408-A 6 30-JUL-2002;
FEATURES
source Location/Qualifiers
1..16
/organism='unknown'
/mol_type='genomic DNA'
Query Match 1.0%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1
|||||
RESULT 192
AR221697/c
LOCUS AR221697 16 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 7 from patent US 6426408.
ACCESSION AR221697
VERSION AR221697.1 GI:23328769
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL Patent: US 6426408-A 7 30-JUL-2002;
FEATURES
source Location/Qualifiers
1..16
/organism='unknown'
/mol_type='genomic DNA'

LOCUS AR221697 16 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 7 from patent US 6426408.
ACCESSION AR221697
VERSION AR221697.1 GI:23328769
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kutuyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL Patent: US 6426408-A 7 30-JUL-2002;
FEATURES Location/Qualifiers
source
1..16
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.0%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1495
|||||
Db 15 AAAAAAAAAAAAAA 1

RESULT 193
AR221698/c
LOCUS AR221698 16 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 8 from patent US 6426408.
ACCESSION AR221698
VERSION AR221698.1 GI:23328770
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kutuyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL Patent: US 6426408-A 8 30-JUL-2002;
FEATURES Location/Qualifiers
source
1..16
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.0%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1495
|||||
Db 15 AAAAAAAAAAAAAA 1

RESULT 194
AR257438/c
LOCUS AR257438 16 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 3 from patent US 6486308.
ACCESSION AR257438
VERSION AR257438.1 GI:27307449
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kutuyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL Patent: US 6486308-A 3 26-NOV-2002;
FEATURES Location/Qualifiers
source
1..16
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.0%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1495
|||||
Db 15 AAAAAAAAAAAAAA 1

RESULT 197
AR257441/c
LOCUS AR257441 16 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 6 from patent US 6486308.
ACCESSION AR257441
VERSION AR257441.1 GI:27307452
KEYWORDS
SOURCE Unknown.

Query Match 1.0%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1495
|||||
Db 15 AAAAAAAAAAAAAA 1

RESULT 195
AR257439/c
LOCUS AR257439 16 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 4 from patent US 6486308.
ACCESSION AR257439
VERSION AR257439.1 GI:27307450
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kutuyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL Patent: US 6486308-A 4 26-NOV-2002;
FEATURES Location/Qualifiers
source
1..16
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.0%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1495
|||||
Db 15 AAAAAAAAAAAAAA 1

RESULT 196
AR257440/c
LOCUS AR257440 16 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 5 from patent US 6486308.
ACCESSION AR257440
VERSION AR257440.1 GI:27307451
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kutuyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL Patent: US 6486308-A 5 26-NOV-2002;
FEATURES Location/Qualifiers
source
1..16
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.0%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1495
|||||
Db 15 AAAAAAAAAAAAAA 1

RESULT 197
AR257441/c
LOCUS AR257441 16 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 6 from patent US 6486308.
ACCESSION AR257441
VERSION AR257441.1 GI:27307452
KEYWORDS
SOURCE Unknown.

Query Match 1.0%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1495
|||||
Db 15 AAAAAAAAAAAAAA 1

ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kutayavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL Patent: US 6486308-A 6 26-NOV-2002;
FEATURES Location/Qualifiers
source 1..16
/organism="unknown"
/mol_type="genomic DNA"
Query Match 1.0%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1495
|||||
DB 15 AAAAAAAAAAAAAA 1

RESULT 198
AR257442/c
LOCUS AR257442 16 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 7 from patent US 6486308.
ACCESSION AR257442
VERSION AR257442.1 GI:27307453
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kutayavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL Patent: US 6486308-A 7 26-NOV-2002;
FEATURES Location/Qualifiers
source 1..16
/organism="unknown"
/mol_type="genomic DNA"
Query Match 1.0%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1495
|||||
DB 15 AAAAAAAAAAAAAA 1

RESULT 199
AR257443/c
LOCUS AR257443 16 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 8 from patent US 6486308.
ACCESSION AR257443
VERSION AR257443.1 GI:27307454
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kutayavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL Patent: US 6486308-A 8 26-NOV-2002;
FEATURES Location/Qualifiers
source 1..16
/organism="unknown"
/mol_type="genomic DNA"
Query Match 1.0%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1495
|||||

DB 15 AAAAAAAAAAAAAA 1

RESULT 200
AX494458
LOCUS AX494458 16 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 223 from Patent WO02059256.
ACCESSION AX494458
VERSION AX494458.1 GI:23340068
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Tuijinder,M., Telerman,A., Anson,R. and Susini,L.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 02059256-A 223 01-AUG-2002;
FEATURES MOLECULAR ENGINEES LAB (PR)
source 1..16
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 1.0%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1477 TGCTAAAAAAAAAA 1491
|||||
DB 2 TGCTAAAAAAAAAA 16

RESULT 201
E34259/c
LOCUS E34259 17 bp DNA linear PAT 31-JAN-2002
DEFINITION Pollinosis-associated gene.
ACCESSION E34259
VERSION E34259.1 GI:18624264
KEYWORDS JP 2000106879-A/3.
SOURCE synthetic construct
synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
Gunji,S., Obayashi,I., Imai,Y., No,N. and Ogawa,K.
TITLE Pollinosis-associated gene
JOURNAL Patent: JP 2000106879-A 3 18-APR-2000;
COMMENT GENOX RESEARCH INC
OS Artificial Sequence
PN JP 2000106879-A/3
PD 18-APR-2000
PF 06-OCT-1998 JP 1998284610
PR
PI TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
PI MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
PI KING NO,
PI KOURU OGAWA
PC C12N15/09,A61K31/00,A61K39/36,A61K45/00,C12Q1/68,C12N15/00 CC
FH Key Location/Qualifiers
FT source 1..17
/organism='Artificial Sequence'.
FEATURES Location/Qualifiers
source 1..17
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 1.0%; Score 15; DB 1; Length 17;

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Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 16 AAAAAAAAAAAAAA 2

RESULT 202
E34260/c
LOCUS E34260 17 bp DNA linear PAT 31-JAN-2002
DEFINITION Follinosis-associated gene.
ACCESSION E34260
VERSION E34260.1 GI:18624265
KEYWORDS JP 2000106879-A/4.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
Gunji,S., Obayashi,I., Inai,Y., No.N. and Ogawa,K.
TITLE Follinosis-associated gene
JOURNAL Patent: JP 2000106879-A 4 18-APR-2000;
GENOX RESEARCH INC
COMMENT OS Artificial Sequence
PN JP 2000106879-A/4
PD 18-APR-2000
PF 06-OCT-1998 JP 1998284610
PR TAKESHI NAGASU, YUJI SUGITA, TOMOKO KASHIWABARA, TADAHIRO OSHIDA,
PI MASAYA OBAYASHI, SHIGEMICHI GUNJI, IZUMI OBAYASHI, YUKIHO INAI,
PI NING NO,
PI KAORU OGAWA
PC C12N15/09,A61K31/00,A61K39/36,A61K45/00,C12Q1/68,C12N15/00 CC
FH Key Location/Qualifiers
FT source 1..17
FT /organism='Artificial Sequence'.

FEATURES
source
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 1..0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 16 AAAAAAAAAAAAAA 2

RESULT 203
E59657/c
LOCUS E59657 17 bp DNA linear PAT 18-JUN-2001
DEFINITION Method for preparing nucleic acid sample for analyzing minor gene,
nucleic acid sample thus prepared and method for analyzing nucleic
acid sample by using the same, and reagent kit and analysis service
for using the same.
E59657
ACCESSION E59657
VERSION E59657.1 GI:13019451
KEYWORDS JP 2000037193-A/3.
SOURCE unidentified
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Takamichi,M., Tsuyoshi,F., Masaharu,K., Takashi,I. and Kazunori,O.
TITLE Method for preparing nucleic acid sample for analyzing minor gene,
nucleic acid sample thus prepared and method for analyzing nucleic
acid sample by using the same, and reagent kit and analysis service
for using the same
JOURNAL Patent: JP 2000037193-A 3 08-FEB-2000;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 16 AAAAAAAAAAAAAA 2

RESULT 204
AR187061/c
LOCUS AR187061 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 2549 from patent US 6346398.
ACCESSION AR187061
VERSION AR187061.1 GI:20233026
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
Patent: US 6346398-A 2549 12-FEB-2002;
JOURNAL Location/Qualifiers
FEATURES source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1..0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 17 AAAAAAAAAAAAAA 3

RESULT 205
AR187064/c
LOCUS AR187064 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 2552 from patent US 6346398.
ACCESSION AR187064
VERSION AR187064.1 GI:20233029
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
Patent: JP 2000037193-A 3 08-FEB-2000;

HITACHI LTD
OS Unidentified
PN JP 200037193-A/3
PD 08-FEB-2000
PF 19-MAY-1999 JP 1999138051
PR TAKAMICHI MATSUMURA, TSUYOSHI FUJITA, MASAHARU KIYAMA, PI
TAKASHI IRIE,
PI KAZUNORI OKANO
PC C12N15/09,C12Q1/68,C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT Source 1..17
FT /organism='Unidentified'.

FEATURES
source
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 1..0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 16 AAAAAAAAAAAAAA 2

RESULT 204
AR187061/c
LOCUS AR187061 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 2549 from patent US 6346398.
ACCESSION AR187061
VERSION AR187061.1 GI:20233026
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
Patent: US 6346398-A 2549 12-FEB-2002;
JOURNAL Location/Qualifiers
FEATURES source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1..0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 17 AAAAAAAAAAAAAA 3

RESULT 205
AR187064/c
LOCUS AR187064 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 2552 from patent US 6346398.
ACCESSION AR187064
VERSION AR187064.1 GI:20233029
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
Patent: JP 2000037193-A 3 08-FEB-2000;
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[illegible]

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source      1. .17
            /organism="unknown"
            /mol_type="unassigned RNA"

Query Match
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Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 17 AAAAAAAAAAAAAA 3

RESULT 211
LOCUS AR323674/c 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 1076 from patent US 6566127.
ACCESSION AR323674
VERSION AR323674.1 GI:33709482
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
  related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 1076 20-MAY-2003;
FEATURES
  source      1. .17
            /organism="unknown"
            /mol_type="unassigned RNA"

Query Match
  1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 212
LOCUS AR397940 17 bp RNA linear PAT 18-DEC-2003
DEFINITION Sequence 321 from patent US 6617438.
ACCESSION AR397940
VERSION AR397940.1 GI:40135343
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 17)
AUTHORS Beigelman,L., Burgin,A.B., Beaudry,A., Karpeisky,A.,
  Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE Oligoribonucleotides with enzymatic activity
JOURNAL Patent: US 6617438-A 321 09-SEP-2003;
FEATURES
  source      1. .17
            /organism="unknown"
            /mol_type="unassigned RNA"

Query Match
  1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 90 CCGCGCGCGCGCGC 104
Db 3 CCGCGCGCGCGCGC 17

RESULT 213
LOCUS AX692524/c 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 5256 from Patent EP1281758.
ACCESSION AX692524
VERSION AX692524.1 GI:29415482
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
  1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
  mdz12
JOURNAL Patent: EP 1281758-A 5256 05-FEB-2003;
  Aeomica, Inc. (US)
FEATURES
  source      1. .17
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            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match
  1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 17 AAAAAAAAAAAAAA 3

RESULT 214
LOCUS BD011731/c 17 bp DNA linear PAT 02-AUG-2002
DEFINITION 795, a novel gene related to pollen allergy.
ACCESSION BD011731
VERSION BD011731.1 GI:22091920
KEYWORDS WO 0065050-A/3.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
  1 (bases 1 to 17)
AUTHORS Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
  Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
  Takahashi,E. and Yokoi,A.
TITLE 795, a novel gene related to pollen allergy
JOURNAL Patent: WO 0065050-A 3 02-NOV-2000;
  GENOX RESEARCH INC, TAKESHI NAGASU, YUJI SUGITA, TOMOKO KASHIWABARA,
  TADAHIRO OSHIDA, MASAYA OBAYASHI, SHIGEMICHI GUNJI, IZUMI OBAYASHI,
  YUKIHO IMAI, NEI YOSHIDA, KAORU OGAWA, KEIKO MATSUI, EIKI
  TAKAHASHI, AKIRA YOKOI
COMMENT OS Artificial Sequence
  PN WO 0065050-A/3
  PD 02-NOV-2000
  PF 26-APR-2000 WO 2000JP002734
  PR 27-APR-1999 JP 99P 120494
  PI TAKESHI NAGASU, YUJI SUGITA, TOMOKO KASHIWABARA, TADAHIRO OSHIDA,
  MASAYA OBAYASHI, SHIGEMICHI GUNJI, IZUMI OBAYASHI, YUKIHO IMAI,
  NEI YOSHIDA,
  PI KAORU OGAWA, KEIKO MATSUI, EIKI TAKAHASHI, AKIRA YOKOI
  PI C12N15/12, C07K14/47, C07K16/18, C12Q1/68, G01N33/50//A61K31/00, PC
  A61P37/00
CC Description of Artificial Sequence:Artificially Synthesized CC
  Primer Sequence
  FH Key Location/Qualifiers
  source      1. .17
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"

Query Match
  1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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QY 1481 AAAAAAAAAAAAAA 1495
Db 16 AAAAAAAAAAAAAA 2

RESULT 215
BD011732/c
LOCUS 17 bp DNA linear PAT 02-AUG-2002
DEFINITION 795, a novel gene related to pollen allergy.
ACCESSION BD011732
VERSION BD011732.1 GI:22091921
KEYWORDS WO 0065050-A/4.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
Takahashi,E. and Yokoi,A.
TITLE 795, a novel gene related to pollen allergy
JOURNAL Patent: WO 0065050-A 4 02-NOV-2000;
GENOX RESEARCH INC,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI
TAKAHASHI,AKIRA YOKOI
COMMENT OS Artificial Sequence
PN WO 0065050-A/4
PD 02-NOV-2000
PF 26-APR-2000 WO 2000JP002734
PR 27-APR-1999 JP 99P 120494
PI TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
PI MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
PI NEI YOSHIDA,
PI KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI PC
C12N15/12,C07K14/47,C07K16/18,C12Q1/68,G01N33/50//A61K31/00, PC
A61P37/00
CC Description of Artificial Sequence:Artificially Synthesized CC
Primer Sequence
FH Key Location/Qualifiers
1. 17
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

FEATURES
source
LOCUS 17 bp DNA linear PAT 27-AUG-2002
DEFINITION 441, a novel gene related to pollen allergy.
ACCESSION BD091743
VERSION BD091743.1 GI:22637354
KEYWORDS WO 0073435-A/3.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K. and Matsui,K.
TITLE 441, a novel gene related to pollen allergy
JOURNAL Patent: WO 0073435-A 3 07-DEC-2000;
GENOX RESEARCH INC,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI

QY 1481 AAAAAAAAAAAAAA 1495
Db 16 AAAAAAAAAAAAAA 2

RESULT 216
BD091743/c
LOCUS 17 bp DNA linear PAT 27-AUG-2002
DEFINITION 441, a novel gene related to pollen allergy.
ACCESSION BD091743
VERSION BD091743.1 GI:22637354
KEYWORDS WO 0073435-A/3.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K. and Matsui,K.
TITLE 441, a novel gene related to pollen allergy
JOURNAL Patent: WO 0073435-A 3 07-DEC-2000;
GENOX RESEARCH INC,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI

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COMMENT OS Artificial Sequence
PN WO 0073435-A/3
PD 07-DEC-2000
PF 18-MAY-2000 WO 2000JP003190
PR 27-MAY-1999 JP 99P 148783
PI TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
PI MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
PI NEI YOSHIDA,
PI KAORU OGAWA,KEIKO MATSUI
PC C12N15/10,C12Q1/68,G01N33/15,G01N33/50
CC Description of Artificial Sequence:Artificially Synthesized CC
Primer Sequence
FH Key Location/Qualifiers
1. 17
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/mol_type="genomic DNA"
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FEATURES
source
Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 16 AAAAAAAAAAAAAA 2

RESULT 217
BD091744/c
LOCUS 17 bp DNA linear PAT 27-AUG-2002
DEFINITION 441, a novel gene related to pollen allergy.
ACCESSION BD091744
VERSION BD091744.1 GI:22637355
KEYWORDS WO 0073435-A/4.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K. and Matsui,K.
TITLE 441, a novel gene related to pollen allergy
JOURNAL Patent: WO 0073435-A 4 07-DEC-2000;
GENOX RESEARCH INC,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI
COMMENT OS Artificial Sequence
PN WO 0073435-A/4
PD 07-DEC-2000
PF 18-MAY-2000 WO 2000JP003190
PR 27-MAY-1999 JP 99P 148783
PI TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
PI MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
PI NEI YOSHIDA,
PI KAORU OGAWA,KEIKO MATSUI
PC C12N15/10,C12Q1/68,G01N33/15,G01N33/50
CC Description of Artificial Sequence:Artificially Synthesized CC
Primer Sequence
FH Key Location/Qualifiers
1. 17
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/mol_type="genomic DNA"
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FEATURES
source
Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 16 AAAAAAAAAAAAAA 2

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RESULT 218
BD091751/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BD091751 17 bp DNA linear PAT 27-AUG-2002
465, a novel gene related to pollen allergy.
BD091751
BD091751.1 GI:22637362
synthetic construct
synthetic construct
artificial sequences.
1 (bases 1 to 17)
Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
Takahashi,E. and Yokoi,A.
465, a novel gene related to pollen allergy
Patent: WO 0073439-A 3 07-DEC-2000;
GENOX RESEARCH INC.TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI
TAKAHASHI,AKIRA YOKOI
OS Artificial Sequence
PN WO 0073439-A/3
PD 07-DEC-2000
PF 18-MAY-2000 WO 2000JP003191
PR 27-MAY-1999 JP 99P 148784
PI TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
PI MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
PI NEI YOSHIDA,
PI KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI PC
C12N15/12,C12Q1/68,A61P37/08,A61K45/00 CC Description
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FH Key Location/Qualifiers.
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FEATURES
source
Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 16 AAAAAAAAAAAAAA 2

RESULT 220
BD091774/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BD091774 17 bp DNA linear PAT 27-AUG-2002
787, a novel gene related to pollen allergy.
BD091774
BD091774.1 GI:22637385
synthetic construct
synthetic construct
artificial sequences.
1 (bases 1 to 17)
Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
Takahashi,E. and Yokoi,A.
787, a novel gene related to pollen allergy
Patent: WO 0073440-A 3 07-DEC-2000;
GENOX RESEARCH INC.TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI
TAKAHASHI,AKIRA YOKOI
OS Artificial Sequence
PN WO 0073440-A/3
PD 07-DEC-2000
PF 18-MAY-2000 WO 2000JP003192
PR 27-MAY-1999 JP 99P 148785
PI TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
PI MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
PI NEI YOSHIDA,
PI KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI PC
C12N15/12,C12Q1/68,C12N5/08,C12N5/06,C07K14/415 CC Description of
Artificial Sequence:Artificially Synthesized CC Primer Sequence
Sequence
FH Key Location/Qualifiers.
1.17
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/db_xref="taxon:32630"

FEATURES
source
Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 16 AAAAAAAAAAAAAA 2

RESULT 221
BD091775/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BD091752 17 bp DNA linear PAT 27-AUG-2002
465, a novel gene related to pollen allergy.
BD091752
BD091752.1 GI:22637363
synthetic construct
synthetic construct
artificial sequences.
1 (bases 1 to 17)
Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
Takahashi,E. and Yokoi,A.
465, a novel gene related to pollen allergy
Patent: WO 0073439-A 4 07-DEC-2000;
GENOX RESEARCH INC.TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI
TAKAHASHI,AKIRA YOKOI
OS Artificial Sequence
PN WO 0073439-A/4
PD 07-DEC-2000
PF 18-MAY-2000 WO 2000JP003191

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LOCUS BD091775 17 bp DNA linear PAT 27-AUG-2002
DEFINITION 787, a novel gene related to pollen allergy.
ACCESSION BD091775
VERSION BD091775.1 GI:22637386
KEYWORDS WO 0073440-A/4.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 17)
AUTHORS Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
Takahashi,E. and Yokoi,A.
TITLE 787, a novel gene related to pollen allergy
JOURNAL Patent: WO 0073440-A 4 07-DEC-2000;
GENOX RESEARCH INC, TAKESHI NAGASU, YUJI SUGITA, TOMOKO KASHIWABARA,
TADAHIRO OSHIDA, MASAYA OBAYASHI, SHIGEMICHI GUNJI, IZUMI OBAYASHI,
YUKIHO IMAI, NEI YOSHIDA, KAORU OGAWA, KEIKO MATSUI, EIKI
TAKAHASHI, AKIRA YOKOI
OS Artificial Sequence
PN WO 0073440-A/4
PD 07-DEC-2000
PF 18-MAY-2000 WO 2000JP003192
PR 27-MAY-1999 JP 99P 148785
PI TAKESHI NAGASU, YUJI SUGITA, TOMOKO KASHIWABARA, TADAHIRO OSHIDA,
MASAYA OBAYASHI, SHIGEMICHI GUNJI, IZUMI OBAYASHI, YUKIHO IMAI,
NEI YOSHIDA,
PI KAORU OGAWA, KEIKO MATSUI, EIKI TAKAHASHI, AKIRA YOKOI PC
C12N15/12, C12Q1/68, C12N5/06, C07K14/415 CC Description of
Artificial Sequence:Artificially Synthesized CC Primer Sequence
FH Key Location/Qualifiers
1. .17
/organism="synthetic construct"
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/db_xref="taxon:32630"

Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 16 AAAAAAAAAAAAAA 2

RESULT 222
BD097335/c
LOCUS BD097335 17 bp DNA linear PAT 27-AUG-2002
DEFINITION Method for examination for allergosis.
ACCESSION BD097335
VERSION BD097335.1 GI:22642910
KEYWORDS WO 0165259-A/7.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 17)
AUTHORS Nagasu,T., Oshida,T., Obayashi,I., Matsui,K. and Sait,H.
TITLE Method for examination for allergosis
JOURNAL Patent: WO 0165259-A 7 07-SEP-2001;
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
NATIONAL CHILDREN'S HOSPITAL, HIROMITSU NAKAUCHI, YUTAKA
FUJIKI, KAZUO FUKAWA, OSAMU KUDO TAKESHI NAGASU, TADAHIRO OSHIDA, IZUMI
OBAYASHI, KEIKO MATSUI, HIROHISA SAITO
OS Artificial Sequence
PN WO 0165259-A/7
PD 07-SEP-2001
PF 23-FEB-2001 WO 2001JP001372
PR 02-MAR-2000 JP 00P 61832
PI TAKESHI NAGASU, TADAHIRO OSHIDA, IZUMI OBAYASHI, KEIKO MATSUI, PI
HIROHISA SAITO
PC GOIN33/53, C12Q1/68, C12N15/12, G01N33/15, A01K67/027, A61K39/395,
A61P37/08
CC Description of Artificial Sequence:Artificially Synthesized CC
Primer Sequence
FH Key Location/Qualifiers
1. .17
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 16 AAAAAAAAAAAAAA 2

RESULT 224
BD142809/c
LOCUS BD142809 17 bp DNA linear PAT 18-SEP-2002
DEFINITION Method of examining allergic disease.
ACCESSION BD142809
VERSION BD142809.1 GI:23237754
KEYWORDS WO 0224903-A/3.

LOCUS BD091775 17 bp DNA linear PAT 27-AUG-2002
DEFINITION 787, a novel gene related to pollen allergy.
ACCESSION BD091775
VERSION BD091775.1 GI:22637386
KEYWORDS WO 0073440-A/4.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 17)
AUTHORS Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
Takahashi,E. and Yokoi,A.
TITLE 787, a novel gene related to pollen allergy
JOURNAL Patent: WO 0073440-A 4 07-DEC-2000;
GENOX RESEARCH INC, TAKESHI NAGASU, YUJI SUGITA, TOMOKO KASHIWABARA,
TADAHIRO OSHIDA, MASAYA OBAYASHI, SHIGEMICHI GUNJI, IZUMI OBAYASHI,
YUKIHO IMAI, NEI YOSHIDA, KAORU OGAWA, KEIKO MATSUI, EIKI
TAKAHASHI, AKIRA YOKOI
OS Artificial Sequence
PN WO 0073440-A/4
PD 07-DEC-2000
PF 18-MAY-2000 WO 2000JP003192
PR 27-MAY-1999 JP 99P 148785
PI TAKESHI NAGASU, YUJI SUGITA, TOMOKO KASHIWABARA, TADAHIRO OSHIDA,
MASAYA OBAYASHI, SHIGEMICHI GUNJI, IZUMI OBAYASHI, YUKIHO IMAI,
NEI YOSHIDA,
PI KAORU OGAWA, KEIKO MATSUI, EIKI TAKAHASHI, AKIRA YOKOI PC
C12N15/12, C12Q1/68, C12N5/06, C07K14/415 CC Description of
Artificial Sequence:Artificially Synthesized CC Primer Sequence
FH Key Location/Qualifiers
1. .17
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 16 AAAAAAAAAAAAAA 2

RESULT 223
BD097336/c
LOCUS BD097336 17 bp DNA linear PAT 27-AUG-2002
DEFINITION Method for examination for allergosis.
ACCESSION BD097336
VERSION BD097336.1 GI:22642910
KEYWORDS WO 0165259-A/7.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 17)
AUTHORS Nagasu,T., Oshida,T., Obayashi,I., Matsui,K. and Sait,H.
TITLE Method for examination for allergosis
JOURNAL Patent: WO 0165259-A 7 07-SEP-2001;
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
NATIONAL CHILDREN'S HOSPITAL, HIROMITSU NAKAUCHI, YUTAKA
FUJIKI, KAZUO FUKAWA, OSAMU KUDO TAKESHI NAGASU, TADAHIRO OSHIDA, IZUMI
OBAYASHI, KEIKO MATSUI, HIROHISA SAITO
OS Artificial Sequence
PN WO 0165259-A/7
PD 07-SEP-2001
PF 23-FEB-2001 WO 2001JP001372
PR 02-MAR-2000 JP 00P 61832
PI TAKESHI NAGASU, TADAHIRO OSHIDA, IZUMI OBAYASHI, KEIKO MATSUI, PI
HIROHISA SAITO
PC GOIN33/53, C12Q1/68, C12N15/12, G01N33/15, A01K67/027, A61K39/395,
A61P37/08
CC Description of Artificial Sequence:Artificially Synthesized CC
Primer Sequence
FH Key Location/Qualifiers
1. .17
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 16 AAAAAAAAAAAAAA 2

RESULT 224
BD142809/c
LOCUS BD142809 17 bp DNA linear PAT 18-SEP-2002
DEFINITION Method of examining allergic disease.
ACCESSION BD142809
VERSION BD142809.1 GI:23237754
KEYWORDS WO 0224903-A/3.

SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE artificial sequences.
AUTHORS 1 (bases 1 to 17)
Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T., Nagasu,T.,
Tsujimoto,G. and Takahashi,E.
TITLE Method of examining allergic disease
JOURNAL Patent: WO 0224903-A 3 28-MAR-2002;
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
NATIONAL CHILDREN'S HOSPITAL, YUJI SUGITA, RYOICHI HASHIDA, KAORU
OGAWA, TOMOKO FUJISHIMA, TAKESHI NAGASU, GOZO TSUJIMOTO, EIKI
TAKAHASHI
COMMENT OS Artificial Sequence
PN WO 0224903-A/3
PD 28-MAR-2002
PF 21-SEP-2001 WO 2001JP008246
PR 25-SEP-2000 JP 00P 291318
PI YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, TOMOKO FUJISHIMA, PI
TAKESHI NAGASU,
PI GOZO TSUJIMOTO, EIKI TAKAHASHI
PC C12N15/09, C12N5/10, C07K14/47, C07K16/18, C12P21/02, C12Q1/02, PC
C12Q1/68,
PC A01K67/027, A61K31/713, A61K45/00, A61K48/00, A61P17/00, A61P37/08,
PC G01N33/15,
PC G01N33/50//C12P21/08, (C12N5/10, C12R1:91), (C12P21/02, C12R1:91)
CC Description of Artificial Sequence:an artificially synthesized

CC sequence primer
FH Key Location/Qualifiers
FT source 1..17
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FEATURES
source
1..17
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/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
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Db 16 AAAAAAAAAAAAAA 2

RESULT 225
BD142810/c
LOCUS 17 bp DNA linear PAT 18-SEP-2002
DEFINITION Method of examining allergic disease.
ACCESSION BD142810
VERSION BD142810.1 GI:23237755
KEYWORDS WO 0224903-A/4.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 17)
AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T., Nagasu,T.,
Tsujimoto,G. and Takahashi,E.
TITLE Method of examining allergic disease
JOURNAL Patent: WO 0224903-A 4 28-MAR-2002;
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
NATIONAL CHILDREN'S HOSPITAL, YUJI SUGITA, RYOICHI HASHIDA, KAORU
OGAWA, TOMOKO FUJISHIMA, TAKESHI NAGASU, GOZO TSUJIMOTO, EIKI
TAKAHASHI
COMMENT OS Artificial Sequence
PN WO 0224903-A/4
PD 28-MAR-2002
PF 21-SEP-2001 WO 2001JP008246
PR 25-SEP-2000 JP 00P 291318
PI YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, TOMOKO FUJISHIMA, PI
TAKESHI NAGASU,

PI GOZO TSUJIMOTO, EIKI TAKAHASHI
PC C12N15/09, C12N5/10, C07K14/47, C07K16/18, C12P21/02, C12Q1/02, PC
C12Q1/68,
PC A01K67/027, A61K31/713, A61K45/00, A61K48/00, A61P17/00, A61P37/08,
PC G01N33/15,
PC G01N33/50//C12P21/08, (C12N5/10, C12R1:91), (C12P21/02, C12R1:91)
CC Description of Artificial Sequence:an artificially synthesized

CC sequence primer
FH Key Location/Qualifiers
FT source 1..17
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source
1..17
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Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
|||||
Db 16 AAAAAAAAAAAAAA 2

RESULT 226
BD143835/c
LOCUS 17 bp DNA linear PAT 17-JAN-2003
DEFINITION Method of examining allergic disease.
ACCESSION BD143835
VERSION BD143835.1 GI:27849593
KEYWORDS JP 2002095500-A/3.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 17)
AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T. and
Tsujimoto,K.
TITLE Method of examining allergic disease
JOURNAL Patent: JP 2002095500-A 3 02-APR-2002;
GENOX RESEARCH INC, THE DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL
OS Artificial Sequence
PN JP 2002095500-A/3
PD 02-APR-2002
PF 25-SEP-2000 JP 200291316
PI YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, MASAYA OBAYASHI, PI
TAKESHI NAGASU,
PI KOZO TSUJIMOTO
PC C12Q1/68, A01K67/027, A61K31/7088, A61K31/711, A61K45/00, A61P37/08, PC
C07K14/47,
PC C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N5/10 PC
C12N15/09, C12P21/02,
PC C12Q1/02, G01N33/15, G01N33/50//C12P21/08, C12N5/00, C12N5/00, PC
C12N15/00
CC Description of Artificial Sequence:an artificially synthesized

CC sequence primer
FH Key Location/Qualifiers
FT source 1..17
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source
1..17
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/db_xref="taxon:32630"

Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
 Db 16 AAAAAAAAAAAAAA 2

RESULT 227
 BD143836/c
 LOCUS 17 bp DNA linear PAT 17-JAN-2003
 DEFINITION Method of examining allergic disease.
 ACCESSION BD143836
 VERSION BD143836.1 GI:27849594
 KEYWORDS JP 2002095500-A/4.
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T. and Teujimoto,K.
 TITLE Method of examining allergic disease
 JOURNAL GENOX RESEARCH INC,THE DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL
 COMMENT OS Artificial Sequence
 PN JP 2002095500-A/4
 PD 02-APR-2002
 PF 25-SEP-2000 JP 2000291316
 PI YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, MASAYA OBAYASHI, PI TAKESHI NAGASU,
 PI KOZO TSUJIMOTO
 PC C12Q1/68, A01K67/027, A61K31/7088, A61K31/711, A61K45/00, A61P37/08, PC C07K14/47, C12N15/09, C12N15/00, A61K31/15, C12N1/19, C12N1/21, C12N5/10, C12N5/10 PC C12Q1/02, G01N33/15, G01N33/50//C12P21/08, C12N5/00, C12N5/00, PC C12N15/00
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CC sequence primer
 CC key
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 FT Location/Qualifiers
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FEATURES
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Query Match 1.0%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
 Db 16 AAAAAAAAAAAAAA 2

RESULT 228
 BD167836/c
 LOCUS 17 bp DNA linear PAT 17-JAN-2003
 DEFINITION Method for examination of allergosis.
 ACCESSION BD167836
 VERSION BD167836.1 GI:27873648
 KEYWORDS WO 0233122-A/3.
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T., Saito,H. and Takahashi,E.
 TITLE Method for examination of allergosis

JOURNAL Patent: WO 0233122-A 3 25-APR-2002;
 GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL, RINAKO NAKAGAWA YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, MASAYA OBAYASHI, TAKESHI NAGASU, HIROHISA SAITO, EIKI TAKAHASHI
 COMMENT OS Artificial Sequence
 PN WO 0233122-A/3
 PD 25-APR-2002
 PF 11-OCT-2001 WO 2001JP008937
 PR 13-OCT-2000 JP 00P 314093
 PI YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, MASAYA OBAYASHI, PI TAKESHI NAGASU,
 PI HIROHISA SAITO, EIKI TAKAHASHI
 PC C12Q1/68, C12N15/09, G01N33/53, G01N33/50, C12Q1/02, A61K48/00, PC A61K39/395,
 PC A01K67/027//C07K16/18, C12N5/10
 CC Description of Artificial Sequence:an artificially synthesized

CC primer anchor
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 FT Location/Qualifiers
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Query Match 1.0%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
 Db 16 AAAAAAAAAAAAAA 2

RESULT 229
 BD167837/c
 LOCUS 17 bp DNA linear PAT 17-JAN-2003
 DEFINITION Method for examination of allergosis.
 ACCESSION BD167837
 VERSION BD167837.1 GI:27873649
 KEYWORDS WO 0233122-A/4.
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T., Saito,H. and Takahashi,E.
 TITLE Method for examination of allergosis
 JOURNAL Patent: WO 0233122-A 4 25-APR-2002;
 GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL, RINAKO NAKAGAWA YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, MASAYA OBAYASHI, TAKESHI NAGASU, HIROHISA SAITO, EIKI TAKAHASHI
 COMMENT OS Artificial Sequence
 PN WO 0233122-A/4
 PD 25-APR-2002
 PF 11-OCT-2001 WO 2001JP008937
 PR 13-OCT-2000 JP 00P 314093
 PI YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, MASAYA OBAYASHI, PI TAKESHI NAGASU,
 PI HIROHISA SAITO, EIKI TAKAHASHI
 PC C12Q1/68, C12N15/09, G01N33/53, G01N33/50, C12Q1/02, A61K48/00, PC A61K39/395,
 PC A01K67/027//C07K16/18, C12N5/10
 CC Description of Artificial Sequence:an artificially synthesized

CC primer anchor
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 FT Location/Qualifiers

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FT source 1..17 /organism='Artificial Sequence'.
FT Location/Qualifiers
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Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 16 AAAAAAAAAAAAAA 2

RESULT 230
BD167908/c
LOCUS
DEFINITION Method of examining allergic disease.
ACCESSION BD167908
VERSION BD167908.1 GI:27873720
KEYWORDS WO 0226962-A/7.
SOURCE synthetic construct
ORGANISM artificial construct
REFERENCE 1 (bases 1 to 17)
AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T., Nagasu,T. and Saito,H.
TITLE Method of examining allergic disease
JOURNAL Patent: WO 0226962-A 7 04-APR-2002; GENOX RESEARCH INC., JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL, MASAKAZU ADACHI, KAZUO MIYANAGA YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, TOMOKO FUJISHIMA, TAKESHI NAGASU, HIROHISA SAITO
COMMENT OS Artificial Sequence
PN WO 0226962-A/7
PD 04-APR-2002
PF 21-SEP-2001 WO 2001JP008247
PR 26-SEP-2000 JP OOP 293021
PI YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, TOMOKO FUJISHIMA, PI TAKESHI NAGASU,
PI HIROHISA SAITO
PC C12N15/09, C12N5/10, C07K14/47, C07K16/18, C12P21/02, C12Q1/02, PC C12Q1/68.
PC A01K67/027, A61K31/713, A61K45/00, A61P17/00, A61P37/08, PC G01N33/15, G01N33/50//C12P21/08, (C12N5/10, C12R1.91), (C12P21/02, C12R1.91)
PC G01N33/50//C12P21/08, (C12N5/10, C12R1.91), (C12P21/02, C12R1.91)
CC Description of Artificial Sequence:an artificially synthesized

CC sequence primer
FH Key Location/Qualifiers
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FEATURES
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Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 16 AAAAAAAAAAAAAA 2

RESULT 231
BD167909/c
LOCUS
DEFINITION Method of examining allergic disease.
ACCESSION BD167909
VERSION BD167909.1 GI:27873721
KEYWORDS WO 0226962-A/8.
SOURCE synthetic construct
ORGANISM artificial construct
REFERENCE 1 (bases 1 to 17)
AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T., Nagasu,T. and Saito,H.
TITLE Method of examining allergic disease
JOURNAL Patent: WO 0226962-A 8 04-APR-2002; GENOX RESEARCH INC., JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL, MASAKAZU ADACHI, KAZUO MIYANAGA YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, TOMOKO FUJISHIMA, TAKESHI NAGASU, HIROHISA SAITO
COMMENT OS Artificial Sequence
PN WO 0226962-A/8
PD 04-APR-2002
PF 21-SEP-2001 WO 2001JP008247
PR 26-SEP-2000 JP OOP 293021
PI YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, TOMOKO FUJISHIMA, PI TAKESHI NAGASU,
PI HIROHISA SAITO
PC C12N15/09, C12N5/10, C07K14/47, C07K16/18, C12P21/02, C12Q1/02, PC C12Q1/68.
PC A01K67/027, A61K31/713, A61K45/00, A61P17/00, A61P37/08, PC G01N33/15, G01N33/50//C12P21/08, (C12N5/10, C12R1.91), (C12P21/02, C12R1.91)
PC G01N33/50//C12P21/08, (C12N5/10, C12R1.91), (C12P21/02, C12R1.91)
CC Description of Artificial Sequence:an artificially synthesized

CC sequence primer
FH Key Location/Qualifiers
FT source 1..17 /organism='Artificial Sequence'.

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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 16 AAAAAAAAAAAAAA 2

RESULT 232
BD168112/c
LOCUS
DEFINITION Method for examination for allergosis.
ACCESSION BD168112
VERSION BD168112.1 GI:27873924
KEYWORDS WO 0233069-A/19.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T. and Saito,H.
TITLE Method for examination for allergosis
JOURNAL Patent: WO 0233069-A 19 25-APR-2003; GENOX RESEARCH INC., JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL, TOMOYUKI FUKASAWA, CHUHEI NOJIRI, NOBUO MATSUHASHI, KOJI NISHIZAWA, YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, MASAYA ODAYASHI, TAKESHI NAGASU, HIROHISA SAITO
COMMENT OS Artificial Sequence
PN WO 0233069-A/19

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PD 25-APR-2002
 PR 28-SEP-2001 WO 2001JP008574
 PR 13-OCT-2000 JP 00P 314093
 PI YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, MASAYA OBYASHI, PI
 TAKESHI NAGASU,
 PI HIROHISA SAITO
 PC C12N15/09, C12N15/63, C12Q1/68, C12Q1/02, G01N33/53, C12N5/10, PC
 A61K39/395,
 PC C07K14/47, C07K16/18//C12P21/02, C12P21/08
 CC Description of Artificial Sequence:an artificially synthesized

CC anchor
 CC primer sequence
 FH key Location/Qualifiers
 FT source 1..17
 FT /organism='Artificial Sequence'.
 FT Location/Qualifiers
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Query Match 1.0%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
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 Db 16 AAAAAAAAAAAAAA 2

RESULT 233
 BD168113/c
 LOCUS 17 bp DNA linear PAT 17-JAN-2003
 DEFINITION Method for examination for allergosis.
 ACCESSION BD168113
 VERSION WO 0233069-A/20.
 KEYWORDS synthetic construct
 SOURCE artificial sequences.
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T. and Saito,H.

TITLE Method for examination for allergosis
 JOURNAL Patent: WO 0233069-A 20 25-APR-2002;
 GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
 NATIONAL CHILDREN'S HOSPITAL, TOMOYUKI FUKASAWA, CHUHEI NOJIRI, NOBUO
 MATSUHASHI, KOJI NISHIZAWA, YUJI SUGITA, RYOICHI HASHIDA, KAORU
 OGAWA, MASAYA OBYASHI, TAKESHI NAGASU, HIROHISA SAITO
 OS Artificial Sequence
 PN WO 0233069-A/20
 PD 25-APR-2002
 PF 28-SEP-2001 WO 2001JP008574
 PR 13-OCT-2000 JP 00P 314093
 PI YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, MASAYA OBYASHI, PI
 TAKESHI NAGASU,
 PI HIROHISA SAITO
 PC C12N15/09, C12N15/63, C12Q1/68, C12Q1/02, G01N33/53, C12N5/10, PC
 A61K39/395,
 PC C07K14/47, C07K16/18//C12P21/02, C12P21/08
 CC Description of Artificial Sequence:an artificially synthesized

CC anchor
 CC primer sequence
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Query Match 1.0%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
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 Db 16 AAAAAAAAAAAAAA 2

RESULT 234
 BD171178/c
 LOCUS 17 bp DNA linear PAT 17-JAN-2003
 DEFINITION Method of examining allergic disease.
 ACCESSION BD171178
 VERSION BD171178.1 GI:27876990
 KEYWORDS WO 0250269-A/3.
 SOURCE synthetic construct
 ORGANISM synthetic construct
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Matsumoto,Y., Imai,Y., Oshida,T., Sugita,Y., Nagasu,T. and Tsujimoto,G.

TITLE Method of examining allergic disease
 JOURNAL Patent: WO 0250269-A 3 27-JUN-2002;
 GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
 NATIONAL CHILDREN'S HOSPITAL, MASAMICHI TAKAGI, AKINORI OTA YOSHIKO
 MATSUMOTO, YUKIHO IMAI, TADAHIRO OSHIDA, YUJI SUGITA, TAKESHI NAGASU,
 GOZO TSUJIMOTO
 OS Artificial Sequence
 PN WO 0250269-A/3
 PD 27-JUN-2002
 PF 21-DEC-2001 WO 2001JP011286
 PR 21-DEC-2000 JP 00P 389476
 PI YOSHIKO MATSUMOTO, YUKIHO IMAI, TADAHIRO OSHIDA, YUJI SUGITA, PI
 TAKESHI NAGASU,
 PI GOZO TSUJIMOTO
 PC C12N15/11, C07K16/18, A61K67/027, A61K31/711, A61K45/00, A61K48/00,
 PC A61P37/08,
 PC C12Q1/68, G01N33/50
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 CC key Location/Qualifiers
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 FT /organism='Artificial Sequence'.
 FT Location/Qualifiers
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 /organism="synthetic construct"
 /mol_type="genomic DNA"
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Query Match 1.0%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
 |||||
 Db 16 AAAAAAAAAAAAAA 2

RESULT 235
 BD171179/c
 LOCUS 17 bp DNA linear PAT 17-JAN-2003
 DEFINITION Method of examining allergic disease.
 ACCESSION BD171179
 VERSION BD171179.1 GI:27876991
 KEYWORDS WO 0250269-A/4.
 SOURCE synthetic construct
 ORGANISM synthetic construct
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Matsumoto,Y., Imai,Y., Oshida,T., Sugita,Y., Nagasu,T. and

Tsujimoto,G.
 TITLE Method of examining allergic disease
 JOURNAL Patent: WO 0250269-A 4 27-JUN-2002;
 GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
 NATIONAL CHILDREN'S HOSPITAL, MASAMICHI TAKAGI, AKINORI OTA YOSHIKO
 MATSUMOTO, YUKIHO IMAI, TADAHIRO OSHIDA, YUJI SUGITA, TAKESHI NAGASU,
 GOZO TSUJIMOTO
 OS Artificial Sequence
 PN WO 0250269-A/4
 PD 27-JUN-2002
 PF 21-DEC-2001 WO 2001JP011286
 PR 21-DEC-2000 JP 00P 389476
 PI YOSHIKO MATSUMOTO, YUKIHO IMAI, TADAHIRO OSHIDA, YUJI SUGITA, PI
 TAKESHI NAGASU,
 PI GOZO TSUJIMOTO
 PC C12N15/11, C07K16/18, A61K67/027, A61K31/711, A61K45/00, A61K48/00,
 PC A61P37/08,
 PC C12Q1/68, G01N33/50
 CC Description of Artificial Sequence:'GT15C', an artificially
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 CC primer sequence
 CC key Location/Qualifiers
 FH source 1..17
 FT /organism='Artificial Sequence'.
 FT Location/Qualifiers
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 /organism="synthetic construct"
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Query Match	Sequence 76 from patent US 5861244.	0.9%; Score 14; DB 1; Length 14;	
Best Local Similarity	AR029887	100.0%; Pred. No. 1.2e+02;	
Matches	AR029887.1 GI:5943101	0; Mismatches 0; Indels 0; Gaps 0;	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 14)		
AUTHORS	Wang, C.-G. and Hepburn, A.G.		
TITLE	Genetic sequence assay using DNA triple strand formation		
JOURNAL	Patent: US 5861244-A 76 19-JAN-1999;		
JOURNAL	Location/Qualifiers		
FEATURES	1..14		
source	/organism="unknown"		
	/mol_type="unassigned DNA"		
Query Match	0.9%; Score 14; DB 1; Length 14;		
Best Local Similarity	100.0%; Pred. No. 1.2e+02;		
Matches	14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1481 AAAAAAAAAAAAAA 1494		
Db	14 AAAAAAAAAAAAAA 1		
RESULT 240			
AR147961/c			
LOCUS	AR147961	14 bp DNA linear	PAT 08-AUG-2001
DEFINITION	Sequence 130 from patent US 6225054.		
ACCESSION	AR147961		
VERSION	AR147961.1 GI:15112051		
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 14)		
AUTHORS	Frudakis, T.N., Smith, J.M. and Reed, S.G.		
TITLE	Compositions and methods for the treatment and diagnosis of breast cancer		
JOURNAL	Patent: US 6225054-A 130 01-MAY-2001;		
JOURNAL	Location/Qualifiers		
FEATURES	1..14		
source	/organism="unknown"		
	/mol_type="unassigned DNA"		
Query Match	0.9%; Score 14; DB 1; Length 14;		
Best Local Similarity	100.0%; Pred. No. 1.2e+02;		
Matches	14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1479 CTAATAAAAAAAAAA 1492		
Db	14 CTAATAAAAAAAAAA 1		
RESULT 241			
AR174026/c			
LOCUS	AR174026	14 bp DNA linear	PAT 17-DEC-2001
DEFINITION	Sequence 16 from patent US 6306624.		
ACCESSION	AR174026		
VERSION	AR174026.1 GI:17914346		
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 14)		
AUTHORS	Petrovich, P. Martin., White, J.A., Beckett, B.R. and Jones, G.		
TITLE	Retinoid metabolizing protein		
JOURNAL	Patent: US 6306624-A 16 23-OCT-2001;		
JOURNAL	Location/Qualifiers		
FEATURES	1..14		
source	/organism="unknown"		
	/mol_type="unassigned DNA"		

artificial sequences.
1 (bases 1 to 14)
Dale,R.M.K., Gattton,S.L. and Arrow,A.
Nucleic acid having blocked terminals modified with an acid-stable
skeleton and therapeutic method thereof
JOURNAL OLIGOS FTC INC
COMMENT OS Artificial Sequence
PN JP 2002534434-A/2
PD 15-OCT-2002
PF 16-DEC-1999 JP 2000592300
PR 30-DEC-1998 US 09/223498,19-JUL-1999 US 09/356069 PT
RODERIC M K DALE,STEVEN L GATTTON,AMY ARROW
PC C07H21/00,A61K9/127,A61K9/50,A61K31/7088,A61K47/44,A61K48/00,
PC A61P3/00,
PC A61P17/02,A61P29/00,A61P31/04,A61P31/10,A61P31/12,A61P35/00,
PC C12N5/10,
PC C12N15/09,C12N15/00,C12N5/00
CC Nucleic acid having blocked terminals modified with an acid-
stable
CC skeleton and therapeutic method thereof
FH Key Location/Qualifiers
FT source 1..14
FT Location/Qualifiers
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
|||||
Db 1 AAAAAAAAAAAAAA 14

RESULT 244
AR219685/c
LOCUS AR219685 14 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 130 from patent US 6423496.
ACCESSION AR219685
VERSION AR219685.1 GI:23323863
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Frudakis,T.N., Smith,J.M. and Reed,S.G.
TITLE Compositions and methods for the treatment and diagnosis of breast cancer
JOURNAL Patent: US 6423496-A 130 23-JUL-2002;
FEATURES
source 1..14
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAATAAAAAAAAAA 1492
|||||
Db 14 CTAATAAAAAAAAAA 1

RESULT 245
AR222460
LOCUS AR222460 14 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 20 from patent US 6429300.
ACCESSION AR222460

VERSION AR222460.1 GI:23329991
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Kurz,M., Lohse,P. and Wagner,R.
TITLE Peptide acceptor ligation methods
JOURNAL Patent: US 6429300-A 20 06-AUG-2002;
FEATURES
source 1..14
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
|||||
Db 1 AAAAAAAAAAAAAA 14

RESULT 246
AR225431/c
LOCUS AR225431 14 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 47 from patent US 6444425.
ACCESSION AR225431
VERSION AR225431.1 GI:27263377
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Reed,S.G., Lodes,M.J., Mohanath,R. and Secrist,H.
TITLE Compounds for therapy and diagnosis of lung cancer and methods for their use
JOURNAL Patent: US 6444425-A 47 03-SEP-2002;
FEATURES
source 1..14
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAATAAAAAAAAAA 1492
|||||
Db 14 CTAATAAAAAAAAAA 1

RESULT 247
AR350783/c
LOCUS AR350783 14 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 130 from patent US 6586570.
ACCESSION AR350783
VERSION AR350783.1 GI:33752423
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Frudakis,T.N., Reed,S.G., Smith,J.M. and Misher,L.
TITLE Compositions and methods for the treatment and diagnosis of breast cancer
JOURNAL Patent: US 6586570-A 130 01-JUL-2003;
FEATURES
source 1..14
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/mol_type="genomic DNA"

Query Match 0.9%; Score 14; DB 1; Length 14;

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Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAATAAAAAAAAAA 1492
DB 14 CTAATAAAAAAAAAA 1

RESULT 248
LOCUS AR364948 14 bp DNA PAT 03-SEP-2003
DEFINITION Sequence 4 from patent US 5453496.
ACCESSION AR364948
VERSION AR364948.1 GI:34428168
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 14)
AUTHORS Caruthers,M.H., Marshall,W.S., Brill,W. and Nielsen,J.
TITLE Polynucleotide phosphorodithioate
JOURNAL Patent: US 5453496-A 4 26-SEP-1995;
FEATURES
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        Location/Qualifiers
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                /organism="unknown"
                /mol_type="genomic DNA"

Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
DB 14 AAAAAAAAAAAAAA 1

RESULT 249
LOCUS AR364949 14 bp DNA PAT 03-SEP-2003
DEFINITION Sequence 5 from patent US 5453496.
ACCESSION AR364949
VERSION AR364949.1 GI:34428169
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 14)
AUTHORS Caruthers,M.H., Marshall,W.S., Brill,W. and Nielsen,J.
TITLE Polynucleotide phosphorodithioate
JOURNAL Patent: US 5453496-A 5 26-SEP-1995;
FEATURES
    source
        Location/Qualifiers
            1..14
                /organism="unknown"
                /mol_type="genomic DNA"

Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
DB 14 AAAAAAAAAAAAAA 1

RESULT 250
LOCUS AR433159/c 14 bp DNA PAT 18-DEC-2003
DEFINITION Sequence 130 from patent US 6656480.
ACCESSION AR433159
VERSION AR433159.1 GI:40195941
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 14)
AUTHORS Frudakis,T.N., Reed,S.G., Smith,J.M., Misher,L.E., Dillon,D.C.,
        Retter,M.W., Wang,A., Skeiky,Y.A., Harlocker,S.L. and Day,C.H.
TITLE Compositions and methods for the therapy and diagnosis of breast
        cancer
JOURNAL Patent: WO 0190152-A 130 29-NOV-2001;
FEATURES
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        Location/Qualifiers
            1..14
                /organism="synthetic construct"
                /mol_type="unassigned DNA"

Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
DB 14 AAAAAAAAAAAAAA 1

RESULT 252
LOCUS AX316793/c 14 bp DNA PAT 14-DEC-2001
DEFINITION Sequence 130 from Patent WO0190152.
ACCESSION AX316793
VERSION AX316793.1 GI:17899884
KEYWORDS
SOURCE synthetic construct
        synthetic construct
        artificial sequences.
ORGANISM
REFERENCE 1
AUTHORS Frudakis,T.N., Reed,S.G., Smith,J.M., Misher,L.E., Dillon,D.C.,
        Retter,M.W., Wang,A., Skeiky,Y.A., Harlocker,S.L. and Day,C.H.
TITLE Compositions and methods for the therapy and diagnosis of breast
        cancer
JOURNAL Patent: WO 0190152-A 130 29-NOV-2001;
FEATURES
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        Location/Qualifiers
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                /mol_type="unassigned DNA"

Unclassified.
1 (bases 1 to 14)
Retter,M.W. and Dillon,D.C.
Compositions and methods for the treatment and diagnosis of breast
cancer
Patent: US 6656480-A 130 02-DEC-2003;
FEATURES
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        Location/Qualifiers
            1..14
                /organism="unknown"
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Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAATAAAAAAAAAA 1492
DB 14 CTAATAAAAAAAAAA 1

RESULT 251
LOCUS AX048406/c 14 bp DNA PAT 12-JAN-2001
DEFINITION Sequence 5 from Patent WO0071747.
ACCESSION AX048406
VERSION AX048406.1 GI:12225570
KEYWORDS
SOURCE synthetic construct
        synthetic construct
        artificial sequences.
ORGANISM
REFERENCE 1
AUTHORS Boenkamp,D., Hoppe,H.U. and Bургstaller,P.
TITLE Detection system for separating constituents of a sample and
        production and use of the same
JOURNAL Patent: WO 0071747-A 5 30-NOV-2000;
FEATURES
    source
        Location/Qualifiers
            1..14
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Region A"

Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
DB 14 AAAAAAAAAAAAAA 1

RESULT 252
LOCUS AX316793 14 bp DNA PAT 14-DEC-2001
DEFINITION Sequence 130 from Patent WO0190152.
ACCESSION AX316793
VERSION AX316793.1 GI:17899884
KEYWORDS
SOURCE synthetic construct
        synthetic construct
        artificial sequences.
ORGANISM
REFERENCE 1
AUTHORS Frudakis,T.N., Reed,S.G., Smith,J.M., Misher,L.E., Dillon,D.C.,
        Retter,M.W., Wang,A., Skeiky,Y.A., Harlocker,S.L. and Day,C.H.
TITLE Compositions and methods for the therapy and diagnosis of breast
        cancer
JOURNAL Patent: WO 0190152-A 130 29-NOV-2001;
FEATURES
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        Location/Qualifiers
            1..14
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/db_xref="taxon:32630"
/notes="Primer"

Query Match      0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAATAAAAAAAAAA 1492
Db 14 CTAATAAAAAAAAAA 1

RESULT 253
AX321516/c
LOCUS      14 bp DNA linear PAT 15-DEC-2001
DEFINITION Sequence 47 from Patent WO0172295.
ACCESSION  AX321516
VERSION     AX321516.1 GI:17905576
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE      Reed,S.G., Lodes,M.J., Mohamath,R., Secrist,H., Benson,D.R.,
          Indrias,C.Y., Henderson,R.A., Fling,S.P., Algate,P.A., Elliot,M.,
          Mannion,J. and Kalos,M.D.
          Compositions and methods for the therapy and diagnosis of lung
          cancer
JOURNAL    Patent: WO 0172295-A 47 04-OCT-2001;
          CORIXA CORPORATION (US)
FEATURES   source
            1..14
            Location/Qualifiers
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              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAATAAAAAAAAAA 1492
Db 14 CTAATAAAAAAAAAA 1

RESULT 254
AX642209/c
LOCUS      14 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 27 from Patent WO2061082.
ACCESSION  AX642209
VERSION     AX642209.1 GI:28474657
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1
AUTHORS    Day,R.
TITLE      Zis-sr nucleic acid and amino acid sequences involved in the
          regulated secretory pathway and/or the regulation of the
          neuroendocrine phenotype (nep)
JOURNAL    Patent: WO 02061082-A 27 08-AUG-2002;
          Universite de Sherbrooke (CA)
FEATURES   source
            1..14
            Location/Qualifiers
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="Oligonucleotide"

Query Match      0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAATAAAAAAAAAA 1492
Db 14 CTAATAAAAAAAAAA 1

RESULT 255
AX59631/c
LOCUS      14 bp DNA linear PAT 03-APR-2003
DEFINITION Sequence 25 from Patent WO02103014.
ACCESSION  AX59631
VERSION     AX59631.1 GI:29161813
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1
AUTHORS    Al-Mahmood,S.
TITLE      Antisense oligonucleotides which can inhibit the formation of
          capillary tubes by endothelial cells
JOURNAL    Patent: WO 02103014-A 25 27-DEC-2002;
          Al-Mahmood, Salman (FR)
FEATURES   source
            1..14
            Location/Qualifiers
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              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="Oligonucleotide anti-sens."

Query Match      0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAATAAAAAAAAAA 1492
Db 14 CTAATAAAAAAAAAA 1

RESULT 256
AX827014
LOCUS      14 bp RNA linear PAT 12-DEC-2003
DEFINITION Sequence 11 from Patent EP1344835.
ACCESSION  AX827014
VERSION     AX827014.1 GI:39837221
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1
AUTHORS    Rabbani,E., Stavrianopoulos,J.G., Donegan,J.J., Coleman,J. and
          Liu,D.
TITLE      Real-time nucleic acid detection processes and compositions
JOURNAL    Patent: EP 1344835-A 11 17-SEP-2003;
          Enzo Life Sciences, Inc. (US)
FEATURES   source
            1..14
            Location/Qualifiers
              /organism="synthetic construct"
              /mol_type="unassigned RNA"
              /db_xref="taxon:32630"
              /note="Description of Artificial Sequence: Primer"

Query Match      0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 1 AAAAAAAAAAAAAA 14

RESULT 257
AX839906
LOCUS      14 bp RNA linear PAT 16-DEC-2003

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DEFINITION Sequence 11 from Patent EP1348713.
ACCESSION AX839906
VERSION AX839906.1 GI:39978437
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Stavrianopoulos,J.G. and Rabbani,E.
TITLE Labeling reagents and labeled targets, target labeling
        processes and other processes for using same in nucleic acid
        determinations and analyses
JOURNAL Patent: EP 1348713-A 11 01-OCT-2003;
        Enzo Life Sciences, Inc. (US)
FEATURES
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        /organism="synthetic construct"
        /mol_type="unassigned RNA"
        /db_xref="taxon:32630"
        /note="Description of Artificial Sequence: Primer"
Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1494
Db 1 AAAAAAAAAAAAAA 14

RESULT 258
BD073883/c
LOCUS BD073883 14 bp DNA linear PAT 27-AUG-2002
DEFINITION Isolation of novel aging factor gene P23.
ACCESSION BD073883
VERSION BD073883.1 GI:22619486
KEYWORDS JP 2001512698-A/8.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 14)
AUTHORS Suishelm,K., Hosier,S. and Kubbies,M.
TITLE Isolation of novel aging factor gene P23
JOURNAL Patent: JP 2001512698-A 8 28-AUG-2001;
        UNIVERSITY OF WASHINGTON
COMMENT OS Unidentified
        PN JP 2001512698-A/8
        PD 28-AUG-2001
        PF 05-AUG-1998 JP 2000506375
        PR 08-AUG-1997 US 08/908873
        PI KAREN SUISHELM,SUZANNE HOSIER,MANFRED KUBBIES PC
        C12Q1/68,C07K14/435,C07K16/18,C12N1/15,C12N1/19,C12N15/09, PC
        C12P21/02,
        PC C12P21/08,C12N15/00
        CC Strandedness: Single;
        CC Topology: Linear;
        CC Isolation of novel aging factor gene P23
        FH Key Location/Qualifiers
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        FT /organism='Unidentified'.
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        /mol_type="genomic DNA"
        /db_xref="taxon:32644"
Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1479 CTAATAAAAAAAAAA 1492
Db 14 CTAATAAAAAAAAAA 1

RESULT 259
BD084127
LOCUS BD084127 14 bp DNA linear PAT 27-AUG-2002
DEFINITION Polymorphisms and new genes in the region of the human
        hemochromatosis gene.
ACCESSION BD084127
VERSION BD084127.1 GI:22629737
KEYWORDS JP 2001525663-A/15.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 14)
AUTHORS Feder,J.N., Kronmal,G.S., Lauer,P.M., Ruddy,D.A., Thomas,W.J.,
        Tsuchihashi,Z. and Wolff,R.K.
TITLE Polymorphisms and new genes in the region of the human
        hemochromatosis gene
JOURNAL Patent: JP 2001525663-A 15 11-DEC-2001;
        PROGENITOR INC
COMMENT OS Homo sapiens (human)
        PN JP 2001525663-A/15
        PD 11-DEC-2001
        PF 30-SEP-1997 JP 1998516815
        PR 01-OCT-1996 US 08/724394,07-MAY-1997 US 08/852495 PI
        JOHN N FEDER,GREGORY S KRONMAL,PETER M LAUER,DAVID A RUDDY, PI
        WINSTON J THOMAS,ZENTA TSUCHIHASHI,ROGER K WOLFF PC
        C07H21/04,C12Q1/68,C12N15/63,C12N15/85,C12P21/02 CC Polymorphisms
        and new genes in the region of the human CC hemochromatosis gene
        FH Key Location/Qualifiers
        FT source 1..14
        FT /organism='Homo sapiens (human)'.
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        /mol_type="genomic DNA"
        /db_xref="taxon:9606"
Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1494
Db 1 AAAAAAAAAAAAAA 14

RESULT 260
BD084336/c
LOCUS BD084336 14 bp DNA linear PAT 27-AUG-2002
DEFINITION Compositions and methods for the treatment and diagnosis of breast
        cancer.
ACCESSION BD084336
VERSION BD084336.1 GI:22629946
KEYWORDS JP 2001521384-A/129.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 14)
AUTHORS Fridakis,T.N., Smith,J.M. and Reed,S.G.
TITLE Compositions and methods for the treatment and diagnosis of breast
        cancer
JOURNAL Patent: JP 2001521384-A 129 06-NOV-2001;
        CORIXA CORP
COMMENT OS Unidentified
        PN JP 2001521384-A/129
        PD 06-NOV-2001
        PF 09-APR-1998 JP 1998543059
        PR 09-APR-1997 US 08/838762,11-DEC-1997 US 08/991789 PI
        TONY N FRIDAKIS,JOHN M SMITH,STEVEN G REED
        PC C07K14/47,C07K14/82,C07K14/15,C12Q1/68,G01N33/574,A61K38/17,
        PC A61K39/00

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CC Strandedness: Single;
CC Topology: Linear;
CC Compositions and methods for the treatment and diagnosis of
CC breast cancer
FH Key Location/Qualifiers
FT source 1..14
FT Location/Qualifiers
FT /organism='Unidentified'.
FEATURES
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/db_xref='taxon:32644'
Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1479 CTAATAAAAAAAAAA 1492
Db 14 CTAATAAAAAAAAAA 1
RESULT 261
BD096963/c
LOCUS BD096963 14 bp DNA linear PAT 27-AUG-2002
DEFINITION Oligonucleotide for SNP detection.
ACCESSION BD096963
VERSION BD096963.1 GI:22642551
KEYWORDS JP 2001346579-A/2.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 14)
AUTHORS Komiya, M. and Asanuma, H.
TITLE Oligonucleotide for SNP detection
JOURNAL Patent: JP 2001346579-A 2 18-DEC-2001;
MAKOTO KOMIYAMA, HIROYUKI ASANUMA
COMMENT OS Artificial Sequence
PN JP 2001346579-A/2
PD 18-DEC-2001
PF 02-JUN-2000 JP 200165441
PI MAKOTO KOMIYAMA, HIROYUKI ASANUMA
PC C12N15/09, C12N15/09, C12Q1/68, G01N33/53, G01N33/566,
PC C12N15/00,
PC C12N15/00
CC Oligonucleotide for SNP detection
FH Key Location/Qualifiers
FT modified base 1.
FT Location/Qualifiers
FT 1..14
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'
Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 1
RESULT 262
BD096965/c
LOCUS BD096965 14 bp DNA linear PAT 27-AUG-2002
DEFINITION Oligonucleotide for SNP detection.
ACCESSION BD096965
VERSION BD096965.1 GI:22642553
KEYWORDS JP 2001346579-A/4.
SOURCE synthetic construct
ORGANISM artificial sequences.

```

```

REFERENCE 1 (bases 1 to 14)
AUTHORS Komiya, M. and Asanuma, H.
TITLE Oligonucleotide for SNP detection
JOURNAL Patent: JP 2001346579-A 4 18-DEC-2001;
MAKOTO KOMIYAMA, HIROYUKI ASANUMA
COMMENT OS Artificial Sequence
PN JP 2001346579-A/4
PD 18-DEC-2001
PF 02-JUN-2000 JP 200165441
PI MAKOTO KOMIYAMA, HIROYUKI ASANUMA
PC C12N15/09, C12N15/09, C12Q1/68, G01N33/53, G01N33/566,
PC C12N15/00,
PC C12N15/00
CC Oligonucleotide for SNP detection
FH Key Location/Qualifiers
FT modified base 1.
FT Location/Qualifiers
FT 1..14
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'
Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 1
RESULT 263
BD132850/c
LOCUS BD132850 14 bp DNA linear PAT 18-SEP-2002
DEFINITION Methods of nucleic acid detection.
ACCESSION BD132850
VERSION BD132850.1 GI:23227795
KEYWORDS JP 2002509443-A/1.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 14)
AUTHORS Weisburg, W.G., Stull, P.D. and Reshatoff, M.R.
TITLE Methods of nucleic acid detection
JOURNAL Patent: JP 2002509443-A 1 26-MAR-2002;
GEN PROBE INC
COMMENT OS Artificial Sequence
PN JP 2002509443-A/1
PD 26-MAR-2002
PF 30-OCT-1998 JP 1999526687
PR 31-OCT-1997 US 60/063969
PI WILLIAM G WEISBURG, PAUL D STULL, MICHAEL R RESHATOFF PC
C12Q1/68
CC Description of Artificial Sequence: synthetic oligonucleotide
FH Key Location/Qualifiers
FT modified base 1.
FT Location/Qualifiers
FT 1..14
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'
Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 1
RESULT 264
BD176795
LOCUS BD176795 14 bp DNA linear PAT 18-MAR-2003

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DEFINITION Method of constructing cDNA tag for identifying expressed gene and method of analyzing gene expression.

ACCESSION BD176795
VERSION BD176795.1 GI:29122507
KEYWORDS WO 02074951-A/42.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1 (bases 1 to 14)
AUTHORS Yamamoto,M., Yamamoto,N., Hirose,K. and Sakai,J.
TITLE Method of constructing cDNA tag for identifying expressed gene and method of analyzing gene expression
JOURNAL Patent: WO 02074951-A 42 26-SEP-2002;

KUREHA CHEMICAL INDUSTRY CO LTD,MIKIO YAMAMOTO,NAOKI YAMAMOTO,

KUNITAKA HIROSE,JUN SAKAI

OS Artificial Sequence

PN WO 02074951-A/42

PD 26-SEP-2002

PF 13-MAR-2002 WO 2002JP002338

PR 15-MAR-2001 JP 01P 073959

PI MIKIO YAMAMOTO,NAOKI YAMAMOTO,KUNITAKA HIROSE,JUN SAKAI PC

C12N15/09,C12Q1/68

CC Synthetic DNA

PH Key Location/Qualifiers

FT source 1..14

FT Location/Qualifiers

FT /organism='Artificial Sequence'.

1..14

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

Query Match 0.9%; Score 14; DB 1; Length 14;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

YQ 1481 AAAAAAAAAAAAAA 1494

|||||

1 AAAAAAAAAAAAAA 14

Db

RESULT 265

BD176801/c

LOCUS

DEFINITION 14 bp DNA linear PAT 18-MAR-2003

Method of constructing cDNA tag for identifying expressed gene and

method of analyzing gene expression.

ACCESSION BD176801

VERSION BD176801.1 GI:29122513

KEYWORDS WO 02074951-A/48.

SOURCE synthetic construct

ORGANISM synthetic construct

artificial sequences.

REFERENCE 1 (bases 1 to 14)

Yamamoto,M., Yamamoto,N., Hirose,K. and Sakai,J.

Method of constructing cDNA tag for identifying expressed gene and

method of analyzing gene expression

Patent: WO 02074951-A 48 26-SEP-2002;

KUREHA CHEMICAL INDUSTRY CO LTD,MIKIO YAMAMOTO,NAOKI YAMAMOTO,

KUNITAKA HIROSE,JUN SAKAI

OS Artificial Sequence

PN WO 02074951-A/48

PD 26-SEP-2002

PF 13-MAR-2002 WO 2002JP002338

PR 15-MAR-2001 JP 01P 073959

PI MIKIO YAMAMOTO,NAOKI YAMAMOTO,KUNITAKA HIROSE,JUN SAKAI PC

C12N15/09,C12Q1/68

CC Synthetic DNA

PH Key Location/Qualifiers

FT source 1..14

FT Location/Qualifiers

FT /organism='Artificial Sequence'.

1..14

/organism="synthetic construct"

source

/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.9%; Score 14; DB 1; Length 14;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAAA 1493

|||||

14 TAAAAAAAAAAAAA 1

Db

RESULT 266

BD176804/c

LOCUS

DEFINITION 14 bp DNA linear PAT 18-MAR-2003

Method of constructing cDNA tag for identifying expressed gene and

method of analyzing gene expression.

ACCESSION BD176804

VERSION BD176804.1 GI:29122516

KEYWORDS WO 02074951-A/51.

SOURCE synthetic construct

ORGANISM synthetic construct

artificial sequences.

REFERENCE 1 (bases 1 to 14)

Yamamoto,M., Yamamoto,N., Hirose,K. and Sakai,J.

Method of constructing cDNA tag for identifying expressed gene and

method of analyzing gene expression

Patent: WO 02074951-A 51 26-SEP-2002;

KUREHA CHEMICAL INDUSTRY CO LTD,MIKIO YAMAMOTO,NAOKI YAMAMOTO,

KUNITAKA HIROSE,JUN SAKAI

OS Artificial Sequence

PN WO 02074951-A/51

PD 26-SEP-2002

PF 13-MAR-2002 WO 2002JP002338

PR 15-MAR-2001 JP 01P 073959

PI MIKIO YAMAMOTO,NAOKI YAMAMOTO,KUNITAKA HIROSE,JUN SAKAI PC

C12N15/09,C12Q1/68

CC Synthetic DNA

PH Key Location/Qualifiers

FT source 1..14

FT Location/Qualifiers

FT /organism='Artificial Sequence'.

1..14

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

Query Match 0.9%; Score 14; DB 1; Length 14;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494

|||||

14 AAAAAAAAAAAAAA 1

Db

RESULT 267

AR056156/c

LOCUS

DEFINITION 15 bp DNA linear PAT 29-SEP-1999

Sequence 360 from patent US 5837542.

ACCESSION AR056156

VERSION AR056156.1 GI:5981733

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 15)

Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and

Draper,K.G.

Intercellular adhesion molecule-1 (ICAM-1) ribozymes

Patent: US 5837542-A 360 17-NOV-1998;

Location/Qualifiers

1..15

source

/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.9%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
|||||
Db 15 AAAAAAAAAAAAAA 2

RESULT 268
AR056159/c
LOCUS AR056159 15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 363 from patent US 5837542.
ACCESSION AR056159
VERSION AR056159.1 GI:5981736
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes
JOURNAL Patent: US 5837542-A 363 17-NOV-1998;
FEATURES Location/Qualifiers
source 1..15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.9%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
|||||
Db 14 AAAAAAAAAAAAAA 1

RESULT 269
AR113914/c
LOCUS AR113914 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 360 from patent US 6132967.
ACCESSION AR113914
VERSION AR113914.1 GI:14094236
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)
JOURNAL Patent: US 6132967-A 360 17-OCT-2000;
FEATURES Location/Qualifiers
source 1..15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.9%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
|||||
Db 15 AAAAAAAAAAAAAA 2

RESULT 270
AR113917/c

LOCUS AR113917 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 363 from patent US 6132967.
ACCESSION AR113917
VERSION AR113917.1 GI:14094239
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)
JOURNAL Patent: US 6132967-A 363 17-OCT-2000;
FEATURES Location/Qualifiers
source 1..15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.9%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
|||||
Db 14 AAAAAAAAAAAAAA 1

RESULT 271
I29065
LOCUS I29065 15 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 3 from patent US 5576427.
ACCESSION I29065
VERSION I29065.1 GI:1819856
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Cook,P.D., Delecki,D.J. and Guinosso,C.
TITLE Acyclic nucleoside analogs and oligonucleotide sequences containing them
JOURNAL Patent: US 5576427-A 3 19-NOV-1996;
FEATURES Location/Qualifiers
source 1..15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.9%; Score 14; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
|||||
Db 1 AAAAAAAAAAAAAA 15

RESULT 272
I29066
LOCUS I29066 15 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 4 from patent US 5576427.
ACCESSION I29066
VERSION I29066.1 GI:1819857
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Cook,P.D., Delecki,D.J. and Guinosso,C.
TITLE Acyclic nucleoside analogs and oligonucleotide sequences containing them
JOURNAL Patent: US 5576427-A 4 19-NOV-1996;
FEATURES Location/Qualifiers

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source      1..15
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      0.9%; Score 14; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
    |||||
Db 1 AAAAAAAAAAAAAA 15

RESULT 273
AR241870/c
LOCUS      AR241870      15 bp      DNA      linear      PAT 20-DEC-2002
DEFINITION Sequence 158 from patent US 6472154.
ACCESSION  AR241870
VERSION     AR241870.1 GI:27287682
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 15)
AUTHORS    Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
TITLE      Polymorphic repeats in human Genes
JOURNAL    Patent: US 6472154-A 158 29-OCT-2002;
FEATURES    Location/Qualifiers
            source
            1..15
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      0.9%; Score 14; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
    |||||
Db 15 AAAAAAAAAAAAAA 1

RESULT 274
AX633195/c
LOCUS      AX633195      15 bp      RNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 334 from Patent EP1260586.
ACCESSION  AX633195
VERSION     AX633195.1 GI:28468809
KEYWORDS    .
SOURCE      unidentified
            unidentified
            unclassified.
REFERENCE   1
AUTHORS     Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
            Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
            Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
            Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
            Woolf,T.
TITLE      Method and reagent for inhibiting the expression of disease related
            genes
JOURNAL    Patent: EP 1260586-A 334 27-NOV-2002;
            RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES    Location/Qualifiers
            source
            1..15
            /organism="unidentified"
            /mol_type="unassigned RNA"
            /db_xref="taxon:32644"

Query Match      0.9%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
    |||||
Db 14 AAAAAAAAAAAAAA 1

RESULT 276
AR002257/c
LOCUS      AR002257      16 bp      DNA      linear      PAT 04-DEC-1998
DEFINITION Sequence 6 from patent US 5741643.
ACCESSION  AR002257
VERSION     AR002257.1 GI:3963811
KEYWORDS    .
SOURCE      Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 16)
AUTHORS     Gryaznov,S.M. and Lloyd,D.H.
TITLE      Oligonucleotide clamps
JOURNAL    Patent: US 5741643-A 6 21-APR-1998;
            RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES    Location/Qualifiers
            source
            1..16
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      0.9%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
    |||||
Db 16 AAAAAAAAAAAAAA 3

RESULT 277
AR045207/c
LOCUS      AR045207      16 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 6 from patent US 5817795.
ACCESSION  AR045207
VERSION     AR045207.1 GI:5966672
KEYWORDS    .

source      1..15
            /organism="unidentified"
            /mol_type="unassigned RNA"
            /db_xref="taxon:32644"

Query Match      0.9%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
    |||||
Db 14 AAAAAAAAAAAAAA 1
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SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Gryaznov, S.M. and Lloyd, D.H.
TITLE Oligonucleotide clamps having diagnostic and therapeutic applications
JOURNAL Patent: US 5817795-A 6 06-OCT-1998;
FEATURES Location/Qualifiers
source 1..16
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.9%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 16 AAAAAAAAAAAAAA 3

RESULT 278
LOCUS AR051238/c 16 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 6 from patent US 5830658.
ACCESSION AR051238
VERSION AR051238.1 GI:5974602
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Gryaznov, S.M.
TITLE Convergent synthesis of branched and multiply connected macromolecular structures
JOURNAL Patent: US 5830658-A 6 03-NOV-1998;
FEATURES Location/Qualifiers
source 1..16
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.9%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 16 AAAAAAAAAAAAAA 3

RESULT 279
LOCUS I16032/c 16 bp DNA linear PAT 03-APR-1996
DEFINITION Sequence 6 from patent US 5473060.
ACCESSION I16032
VERSION I16032.1 GI:1250940
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Gryaznov, S.M. and Lloyd, D.H.
TITLE Oligonucleotide clamps having diagnostic applications
JOURNAL Patent: US 5473060-A 6 05-DEC-1995;
FEATURES Location/Qualifiers
source 1..16
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.9%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 16 AAAAAAAAAAAAAA 3

RESULT 280
LOCUS I28367/c 16 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 6 from patent US 5571677.
ACCESSION I28367
VERSION I28367.1 GI:1819143
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Gryaznov, S.M.
TITLE Convergent synthesis of branched and multiply connected macromolecular structures
JOURNAL Patent: US 5571677-A 6 05-NOV-1996;
FEATURES Location/Qualifiers
source 1..16
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.9%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 16 AAAAAAAAAAAAAA 3

RESULT 281
LOCUS AX359760 16 bp DNA linear PAT 13-FEB-2002
DEFINITION Sequence 64 from Patent WO200691.
ACCESSION AX359760
VERSION AX359760.1 GI:18675467
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Vernet, C.A., Tchernev, V., Putturajan, M., Malyankar, U.M., Gusev, V., Herrmann, J.L., Macdougall, J.R., Rastelli, L., Zhong, H., Shenoy, S., Gerlach, V.L., Gangolli, E.A., Stone, D.J. and Smithson, G.
TITLE Novel polynucleotides and polypeptides encoded thereby
JOURNAL Patent: WO 0200691-A 64 03-JAN-2002;
FEATURES Location/Qualifiers
source 1..16
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.9%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 16 AAAAAAAAAAAAAA 14

RESULT 282
LOCUS A12730/c 15 bp DNA linear PAT 29-SEP-1994
DEFINITION Oligonucleotide.
ACCESSION A12730

QY 1481 AAAAAAAAAAAAAA 1494
Db 16 AAAAAAAAAAAAAA 3

RESULT 280
LOCUS I28367/c 16 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 6 from patent US 5571677.
ACCESSION I28367
VERSION I28367.1 GI:1819143
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Gryaznov, S.M.
TITLE Convergent synthesis of branched and multiply connected macromolecular structures
JOURNAL Patent: US 5571677-A 6 05-NOV-1996;
FEATURES Location/Qualifiers
source 1..16
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.9%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 16 AAAAAAAAAAAAAA 3

RESULT 281
LOCUS AX359760 16 bp DNA linear PAT 13-FEB-2002
DEFINITION Sequence 64 from Patent WO200691.
ACCESSION AX359760
VERSION AX359760.1 GI:18675467
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Vernet, C.A., Tchernev, V., Putturajan, M., Malyankar, U.M., Gusev, V., Herrmann, J.L., Macdougall, J.R., Rastelli, L., Zhong, H., Shenoy, S., Gerlach, V.L., Gangolli, E.A., Stone, D.J. and Smithson, G.
TITLE Novel polynucleotides and polypeptides encoded thereby
JOURNAL Patent: WO 0200691-A 64 03-JAN-2002;
FEATURES Location/Qualifiers
source 1..16
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.9%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db 16 AAAAAAAAAAAAAA 14

RESULT 282
LOCUS A12730/c 15 bp DNA linear PAT 29-SEP-1994
DEFINITION Oligonucleotide.
ACCESSION A12730

VERSION A12730.1 GI:640594
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 15)
AUTHORS PRODUCTION OF HUMAN SOMATOMEDIN C
TITLE PATENT: WO 8605810-A 9 09-OCT-1986;
JOURNAL
FEATURES Location/Qualifiers
source
1. .15
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 0.9%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1034 ATATAACGTTTCGG 1048
Db 15 ACATAACGTTTCGG 1

RESULT 283
A25390/c
LOCUS A25390 15 bp DNA linear PAT 03-MAR-1995
DEFINITION Oligonucleotide.
ACCESSION A25390
VERSION A25390.1 GI:833580
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 15)
AUTHORS
TITLE METHOD FOR SELECTING RECOMBINANT MICRO-ORGANISMS OF WHICH THE
JOURNAL SURFACE COMPRISES AT LEAST ONE MOLECULE HAVING ENZYMIC ACTIVITY
FEATURES Patent: WO 9311242-A 4 10-JUN-1993;
source Location/Qualifiers
1. .15
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 0.9%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 298 CTTCTGGCTGGCTGG 312
Db 15 CTTCCGGCTGGCTGG 1

RESULT 284
AR041957
LOCUS AR041957 15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 747 from patent US 5811300.
ACCESSION AR041957
VERSION AR041957.1 GI:5962453
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Sullivan, S., Draper, K., Kisich, K., Stinchcomb, D.T. and McSwiggen, J.
TITLE TNF- α ribozymes
JOURNAL Patent: US 5811300-A 747 22-SEP-1998;
FEATURES Location/Qualifiers
source
1. .15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.9%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1334 ACCTTGTTCCCTCCT 1348
Db 1 ACCTTGTTCCCTCCT 15

RESULT 285
AR056160/c
LOCUS AR056160 15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 364 from patent US 5837542.
ACCESSION AR056160
VERSION AR056160.1 GI:5981737
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Grimm, S., Stinchcomb, D.T., McSwiggen, J., Sullivan, S. and
TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes
JOURNAL Patent: US 5837542-A 364 17-NOV-1998;
FEATURES Location/Qualifiers
source
1. .15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.9%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAAA 1494
Db 15 TGAATAAAAAAATAAAAA 1

RESULT 286
AR056161/c
LOCUS AR056161 15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 365 from patent US 5837542.
ACCESSION AR056161
VERSION AR056161.1 GI:5981738
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Grimm, S., Stinchcomb, D.T., McSwiggen, J., Sullivan, S. and
TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes
JOURNAL Patent: US 5837542-A 365 17-NOV-1998;
FEATURES Location/Qualifiers
source
1. .15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.9%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1479 CTAAAAAATAAAAAA 1493
Db 15 CTGAAAAAATAAAAAA 1

RESULT 287
AR084518
LOCUS AR084518 15 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 7 from patent US 5981185.
ACCESSION AR084518
VERSION AR084518.1 GI:10011289

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
TITLE Oligonucleotide repeat arrays
JOURNAL Patent: US 5981185-A 7-09-NOV-1999;
FEATURES
source
Location/Qualifiers
1. .15
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.9%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
DB 1 AAAAAAAAAAAAAA 15

RESULT 288
LOCUS AR084532 15 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 21 from patent US 5981185.
ACCESSION AR084532
VERSION AR084532.1 GI:10011303
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
TITLE Oligonucleotide repeat arrays
JOURNAL Patent: US 5981185-A 21-09-NOV-1999;
FEATURES
source
Location/Qualifiers
1. .15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.9%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1479 CTAATAAAAAAAAAA 1493
DB 15 CTAATAAAAAAAAAA 1

RESULT 291
LOCUS BD244856 15 bp DNA linear PAT 17-JUL-2003
DEFINITION Oligonucleotide primer capable of making the non-specific double strand formation unstable.
ACCESSION BD244856
VERSION BD244856.1 GI:33054626
KEYWORDS JP 2002532063-A/1.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 15)
AUTHORS Pelletier,J. and Das,M.
TITLE Oligonucleotide primer capable of making the non-specific double strand formation unstable
JOURNAL Patent: JP 2002532063-A 1 02-OCT-2002;
COMMENT MCGILL UNIVERSITY
OS Artificial Sequence
FN JP 2002532063-A/1
PD 02-OCT-2002
PF 06-OCT-1999 JP 2000574722
PR 07-OCT-1998 CA 2246623
PI JERRY PELLETIER,MANJULA DAS
PC C12N15/09,C12Q1/68,C12N15/00
FH Description of Artificial Sequence: synthetic oligonucleotide
CC Key Location/Qualifiers
FT source 1. .15
FEATURES
source
Location/Qualifiers
1. .15
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.9%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.8e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAAA 1494
DB 15 TAAAAAAAAAAAAA 1

RESULT 290
LOCUS AR113919/c 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 365 from patent US 6132967.
ACCESSION AR113919
VERSION AR113919.1 GI:14094241
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)
JOURNAL Patent: US 6132967-A 365 17-OCT-2000;
FEATURES
source
Location/Qualifiers
1. .15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.9%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1479 CTAATAAAAAAAAAA 1493
DB 15 CTAATAAAAAAAAAA 1

RESULT 291
LOCUS BD244856 15 bp DNA linear PAT 17-JUL-2003
DEFINITION Oligonucleotide primer capable of making the non-specific double strand formation unstable.
ACCESSION BD244856
VERSION BD244856.1 GI:33054626
KEYWORDS JP 2002532063-A/1.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 15)
AUTHORS Pelletier,J. and Das,M.
TITLE Oligonucleotide primer capable of making the non-specific double strand formation unstable
JOURNAL Patent: JP 2002532063-A 1 02-OCT-2002;
COMMENT MCGILL UNIVERSITY
OS Artificial Sequence
FN JP 2002532063-A/1
PD 02-OCT-2002
PF 06-OCT-1999 JP 2000574722
PR 07-OCT-1998 CA 2246623
PI JERRY PELLETIER,MANJULA DAS
PC C12N15/09,C12Q1/68,C12N15/00
FH Description of Artificial Sequence: synthetic oligonucleotide
CC Key Location/Qualifiers
FT source 1. .15
FEATURES
source
Location/Qualifiers
1. .15
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.9%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.8e+02;

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Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 1 AAAAAAAAAAAAAA 15

RESULT 292
AR241876/c
LOCUS AR241876 15 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 164 from patent US 6472154.
ACCESSION AR241876
VERSION AR241876.1 GI:27287688
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
TITLE Polymorphic repeats in human genes
JOURNAL Patent: US 6472154-A 164 29-OCT-2002;
FEATURES
    Location/Qualifiers
    source 1..15
    /organism="unknown"
    /mol_type="genomic DNA"

Query Match 0.9%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 293
AR278935
LOCUS AR278935 15 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 13 from patent US 6514693.
ACCESSION AR278935
VERSION AR278935.1 GI:29713578
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Lansdorp,P.
TITLE Method for detecting multiple copies of a repeat sequence in a
JOURNAL Patent: US 6514693-A 13 04-FEB-2003;
FEATURES
    Location/Qualifiers
    source 1..15
    /organism="unknown"
    /mol_type="genomic DNA"

Query Match 0.9%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 26 GGCGGCGCGCGCGC 40
Db 1 GGCGGCGCGCGCGC 15

RESULT 294
AX633203/c
LOCUS AX633203 15 bp RNA linear PAT 21-FEB-2003
DEFINITION Sequence 342 from Patent EP1260586.
ACCESSION AX633203
VERSION AX633203.1 GI:28468817
KEYWORDS
SOURCE unidentified
ORGANISM unidentified

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 1 AAAAAAAAAAAAAA 15

RESULT 295
AX633205/c
LOCUS AX633205 15 bp RNA linear PAT 21-FEB-2003
DEFINITION Sequence 344 from Patent EP1260586.
ACCESSION AX633205
VERSION AX633205.1 GI:28468819
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
Unclassified.
REFERENCE 1
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
Mcswiggen,J.A., Modak,A., Favco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Woolf,T.
TITLE Method and reagent for inhibiting the expression of disease related
JOURNAL Patent: EP 1260586-A 344 27-NOV-2002;
FEATURES
    Location/Qualifiers
    source 1..15
    /organism="unidentified"
    /mol_type="unassigned RNA"
    /db_xref="taxon:32644"

Query Match 0.9%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAAA 1494
Db 15 TAAAAAAAAAAAAA 1

RESULT 296
AX637368
LOCUS AX637368 15 bp RNA linear PAT 21-FEB-2003
DEFINITION Sequence 4507 from Patent EP1260586.
ACCESSION AX637368
VERSION AX637368.1 GI:28472982
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
Unclassified.
REFERENCE 1
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
```

Karpisky, A., Draper, K.G., Kisich, K., Matulic-Adamic, J.,
McSwiggen, J.A., Modak, A., Pavco, P., Beigelman, L., Sullivan, S.M.,
Sweedler, D., Thompson, J.D., Tracz, D., Usman, N., Wincott, F.E. and
Wolfe, T.

TITLE Method and reagent for inhibiting the expression of disease related

Genes

Patent: EP 1260586-A 4507 27-NOV-2002;

RIBOZYME PHARMACEUTICALS, INC. (US)

Location/Qualifiers

1. 15

/organism="unidentified"

/mol_type="unassigned RNA"

/db_xref="taxon:32644"

Query Match 0.9%; Score 13.4; DB 1; Length 15;

Best Local Similarity 93.3%; Pred. No. 1.8e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1334 ACCTGTTCCCTCCT 1348

Db 1 ACCTGTTGCTCCT 15

RESULT 297

A52267/c

LOCUS

DEFINITION 14 bp DNA linear PAT 12-DEC-1997

ACCESSION Sequence 57 from Patent EP0705842.

VERSION A52267

KEYWORDS A52267.1 GI:2852045

SOURCE unidentified

ORGANISM unclassified.

REFERENCE 1

AUTHORS Bartnik, E.D. and Margerie, D.D.

TITLE Regulated genes by stimulation of chondrocytes with 1L-1beta

JOURNAL Patent: EP 0705842-A 57 10-APR-1996;

COMMENT HOECHST AG (DE)

Other publication ZA 9508381 960424

Other publication JP 8191693 960730

Other publication CA 2159957 960407

Other publication AU 3308695 960418.

FEATURES

source

1. 14

/organism="unidentified"

/mol_type="unassigned DNA"

/db_xref="taxon:32644"

Query Match 0.9%; Score 13.2; DB 1; Length 14;

Best Local Similarity 92.9%; Pred. No. 1.6e+02;

Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAATAAAAAAAAAA 1492

Db 14 CBAATAAAAAAAAAA 1

RESULT 298

AR064009/c

LOCUS

DEFINITION 14 bp DNA linear PAT 29-SEP-1999

ACCESSION Sequence 10 from patent US 5846773.

VERSION AR064009

KEYWORDS AR064009.1 GI:5993317

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 14)

AUTHORS Lee, M.-E. and Hsieh, C.-M.

TITLE Single gene encoding aortic-specific and striated-specific muscle

cell isoforms and uses thereof

Patent: US 5846773-A 10 08-DEC-1998;

JOURNAL Location/Qualifiers

FEATURES

source

1. 14

/organism="unknown"

/mol_type="unassigned DNA"

Query Match

Best Local Similarity 0.9%; Score 13.2; DB 1; Length 14;

Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAATAAAAAAAAAA 1492

Db 14 CBAATAAAAAAAAAA 1

RESULT 299

BD235627/c

LOCUS

DEFINITION 14 bp DNA linear PAT 17-JUL-2003

ACCESSION Single gene encoding aorta-specific muscular cell isoform and

VERSION BD235627.1 GI:33045397

KEYWORDS JP 2002522074-A/3.

SOURCE synthetic construct

ORGANISM artificial construct

REFERENCE 1 (bases 1 to 14)

AUTHORS Lee, M.E. and Hsieh, C.M.

TITLE Single gene encoding aorta-specific muscular cell isoform and

striated muscle-specific isoform, regulatory sequence thereof and

utilization of the same

Patent: JP 2002522074-A 3 23-JUL-2002;

JOURNAL PRESIDENT AND FELLOWS OF HARVARD COLLEGE

COMMENT OS Artificial Sequence

PN JP 2002522074-A/3

PD 23-JUL-2002

PF 11-MAY-1999 JP 2000565124

PR 14-AUG-1998 US 09/134250, 30-APR-1999 US 09/303069 PI

MU EN LEE, CHUNG MING HSIEH

PC C12N15/09, C07K14/47, C12Q1/66, C12Q1/68, G01N33/15, G01N33/50, PC

G01N33/68,

PC C12N15/00

CC Synthetic Poly T Anchoring Primer

PH Key Location/Qualifiers

FT source 1. 14

/organism="Artificial Sequence".

FEATURES

source

1. 14

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

Query Match

Best Local Similarity 0.9%; Score 13.2; DB 1; Length 14;

Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAATAAAAAAAAAA 1492

Db 14 CBAATAAAAAAAAAA 1

RESULT 300

E13664/c

LOCUS

DEFINITION 14 bp DNA linear PAT 27-APR-1998

ACCESSION E13664

VERSION E13664.1 GI:3252441

KEYWORDS JP 1997224671-A/2.

SOURCE unidentified

ORGANISM unidentified

REFERENCE 1 (bases 1 to 14)

AUTHORS Shibata, D., Kato, T. and Ota, H.

TITLE DNA CODING NEW CYTOCHROME P450

```
JOURNAL Patent: JP 1997224671-A 2 02-SEP-1997;
COMMENT MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO:KK
OS None
OC Artificial sequences.
PN JP 1997224671-A/2
PD 02-SEP-1997
PF 19-FEB-1996 JP 1996031075
PI SHIBATA DAISUKE, KATO TOMOHIKO, OTA HIROYUKI
PC C12N15/09,C12N9/02,C12N9/02,C12R1:91);
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
FH Key Location/Qualifiers
FH source 1..14
FH /organism='Artificial sequences'.
FT Location/Qualifiers
FT source 1..14
FT /organism='unidentified'
FT /mol_type='genomic DNA'
FT /db_xref='taxon:32644'

Query Match 0.9%; Score 13.2; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAATAAAAAAAAAA 1492
Db 14 CBAATAAAAAAAAAA 1

RESULT 301
E13669/c
LOCUS AR212269/c 14 bp DNA linear PAT 27-APR-1998
DEFINITION Sequence 10 from patent US 6399753.
ACCESSION AR212269
VERSION AR212269.1 GI:3252446
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 14)
AUTHORS Lee,M.-E. and Ota,H.
TITLE DNA CODING NEW DNA-CONNECTED PROTEIN
JOURNAL Patent: JP 1997224672-A 2 02-SEP-1997;
COMMENT MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO:KK
OS None
OC Artificial sequences.
PN JP 1997224672-A/2
PD 02-SEP-1997
PF 21-FEB-1996 JP 1996033973
PI SHIBATA DAISUKE, KATO TOMOHIKO, OTA HIROYUKI
PC C12N15/09,A01H5/00,C07H21/04,C07K14/415//C12N5/10,C12Q1/68; CC
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
FH Key Location/Qualifiers
FH source 1..14
FH /organism='Artificial sequences'.
FT Location/Qualifiers
FT source 1..14
FT /organism='unidentified'
FT /mol_type='genomic DNA'
FT /db_xref='taxon:32644'

Query Match 0.9%; Score 13.2; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAATAAAAAAAAAA 1492
Db 14 CBAATAAAAAAAAAA 1

RESULT 302
AR195060/c
LOCUS AR212269/c 14 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 10 from patent US 6399753.
ACCESSION AR212269
VERSION AR212269.1 GI:20244497
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 14)
AUTHORS Lee,M.-E. and Hsieh,C.-M.
TITLE Aortic-specific enhancer sequence and uses thereof
JOURNAL Patent: US 6350592-A 10 26-FEB-2002;
FEATURES
source 1..14
/organism='unassigned DNA'
/mol_type='unassigned DNA'

Query Match 0.9%; Score 13.2; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAATAAAAAAAAAA 1492
Db 14 CBAATAAAAAAAAAA 1

RESULT 303
AR212269/c
LOCUS AR212269/c 14 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 10 from patent US 6399753.
ACCESSION AR212269
VERSION AR212269.1 GI:21515800
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 14)
AUTHORS Lee,M.-E. and Hsieh,C.-M.
TITLE Striated-specific muscle cell polypeptides
JOURNAL Patent: US 6399753-A 10 04-JUN-2002;
FEATURES
source 1..14
/organism='unassigned DNA'
/mol_type='unassigned DNA'

Query Match 0.9%; Score 13.2; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAATAAAAAAAAAA 1492
Db 14 CBAATAAAAAAAAAA 1

RESULT 304
AR266627/c
LOCUS AR266627/c 14 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 65 from patent US 6495319.
ACCESSION AR266627
VERSION AR266627.1 GI:29695691
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 14)
AUTHORS McClelland,M., Welsh,J. and Trenkle,T.
TITLE Reduced complexity nucleic acid targets and methods of using same
JOURNAL Patent: US 6495319-A 65 17-DEC-2002;
FEATURES
source 1..14
/organism='unassigned DNA'
/mol_type='unassigned DNA'
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source      1. .14
/organism="unknown"
/mol_type="genomic DNA"

Query Match      0.9%; Score 13.2; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAAA 1493
Db 14 BAAAAAATAAAAAA 1

RESULT 305
BD057045/c
LOCUS      14 bp DNA linear PAT 27-AUG-2002
DEFINITION A single gene encoding aortic-specific and striated-specific muscle
cell isoforms and uses thereof.
ACCESSION  BD057045
VERSION     BD057045.1 GI:22602651
KEYWORDS   JP 2001511016-A/3.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 14)
AUTHORS    Lee,M.E. and Heieh,C.M.
TITLE      A single gene encoding aortic-specific and striated-specific muscle
cell isoforms and uses thereof
JOURNAL    Patent: JP 2001511016-A 3 07-AUG-2001;
            PRESIDENT AND FELLOWS OF HARVARD COLLEGE
COMMENT    FN JP 2001511016-A/3
            PD 07-AUG-2001
            PF 06-FEB-1998 JP 1998534965
            PR 06-FEB-1997 US 08/795868
            PI MU EN LEE,CHUNG MING HSIEH
            PC C12N15/09,C07K14/47,C12N5/10,C12N15/00,C12N5/00 CC
            CC Topology: Linear;
            FH Key Location/Qualifiers.
FEATURES
source      1. .14
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match      0.9%; Score 13.2; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAAAAAATAAAAA 1492
Db 14 CBAATAAAAAA 1

RESULT 306
E32457
LOCUS      18 bp DNA linear PAT 18-JUN-2001
DEFINITION Mammal-derived tissue specific physiologically active protein.
ACCESSION  E32457
VERSION     E32457.1 GI:13018693
KEYWORDS   JP 2000037190-A/17.
SOURCE     synthetic construct
            artificial sequences.
ORGANISM   1 (bases 1 to 18)
            Jun,N., Yusuke,N. and Toshihiro,T.
            Mammal-derived tissue specific physiologically active protein
            Patent: JP 2000037190-A 17 08-FEB-2000;
            JAPAN TOBACCO INC
COMMENT    OS Artificial Sequence
            FN JP 2000037190-A/17
            PD 08-FEB-2000

PF 23-JUL-1998 JP 1998225228
PR JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
PC C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
C12N15/02
PC C12P21/02,C12P21/08/(C12N5/10,C12R1:91), (C12P21/08,C12R1:91),
PC C12N15/00,
PC C12N5/00,C12N15/00, (C12N5/00,C12R1:91)
CC
CF Key Location/Qualifiers
FH primer bind (1)-(18).
FT Location/Qualifiers
1. .18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match      0.9%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1085 GTTTTCTTTTGTCTGA 1102
Db 1 GTTTTCTTTTGTCTGA 18

RESULT 307
AR012009/c
LOCUS      13 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 3 from patent US 5763183.
ACCESSION  AR012009
VERSION     AR012009.1 GI:3969999
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE   1 (bases 1 to 13)
AUTHORS    Pesonen,U., Koulu,M., Linnoila,M., Goldman,D. and Virkkunen,M.
TITLE      Allelic variation of the serotonin 5HT7 receptor
JOURNAL    Patent: US 5763183-A 3 09-JUN-1998;
FEATURES
source      1. .13
/organism="unknown"
/mol_type="unassigned DNA"

Query Match      0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAATAAAAA 1493
Db 13 AAAAAAATAAAAA 1

RESULT 308
AR012010/c
LOCUS      13 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 4 from patent US 5763183.
ACCESSION  AR012010
VERSION     AR012010.1 GI:3970000
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE   1 (bases 1 to 13)
AUTHORS    Pesonen,U., Koulu,M., Linnoila,M., Goldman,D. and Virkkunen,M.
TITLE      Allelic variation of the serotonin 5HT7 receptor
JOURNAL    Patent: US 5763183-A 4 09-JUN-1998;
FEATURES
source      1. .13
/organism="unknown"
/mol_type="unassigned DNA"

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Query Match      0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
Db 13 AAAAAAAAAAAAAA 1

RESULT 309
AR145368
LOCUS      AR145368      13 bp      DNA      linear      PAT 08-AUG-2001
DEFINITION Sequence 1 from patent US 6211354.
ACCESSION  AR145368
VERSION     AR145368.1 GI:15107235
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 13)
AUTHORS   Horie,R. and Ishiguro,T.
TITLE     Optically active DNA probe having phosphonic diester linkage
JOURNAL   Patent: US 6211354-A 1 03-APR-2001;
FEATURES   Location/Qualifiers
            source
            1..13
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
Db 1 AAAAAAAAAAAAAA 13

RESULT 310
AR179431/c
LOCUS      AR179431      13 bp      DNA      linear      PAT 20-APR-2002
DEFINITION Sequence 6 from patent US 6326175.
ACCESSION  AR179431
VERSION     AR179431.1 GI:20220986
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 13)
AUTHORS   Guegler,K., Tan,R. and Rose,M.J.
TITLE     Methods and compositions for producing full length cDNA libraries
JOURNAL   Patent: US 6326175-A 6 04-DEC-2001;
FEATURES   Location/Qualifiers
            source
            1..13
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
Db 13 AAAAAAAAAAAAAA 1

RESULT 311
E66853
LOCUS      E66853      13 bp      DNA      linear      PAT 18-JUN-2001
DEFINITION DNA probe having optically active diphosphate bond.
ACCESSION  E66853
VERSION     E66853.1 GI:13018113
KEYWORDS   JP 1999322783-A/1.
SOURCE     synthetic construct

ORGANISM      synthetic construct
artificial sequences.
1 (bases 1 to 13)
Ryuichi,H. and Takahiko,I.
DNA probe having optically active diphosphate bond
Patent: JP 1999322783-A 1 24-NOV-1999;
TOSOH CORP
OS Artificial Sequence
PN JP 1999322783-A/1
PD 24-NOV-1999
PF 06-MAY-1998 JP 1998123298
PR
PI RYUICHI HORIE,TAKAHIKO ISHIGURO
PC C07H21/04,C12N15/09,C12Q1/68,C12Q1/78,G01N33/50, PC
G01N33/533,
PC G01N33/566,G01N33/58
CC
FH Key Location/Qualifiers
FT source 1..13 /organism='Artificial Sequence'.
FEATURES
source
1..13
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match      0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
Db 1 AAAAAAAAAAAAAA 13

RESULT 312
E66854
LOCUS      E66854      13 bp      DNA      linear      PAT 18-JUN-2001
DEFINITION DNA probe having optically active diphosphate bond.
ACCESSION  E66854
VERSION     E66854.1 GI:13018114
KEYWORDS   JP 1999322783-A/2.
SOURCE     synthetic construct
artificial sequences.
1 (bases 1 to 13)
Ryuichi,H. and Takahiko,I.
DNA probe having optically active diphosphate bond
Patent: JP 1999322783-A 2 24-NOV-1999;
TOSOH CORP
OS Artificial Sequence
PN JP 1999322783-A/2
PD 24-NOV-1999
PF 06-MAY-1998 JP 1998123298
PR
PI RYUICHI HORIE,TAKAHIKO ISHIGURO
PC C07H21/04,C12N15/09,C12Q1/68,C12Q1/78,G01N33/50, PC
G01N33/533,
PC G01N33/566,G01N33/58
CC
FH Key Location/Qualifiers
FT source 1..13 /organism='Artificial Sequence'.
FEATURES
source
1..13
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match      0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1481 AAAAAAAAAAAAA 1493
Db 1 AAAAAAAAAAAAA 13

RESULT 313
LOCUS AR205695 13 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 6 from patent US 6369199.
ACCESSION AR205695
VERSION AR205695.1 GI:21503343
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 13)
AUTHORS Guegler,K., Tan,R. and Rose,M.J.
TITLE Fusion protein comprising an eIF-4E domain and an eIF-4G domain
JOURNAL joined by a linker domain
FEATURES
    Patent: US 6369199-A 6 09-APR-2002;
    Location/Qualifiers
        source
            1..13
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAA 1493
Db 13 AAAAAAAAAAAAA 1

RESULT 316
LOCUS AX048405 13 bp DNA linear PAT 12-JAN-2001
DEFINITION Sequence 4 from Patent WO0071747.
ACCESSION AX048405
VERSION AX048405.1 GI:12225569
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
TITLE Detection system for separating constituents of a sample and
JOURNAL Production and use of the same
FEATURES
    Patent: WO 0071747-A 4 30-NOV-2000;
    Aventis Research & Technologies GmbH & Co. KG (DE)
    Location/Qualifiers
        source
            1..13
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Region A"

Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAA 1493
Db 13 AAAAAAAAAAAAA 1

RESULT 317
LOCUS AX104675 13 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 867 from Patent WO0122972.
ACCESSION AX104675
VERSION AX104675.1 GI:13920872
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 867 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
FEATURES
    GmbH (DE)
    Location/Qualifiers
        source
            1..13
                /organism="synthetic construct"

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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
11_13
/notes="FITC moiety attached at 3' end of sequence.
Has phosphodiester backbone."
misc_feature
    0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match
AX235509/c
LOCUS
DEFINITION
Sequence 25 from Patent WO0149687.
ACCESSION
AX235509
VERSION
AX235509.1 GI:15593971
KEYWORDS
.
SOURCE
synthetic construct
ORGANISM
synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS
Wang,J. and Herdewijn,P.
TITLE
Cyclohexene nucleic acids
JOURNAL
Patent: WO 0149687-A 25 12-JUL-2001;
UNIVERSITY OF IOWA RESEARCH & DEVELOPMENT (BE)
GmbH (DE)
FEATURES
source
    1..13
    /organism="synthetic construct"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"
misc_feature
    11_13
    /notes="Biotin moiety attached at 3' end of sequence.
Has phosphorothioate and phosphodiester chimeric backbone
with phosphodiester on 3' end."
Query Match
AX235509/c
LOCUS
DEFINITION
Sequence 25 from Patent WO0149687.
ACCESSION
AX235509
VERSION
AX235509.1 GI:15593971
KEYWORDS
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SOURCE
synthetic construct
ORGANISM
synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS
Wang,J. and Herdewijn,P.
TITLE
Cyclohexene nucleic acids
JOURNAL
Patent: WO 0149687-A 25 12-JUL-2001;
UNIVERSITY OF IOWA RESEARCH & DEVELOPMENT (BE)
K.U. LEUVEN RESEARCH & DEVELOPMENT (BE)
Location/Qualifiers
    1..13
    /organism="synthetic construct"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"
    /notes="DNA complement"
Query Match
    0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 13;

AX104676
LOCUS
DEFINITION
Sequence 868 from Patent WO0122972.
ACCESSION
AX104676
VERSION
AX104676.1 GI:13920873
KEYWORDS
.
SOURCE
synthetic construct
ORGANISM
synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS
Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE
Immunostimulatory nucleic acids
JOURNAL
Patent: WO 0122972-A 868 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
FEATURES
source
    1..13
    /organism="synthetic construct"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"
misc_feature
    11_13
    /notes="Biotin moiety attached at 3' end of sequence.
Has phosphorothioate and phosphodiester chimeric backbone
with phosphodiester on 3' end."
Query Match
AX104676/c
LOCUS
DEFINITION
Sequence 868 from Patent WO0122972.
ACCESSION
AX104676
VERSION
AX104676.1 GI:13920873
KEYWORDS
.
SOURCE
synthetic construct
ORGANISM
synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS
Wang,J. and Herdewijn,P.
TITLE
Cyclohexene nucleic acids
JOURNAL
Patent: WO 0149687-A 26 12-JUL-2001;
K.U. LEUVEN RESEARCH & DEVELOPMENT (BE)
Location/Qualifiers
    1..13
    /organism="synthetic construct"
    /mol_type="unassigned RNA"
    /db_xref="taxon:32630"
    /note="oligomer used in this study"
Query Match
    0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AX355807
LOCUS
DEFINITION
Sequence 835 from Patent WO0197843.
ACCESSION
AX355807
VERSION
AX355807.1 GI:18620475
KEYWORDS
.
SOURCE
synthetic construct
ORGANISM
synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS
Weiner,G. and Hartmann,G.
TITLE
Methods for enhancing antibody-induced cell lysis and treating
cancer
JOURNAL
Patent: WO 0197843-A 835 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
Location/Qualifiers
    1..13
    /organism="synthetic construct"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"
    /note="Synthetic oligonucleotide-phosphodiester backbone"
misc_feature
    13
    /note="FITC labeled"
Query Match
    0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AX355807/c
LOCUS
DEFINITION
Sequence 835 from Patent WO0197843.
ACCESSION
AX355807
VERSION
AX355807.1 GI:18620475
KEYWORDS
.
SOURCE
synthetic construct
ORGANISM
synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS
Weiner,G. and Hartmann,G.
TITLE
Methods for enhancing antibody-induced cell lysis and treating
cancer
JOURNAL
Patent: WO 0197843-A 835 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
Location/Qualifiers
    1..13
    /organism="synthetic construct"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"
    /note="Synthetic oligonucleotide-phosphodiester backbone"
misc_feature
    13
    /note="FITC labeled"
Query Match
    0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
DB 13 AAAAAAAAAAAAAA 1

RESULT 320
AX235510/c
LOCUS
DEFINITION
Sequence 26 from Patent WO0149687.
ACCESSION
AX235510
VERSION
AX235510.1 GI:15593972
KEYWORDS
.
SOURCE
synthetic construct
ORGANISM
synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS
Wang,J. and Herdewijn,P.
TITLE
Cyclohexene nucleic acids
JOURNAL
Patent: WO 0149687-A 26 12-JUL-2001;
K.U. LEUVEN RESEARCH & DEVELOPMENT (BE)
Location/Qualifiers
    1..13
    /organism="synthetic construct"
    /mol_type="unassigned RNA"
    /db_xref="taxon:32630"
    /note="oligomer used in this study"
Query Match
    0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
DB 13 AAAAAAAAAAAAAA 1

RESULT 321
AX355807/c
LOCUS
DEFINITION
Sequence 835 from Patent WO0197843.
ACCESSION
AX355807
VERSION
AX355807.1 GI:18620475
KEYWORDS
.
SOURCE
synthetic construct
ORGANISM
synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS
Weiner,G. and Hartmann,G.
TITLE
Methods for enhancing antibody-induced cell lysis and treating
cancer
JOURNAL
Patent: WO 0197843-A 835 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
Location/Qualifiers
    1..13
    /organism="synthetic construct"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"
    /note="Synthetic oligonucleotide-phosphodiester backbone"
misc_feature
    13
    /note="FITC labeled"
Query Match
    0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
DB 13 AAAAAAAAAAAAAA 1
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RESULT 322
AX355808/c
LOCUS AX355808 13 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 836 from Patent WO0197843.
ACCESSION AX355808
VERSION AX355808.1 GI:18620476
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Bratzler, R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 867 11-JUL-2002;
FEATURES
source
    /organism="synthetic construct"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"
    /note="Synthetic oligonucleotide-chimeric
    phosphorothioate/phosphodiester backbone with
    phosphodiester on 3' end"
misc_difference 13
    /note="FITC labeled"
Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
Db 13 AAAAAAAAAAAAAA 1

RESULT 323
AX547728/c
LOCUS AX547728 13 bp DNA linear PAT 15-JAN-2003
DEFINITION Sequence 867 from Patent WO02053141.
ACCESSION AX547728
VERSION AX547728.1 GI:25812872
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Bratzler, R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 867 11-JUL-2002;
FEATURES
source
    /organism="synthetic construct"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"
    /note="Has phosphodiester backbone."
misc_feature 11..13
    /note="Conjugated to FITC moiety."
Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
Db 13 AAAAAAAAAAAAAA 1

RESULT 324
AX547729/c
LOCUS AX547729 13 bp DNA linear PAT 15-JAN-2003
DEFINITION Sequence 868 from Patent WO02053141.
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ACCESSION AX547729
VERSION AX547729.1 GI:25812873
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Bratzler, R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 868 11-JUL-2002;
FEATURES
source
    /organism="synthetic construct"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"
    /note="Has phosphorothioate and phosphodiester chimeric
    backbone with phosphodiester on 3' end."
misc_feature 11..13
    /note="Conjugated to biotin moiety."
Query Match 0.9%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
Db 13 AAAAAAAAAAAAAA 1

RESULT 325
AR124885/c
LOCUS AR124885 14 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 3 from patent US 6172211.
ACCESSION AR124885
VERSION AR124885.1 GI:14110246
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 14)
AUTHORS Georgiev, G.P., Kiselev, S.L., Prokhorchouk, E.B. and Ostermann, E.
TITLE Nucleic acid encoding tag7 polypeptide
JOURNAL Patent: US 6172211-A 3 09-JAN-2001;
FEATURES
source
    /organism="unknown"
    /mol_type="unassigned DNA"
Query Match 0.9%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAAA 1492
Db 13 TAAAAAAAAAAAAA 1

RESULT 326
AR174027/c
LOCUS AR174027 14 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 17 from patent US 6306624.
ACCESSION AR174027
VERSION AR174027.1 GI:17914347
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 14)
AUTHORS Petkovich, P., Martin, J.A., Beckett, B.R. and Jones, G.
TITLE Retinoid metabolizing protein
JOURNAL Patent: US 6306624-A 17 23-OCT-2001;
FEATURES
    Location/Qualifiers
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source 1. .14
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.9%; Score 13; DB 1; Length 14;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAA 1492
|||||
Db 13 TAAAAAATAAAAA 1

RESULT 327
AR174028/c
LOCUS AR174028 14 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 18 from patent US 6306624.
ACCESSION AR174028
VERSION AR174028.1 GI:17914348
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Petkovich,P.Martin., White,J.A., Beckett,B.R. and Jones,G.
TITLE Retinoid metabolizing protein
JOURNAL Patent: US 6306624-A 18 23-OCT-2001;
FEATURES
Location/Qualifiers
source 1. .14
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.9%; Score 13; DB 1; Length 14;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAA 1492
|||||
Db 13 TAAAAAATAAAAA 1

RESULT 328
AR174029/c
LOCUS AR174029 14 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 19 from patent US 6306624.
ACCESSION AR174029
VERSION AR174029.1 GI:17914349
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Petkovich,P.Martin., White,J.A., Beckett,B.R. and Jones,G.
TITLE Retinoid metabolizing protein
JOURNAL Patent: US 6306624-A 19 23-OCT-2001;
FEATURES
Location/Qualifiers
source 1. .14
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.9%; Score 13; DB 1; Length 14;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAA 1492
|||||
Db 13 TAAAAAATAAAAA 1

RESULT 329
AR228386
LOCUS AR228386 14 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 18 from patent US 6448039.
ACCESSION AR228386
VERSION AR228386.1 GI:27267215
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Nelson,P.J., Krensky,A.M. and Ortiz,B.D.
TITLE Enhancer sequences for late T cell expressed genes
JOURNAL Patent: US 6448039-A 18 10-SEP-2002;
FEATURES
Location/Qualifiers
source 1. .14
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 0.9%; Score 13; DB 1; Length 14;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1179 GACTGGAGGGCAG 1191
|||||
Db 1 GACTGGAGGGCAG 13

RESULT 330
AR241806/c
LOCUS AR241806 14 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 94 from patent US 6472154.
ACCESSION AR241806
VERSION AR241806.1 GI:27287618
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
TITLE Polymorphic repeats in human genes
JOURNAL Patent: US 6472154-A 94 29-OCT-2002;
FEATURES
Location/Qualifiers
source 1. .14
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 0.9%; Score 13; DB 1; Length 14;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAATAAAAA 1493
|||||
Db 13 AAAAAAATAAAAA 1

RESULT 331
AR349924/c
LOCUS AR349924 14 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 18 from patent US 6586204.
ACCESSION AR349924
VERSION AR349924.1 GI:33750834
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Lehar,S.M. and Guild,B.C.
TITLE Apoptosis gene BIZ4, compositions, and methods of use
JOURNAL Patent: US 6586204-A 18 01-JUL-2003;
FEATURES
Location/Qualifiers
source 1. .14
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 0.9%; Score 13; DB 1; Length 14;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAATAAAAA 1493
|||||
Db 13 AAAAAAATAAAAA 1
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RESULT 334	AX482598	Sequence 32 from Patent WO02055547.	14 bp	DNA	linear	PAT 16-AUG-2002
AX482598/c	LOCUS	AX482598				
	DEFINITION	Sequence 32 from Patent WO02055547.	14 bp	DNA	linear	PAT 16-AUG-2002
	ACCESSION	AX482598				
	VERSION	AX482598.1	GI:22317052			
	KEYWORDS	.				
	SOURCE	synthetic construct				
	ORGANISM	synthetic construct				
		artificial sequences.				

RESULT 336	
BD073886/C	
LOCUS.	
DEFINITION	

Qy 1480 TAAAAAAAAAAAAA 1492

 Db 13 TAAAAAAAAAAAAA 1

RESULT 336
 BD073886/c
 LOCUS.
 DEFINITION Isolation of novel aging factor gene p23.
 14 bp DNA linear PAT 27-AUG-2002

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ACCESSION BD073886
VERSION BD073886.1 GI:22619489
KEYWORDS JP 2001512698-A/11.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 14)
AUTHORS Suishelm,K., Hosier,S. and Kubbies,M.
TITLE Isolation of novel aging factor gene P23
JOURNAL Patent: JP 2001512698-A 11 28-AUG-2001;
UNIVERSITY OF WASHINGTON
COMMENT OS Unidentified
PN JP 2001512698-A/11
PD 28-AUG-2001
PP 05-AUG-1998 JP 2000506375
PR 08-AUG-1997 US 08/908873
PI KAREN SUISHELM,SUZANNE HOSIER,MANFRED KUBBIES PC
C12Q1/68,C07K14/435,C07K16/18,C12N1/15,C12N1/19,C12N15/09, PC
C12P21/02,
PC C12P21/08,C12N15/00
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CC Topology: Linear;
CC Isolation of novel aging factor gene P23
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Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1480 TAAAAA 1492
Db 13 TAAAAA 1
RESULT 338
BD073889/c
LOCUS
DEFINITION Tumor proliferation inhibition- and apoptosis-associated gene and
polypeptide and method of using the same.
ACCESSION BD078858
VERSION BD078858.1 GI:22624461
KEYWORDS JP 2001509384-A/3.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 14)
AUTHORS Georgiev,G. Kiselev,S. Prokhorchouk,E. and Ostermann,E.
TITLE Tumor proliferation inhibition- and apoptosis-associated gene and
polypeptide and method of using the same
JOURNAL Patent: JP 2001509384-A 3 24-JUL-2001;
COMMENT BOEHRINGER INGELHEIM INTERNATIONAL GMBH
OS Unidentified
PN JP 2001509384-A/3
PD 24-JUL-2001
PP 10-JUL-1998 JP 2000502182
PR 11-JUL-1997 US 08/893764
PI GEORGII GEORGIEV,SERGEI KISELEV,EGOR PROKHORCHOUK,ELINBORG PI
OSTERMANN
PC C12N15/09,A61K35/76,A61K38/00,A61K48/00,A61P35/00,C07K14/525,
PC C07K16/24,
PC C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12P21/02,C12P21/08 PC
,C12Q1/68,G01N33/53,
PC C12N15/00,A61K37/02,C12N5/00
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CC and
CC polypeptide and method of using the same
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Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1480 TAAAAA 1492
Db 13 TAAAAA 1
RESULT 339
BD084126/c
LOCUS
DEFINITION Polymorphisms and new genes in the region of the human
hemochromatosis gene.
ACCESSION BD084126
VERSION BD084126.1 GI:22629736
KEYWORDS JP 2001525663-A/14.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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ACCESSION BD073886
VERSION BD073886.1 GI:22619489
KEYWORDS JP 2001512698-A/11.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 14)
AUTHORS Suishelm,K., Hosier,S. and Kubbies,M.
TITLE Isolation of novel aging factor gene P23
JOURNAL Patent: JP 2001512698-A 11 28-AUG-2001;
UNIVERSITY OF WASHINGTON
COMMENT OS Unidentified
PN JP 2001512698-A/11
PD 28-AUG-2001
PP 05-AUG-1998 JP 2000506375
PR 08-AUG-1997 US 08/908873
PI KAREN SUISHELM,SUZANNE HOSIER,MANFRED KUBBIES PC
C12Q1/68,C07K14/435,C07K16/18,C12N1/15,C12N1/19,C12N15/09, PC
C12P21/02,
PC C12P21/08,C12N15/00
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CC Topology: Linear;
CC Isolation of novel aging factor gene P23
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1480 TAAAAA 1492
Db 13 TAAAAA 1
RESULT 337
BD073889/c
LOCUS
DEFINITION Isolation of novel aging factor gene P23.
ACCESSION BD073889
VERSION BD073889.1 GI:22619492
KEYWORDS JP 2001512698-A/14.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 14)
AUTHORS Suishelm,K., Hosier,S. and Kubbies,M.
TITLE Isolation of novel aging factor gene P23
JOURNAL Patent: JP 2001512698-A 14 28-AUG-2001;
UNIVERSITY OF WASHINGTON
COMMENT OS Unidentified
PN JP 2001512698-A/14
PD 28-AUG-2001
PP 05-AUG-1998 JP 2000506375
PR 08-AUG-1997 US 08/908873
PI KAREN SUISHELM,SUZANNE HOSIER,MANFRED KUBBIES PC
C12Q1/68,C07K14/435,C07K16/18,C12N1/15,C12N1/19,C12N15/09, PC
C12P21/02,
PC C12P21/08,C12N15/00
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CC Topology: Linear;
CC Isolation of novel aging factor gene P23
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source
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Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Feder,J.N., Kronmal,G.S., Lauer,P.M., Ruddy,D.A., Thomas,W.J.,
TITLE Tsuchihashi,Z. and Wolff,R.K.
JOURNAL Polymorphisms and new genes in the region of the human
hemochromatosis gene
COMMENT Patent: JP 2001525663-A 14 11-DEC-2001;
PROGENITOR INC
OS Homo sapiens (human)
PN JP 2001525663-A/14
PD 11-DEC-2001
PF 30-SEP-1997 JP 1998516815
PR 01-OCT-1996 US 08/724394,07-MAY-1997 US 08/852495 PI
JOHN N FEDER,GREGORY S KONNALL,PETER M LAUER,DAVID A RUDDY, PI
WINSTON J THOMAS,ZENTA TSUCHIHASHI,ROGER K WOLFF PC
C07H21/04,C12Q1/68,C12N15/63,C12N15/85,C12P21/02 CC Polymorphisms
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DB 14 AAAAAAAAAAAAAA 2
RESULT 340
BD176796
LOCUS 14 bp DNA linear PAT 18-MAR-2003
DEFINITION Method of constructing cDNA tag for identifying expressed gene and
method of analyzing gene expression.
ACCESSION BD176796.1 GI:29122508
VERSION WO 02074951-A/43.
KEYWORDS synthetic construct
SOURCE artificial sequences.
ORGANISM 1 (bases 1 to 14)
REFERENCE Yamamoto,M., Yamamoto,N., Hirose,K. and Sakai,J.
AUTHORS Method of constructing cDNA tag for identifying expressed gene and
TITLE Method of analyzing gene expression
JOURNAL Patent: WO 02074951-A 43 26-SEP-2002;
KUREHA CHEMICAL INDUSTRY CO LTD,MIKIO YAMAMOTO,NAOKI YAMAMOTO,
COMMENT KUNITAKA HIROSE,JUN SAKAI
OS Artificial Sequence
PN WO 02074951-A/43
PD 26-SEP-2002
PF 13-MAR-2002 WO 2002JP002338
PR 15-MAR-2001 JP 01P 073959
PI MIKIO YAMAMOTO,NAOKI YAMAMOTO,KUNITAKA HIROSE,JUN SAKAI PC
C12N15/09,C12Q1/68
CC Synthetic DNA
FH Key Location/Qualifiers
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DB 14 AAAAAAAAAAAAAA 2
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BD176796
LOCUS 14 bp DNA linear PAT 18-MAR-2003
DEFINITION Method of constructing cDNA tag for identifying expressed gene and
method of analyzing gene expression.
ACCESSION BD176796.1 GI:29122508
VERSION WO 02074951-A/43.
KEYWORDS synthetic construct
SOURCE artificial sequences.
ORGANISM 1 (bases 1 to 14)
REFERENCE Yamamoto,M., Yamamoto,N., Hirose,K. and Sakai,J.
AUTHORS Method of constructing cDNA tag for identifying expressed gene and
TITLE Method of analyzing gene expression
JOURNAL Patent: WO 02074951-A 43 26-SEP-2002;
KUREHA CHEMICAL INDUSTRY CO LTD,MIKIO YAMAMOTO,NAOKI YAMAMOTO,
COMMENT KUNITAKA HIROSE,JUN SAKAI
OS Artificial Sequence
PN WO 02074951-A/43
PD 26-SEP-2002
PF 13-MAR-2002 WO 2002JP002338
PR 15-MAR-2001 JP 01P 073959
PI MIKIO YAMAMOTO,NAOKI YAMAMOTO,KUNITAKA HIROSE,JUN SAKAI PC
C12N15/09,C12Q1/68
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DB 14 AAAAAAAAAAAAAA 2

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DB 1 AAAAAAAAAAAAAA 13
RESULT 341
BD176797
LOCUS 14 bp DNA linear PAT 18-MAR-2003
DEFINITION Method of constructing cDNA tag for identifying expressed gene and
method of analyzing gene expression.
ACCESSION BD176797.1 GI:29122509
VERSION WO 02074951-A/44.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 14)
AUTHORS Yamamoto,M., Yamamoto,N., Hirose,K. and Sakai,J.
TITLE Method of constructing cDNA tag for identifying expressed gene and
JOURNAL Method of analyzing gene expression
COMMENT Patent: WO 02074951-A 44 26-SEP-2002;
KUREHA CHEMICAL INDUSTRY CO LTD,MIKIO YAMAMOTO,NAOKI YAMAMOTO,
KUNITAKA HIROSE,JUN SAKAI
OS Artificial Sequence
PN WO 02074951-A/44
PD 26-SEP-2002
PF 13-MAR-2002 WO 2002JP002338
PR 15-MAR-2001 JP 01P 073959
PI MIKIO YAMAMOTO,NAOKI YAMAMOTO,KUNITAKA HIROSE,JUN SAKAI PC
C12N15/09,C12Q1/68
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FH Key Location/Qualifiers
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|||||
DB 1 AAAAAAAAAAAAAA 13
RESULT 342
BD176798
LOCUS 14 bp DNA linear PAT 18-MAR-2003
DEFINITION Method of constructing cDNA tag for identifying expressed gene and
method of analyzing gene expression.
ACCESSION BD176798.1 GI:29122510
VERSION WO 02074951-A/45.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 14)
AUTHORS Yamamoto,M., Yamamoto,N., Hirose,K. and Sakai,J.
TITLE Method of constructing cDNA tag for identifying expressed gene and
JOURNAL Method of analyzing gene expression
COMMENT Patent: WO 02074951-A 45 26-SEP-2002;
KUREHA CHEMICAL INDUSTRY CO LTD,MIKIO YAMAMOTO,NAOKI YAMAMOTO,
KUNITAKA HIROSE,JUN SAKAI
OS Artificial Sequence
PN WO 02074951-A/45
PD 26-SEP-2002
PF 13-MAR-2002 WO 2002JP002338

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PR 15-MAR-2001 JP 01P 073959
PI MIKIO YAMAMOTO,NAOKI YAMAMOTO,KUNITAKA HIROSE,JUN SAKAI PC
C12N15/09,C12Q1/68
CC Synthetic DNA
FH Key Location/Qualifiers
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
Db 1 AAAAAAAAAAAAAA 13

RESULT 343
BD176802/c
LOCUS      14 bp DNA linear PAT 18-MAR-2003
DEFINITION Method of constructing cDNA tag for identifying expressed gene and
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ACCESSION  BD176802
VERSION     BD176802.1 GI:29122514
KEYWORDS    WO 02074951-A/49.
SOURCE      synthetic construct
ORGANISM    artificial sequences.
REFERENCE   1 (bases 1 to 14)
AUTHORS     Yamamoto,M., Yamamoto,N., Hirose,K. and Sakai,J.
TITLE       Method of constructing cDNA tag for identifying expressed gene and
            method of analyzing gene expression
JOURNAL     Patent: WO 02074951-A 49 26-SEP-2002;
            KUREHA CHEMICAL INDUSTRY CO LTD,MIKIO YAMAMOTO,NAOKI YAMAMOTO,
            KUNITAKA HIROSE,JUN SAKAI
COMMENT     OS Artificial Sequence
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            PD 26-SEP-2002
            PF 13-MAR-2002 WO 2002JP002338
            PR 15-MAR-2001 JP 01P 073959
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QY 1481 AAAAAAAAAAAAAA 1493
Db 13 AAAAAAAAAAAAAA 1

RESULT 344
BD176803/c
LOCUS      14 bp DNA linear PAT 18-MAR-2003
DEFINITION Method of constructing cDNA tag for identifying expressed gene and
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ACCESSION  BD176803
VERSION     BD176803.1 GI:29122515

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KEYWORDS    WO 02074951-A/50.
SOURCE      synthetic construct
ORGANISM    artificial sequences.
REFERENCE   1 (bases 1 to 14)
AUTHORS     Yamamoto,M., Yamamoto,N., Hirose,K. and Sakai,J.
TITLE       Method of constructing cDNA tag for identifying expressed gene and
            method of analyzing gene expression
JOURNAL     Patent: WO 02074951-A 50 26-SEP-2002;
            KUREHA CHEMICAL INDUSTRY CO LTD,MIKIO YAMAMOTO,NAOKI YAMAMOTO,
            KUNITAKA HIROSE,JUN SAKAI
COMMENT     OS Artificial Sequence
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            PD 26-SEP-2002
            PF 13-MAR-2002 WO 2002JP002338
            PR 13-MAR-2001 JP 01P 073959
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1493
Db 13 AAAAAAAAAAAAAA 1

RESULT 345
AR056155/c
LOCUS      15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 359 from patent US 5837542.
ACCESSION  AR056155
VERSION     AR056155.1 GI:5981732
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 15)
AUTHORS     Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
            Draper,K.G.
TITLE       Intercellular adhesion molecule-1 (ICAM-1) ribozymes
JOURNAL     Patent: US 5837542-A 359 17-NOV-1998;
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RESULT 346
AR084519
LOCUS      15 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 8 from patent US 5981185.
ACCESSION  AR084519
VERSION     AR084519.1 GI:10011290
KEYWORDS

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QY 1078 TTTTGGGTTTTG 1090					
Db 13 TTTTGGGTTTTG 1					
RESULT 349					
LOCUS AR104533/c					
DEFINITION Sequence 45 from patent US 6093809.					
ACCESSION AR104533					
VERSION AR104533.1 GI:12817241					
KEYWORDS Unknown.					
SOURCE Unknown.					
ORGANISM Unclassified.					
REFERENCE 1 (bases 1 to 15)					
AUTHORS Cech,T.R. and Lingner,J.					
TITLE Telomerase					
JOURNAL Patent: US 6093809-A 45 25-JUL-2000;					
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ACCESSION AR113913					
VERSION AR113913.1 GI:14094235					
KEYWORDS Unknown.					
SOURCE Unknown.					
ORGANISM Unclassified.					
REFERENCE 1 (bases 1 to 15)					
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.					
TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)					
JOURNAL Patent: US 6132967-A 359 17-OCT-2000;					
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QY 1481 AAAAAAAAAAAAAA 1493					
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LOCUS AR175792/c					
DEFINITION Sequence 43 from patent US 6309867.					
ACCESSION AR175792					
VERSION AR175792.1 GI:17917091					
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SOURCE Unknown.					
ORGANISM Unclassified.					
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KEYWORDS Unknown.					
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VERSION AR175792.1 GI:17917091					
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VERSION AR175792.1 GI:17917091					
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SOURCE Unknown.					
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VERSION AR175792.1 GI:17917091					
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ORGANISM Unclassified.					
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Db 15 AAAAAAAAAAAAAA 3					
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KEYWORDS Unknown.					
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VERSION AR175792.1 GI:17917091					
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VERSION AR175792.1 GI:17917091					
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SOURCE Unknown.					
ORGANISM Unclassified.					

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ACCESSION	AR104533		
VERSION	AR104533.1	GI:12817241	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 15)		
AUTHORS	Cech,T.R. and Lingner,J.		
TITLE	Telomerase		
JOURNAL	Patent: US 6093809-A 45 25-JUL-2000;		
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	/mol_type="unassigned DNA"		
Query Match	0.9%;	Score 13;	DB 1; Length 15;
Best Local Similarity	100.0%;	Pred. No. 2.1e+02;	
Matches	13;	Conservative 0;	Mismatches 0; Indels 0; Gaps 0;
QY	1078	TTTTGGGGTTTG	1090
Db	13	TTTTGGGGTTTG	1
RESULT 350			
LOCUS	AR113913/C	15 bp	DNA
DEFINITION	Sequence 359 from patent US 6132967.		linear
ACCESSION	AR113913		
VERSION	AR113913.1	GI:14094235	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 15)		
AUTHORS	Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.		
TITLE	Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)		
JOURNAL	Patent: US 6132967-A 359 17-OCT-2000;		
FEATURES	Location/Qualifiers		
source	1..15		
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	/mol_type="unassigned DNA"		
Query Match	0.9%;	Score 13;	DB 1; Length 15;
Best Local Similarity	100.0%;	Pred. No. 2.1e+02;	
Matches	13;	Conservative 0;	Mismatches 0; Indels 0; Gaps 0;
QY	1481	AAAAAAAAAAAAAA	1493
Db	15	AAAAAAAAAAAAAA	3
RESULT 351			
LOCUS	AR175792	15 bp	DNA
DEFINITION	Sequence 43 from patent US 6309867.		linear
ACCESSION	AR175792		
VERSION	AR175792.1	GI:17917091	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		

```

REFERENCE 1 (bases 1 to 15)
AUTHORS Cech,T.R. and Nakamura,T.
TITLE Telomerase
JOURNAL Patent: US 6309867-A 43 30-OCT-2001;
FEATURES
source
    Location/Qualifiers
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    /organism="unknown"
    /mol_type="unassigned DNA"

Query Match
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1078 TTTTGGGGTTTGG 1090
Db 13 TTTTGGGGTTTGG 1

RESULT 352
AR175794/c
LOCUS AR175794 15 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 45 from patent US 6309867.
ACCESSION AR175794
VERSION AR175794.1 GI:17917093
KEYWORDS
SOURCE Unknown.
ORGANISM
    Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Cech,T.R. and Nakamura,T.
TITLE Telomerase
JOURNAL Patent: US 6309867-A 45 30-OCT-2001;
FEATURES
source
    Location/Qualifiers
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    /mol_type="unassigned DNA"

Query Match
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1078 TTTTGGGGTTTGG 1090
Db 13 TTTTGGGGTTTGG 1

RESULT 353
E36806/c
LOCUS E36806 15 bp DNA linear PAT 18-JUN-2001
DEFINITION Human telomerase catalytic subunit promoter.
ACCESSION E36806
VERSION E36806.1 GI:13022769
KEYWORDS
SOURCE unidentified
ORGANISM
    unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Thomas,R.S., Jochimu,R., Toru,N., Karen,B.C., Greg,B.M.,
TITLE Calvin,B.H. and William,H.A.
JOURNAL Human telomerase catalytic subunit promoter
    Patent: JP 199253177-A 14 21-SEP-1999;
COMMENT JERON CORP UNIVERSITY TECHNOLOGY CORP
OS Unidentified
EN JP 199253177-A/14
PD 21-SEP-1999
PF 15-OCT-1998 JP 1998320169
PR 01-OCT-1996 US 08/724,643,18-APR-1997 US 08/844,419, PR
25-APR-1997 US 08/846,017,06-MAY-1997 US 08/851,843, PR
09-MAY-1997 US 08/854,050,14-AUG-1997 US 08/911,312, PR
14-AUG-1997 US 08/912,951,14-AUG-1997 US 08/915,503 PI THOMAS
R SECHI, JOCHIMU RINGNER, TORU NAKAMURA, KAREN B CHAPMAN, PI GREG B
MORIN,
PI CALVIN B HARBEL, WILLIAM H ANDREWS

PC C12N15/09,A61K31/70,A61K38/55,A61K39/395,A61K39/395,A61K48/00,
PC C12Q1/02,
PC C12Q1/48,C12Q1/68,G01N33/15,G01N33/48,G01N33/50//C07K14/47, PC
C07K16/40,
PC C12N1/19,C12N1/21,C12N5/10,C12N9/12,C12P21/08,(C12N1/19, PC
C12R1:84),
PC (C12N1/21,C12R1:19),(C12N9/12,C12R1:19),(C12N9/12,C12R1:84),
PC (C12N9/12,C12R1:91),C12N15/00,A61K37/64,C12N5/00 CC
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..15
    /organism='Unidentified'.
FEATURES
source
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    /mol_type="genomic DNA"
    /db_xref="taxon:32644"

Query Match
Best Local Similarity 0.9%; Score 13; DB 1; Length 15;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1078 TTTTGGGGTTTGG 1090
Db 13 TTTTGGGGTTTGG 1

RESULT 354
AR282617/c
LOCUS AR282617 15 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 13 from patent US 6521747.
ACCESSION AR282617
VERSION AR282617.1 GI:29719215
KEYWORDS
SOURCE Unknown.
ORGANISM
    Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Anastasio,A.E., Finkel,K., Koshy,B. and Lee,H.
TITLE Haplotypes of the AGTR1 gene
JOURNAL Patent: US 6521747-A 13 18-FEB-2003;
FEATURES
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    /mol_type="genomic DNA"

Query Match
Best Local Similarity 0.9%; Score 13; DB 1; Length 15;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1106 TTCCTGTACCTTTT 1120
Db 15 TTCCTGTTCCTTTT 1

RESULT 355
AR359628/c
LOCUS AR359628 15 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 2 from patent US 6593306.
ACCESSION AR359628
VERSION AR359628.1 GI:33766351
KEYWORDS
SOURCE Unknown.
ORGANISM
    Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Chen,S.-F., Maine,I., Kerwin,S.M., Fletcher,T.M., Salazar,M.,
TITLE Mamiya,B., Wajima,M. and Windle,B.E.
JOURNAL Methods for modulation and inhibition of telomerase
    Patent: US 6593306-A 2 15-JUL-2003;
FEATURES
source
    Location/Qualifiers
    1..15

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/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 0.9%; Score 13; DB 1; Length 15;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1078 TTTTGGGTTTTC 1090
DB 13 TTTTGGGTTTTC 1

RESULT 356
LOCUS AR390483/C 15 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 113 from patent US 6610839.
ACCESSION AR390483
VERSION AR390483.1 GI:40112407
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Morin,G.B. and Andrews,W.H.
TITLE Promoter for telomerase reverse transcriptase
JOURNAL Patent: US 6610839-A 113 26-AUG-2003;
FEATURES
    Location/Qualifiers
    1..15
    /organism="unknown"
    /mol_type="genomic DNA"

Query Match
Best Local Similarity 0.9%; Score 13; DB 1; Length 15;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1078 TTTTGGGTTTTC 1090
DB 13 TTTTGGGTTTTC 1

RESULT 357
LOCUS AR393097/C 15 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 113 from patent US 6617110.
ACCESSION AR393097
VERSION AR393097.1 GI:40118374
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
        Harley,C.B. and Andrews,W.H.
TITLE Cells immortalized with telomerase reverse transcriptase for use in
        drug screening
JOURNAL Patent: US 6617110-A 113 09-SEP-2003;
FEATURES
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1078 TTTTGGGTTTTC 1090
DB 13 TTTTGGGTTTTC 1

RESULT 358
LOCUS AX033371/C 15 bp RNA linear PAT 21-SEP-2000
DEFINITION Sequence 3 from Patent WO0046601.
ACCESSION AX033371
VERSION AX033371.1 GI:10280145
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Larsen,F. and Skaanseng,M.
TITLE Detecting telomerase activity
JOURNAL Patent: WO 0046601-A 3 10-AUG-2000;
        LARSEN FRANK (NO) ; SKAANSENG MARIANNE (NO)
FEATURES
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    /db_xref="taxon:32644"
    /note="Euplotes"

Query Match
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1078 TTTTGGGTTTTC 1090
DB 13 TTTTGGGTTTTC 1

RESULT 359
LOCUS AX033372/C 15 bp RNA linear PAT 21-SEP-2000
DEFINITION Sequence 4 from Patent WO0046601.
ACCESSION AX033372
VERSION AX033372.1 GI:10280146
KEYWORDS
SOURCE Oxytricha sp.
ORGANISM Oxytricha sp.
REFERENCE 1
AUTHORS Larsen,F. and Skaanseng,M.
TITLE Detecting telomerase activity
JOURNAL Patent: WO 0046601-A 4 10-AUG-2000;
        LARSEN FRANK (NO) ; SKAANSENG MARIANNE (NO)
FEATURES
    Location/Qualifiers
    1..15
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    /mol_type="unassigned RNA"
    /db_xref="taxon:99928"

Query Match
Best Local Similarity 0.9%; Score 13; DB 1; Length 15;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1078 TTTTGGGTTTTC 1090
DB 13 TTTTGGGTTTTC 1

RESULT 360
LOCUS AX391450/C 15 bp DNA linear PAT 23-MAR-2002
DEFINITION Sequence 13 from Patent EP1184456.
ACCESSION AX391450
VERSION AX391450.1 GI:19700060
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Anastasio,A.E., Koshy,B., Finkel,K. and Lee,H.H.
        Haplotypes of the agr1 gene

```

JOURNAL Patent: EP 1184456-A 13 06-MAR-2002;
Genaissance Pharmaceuticals, Inc. (US)
FEATURES Location/Qualifiers
source 1..15
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.9%; Score 13; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 2.1e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1106 TTCCTCTTACCTTT 1120
|:|||||
Db 15 TVCCTCTTCCCTTT 1

RESULT 361
AX633193/c
LOCUS 15 bp RNA linear PAT 21-FEB-2003
DEFINITION Sequence 332 from Patent EP1260586.
ACCESSION AX633193
VERSION AX633193.1 GI:28468807
KEYWORDS
SOURCE unclassified
ORGANISM unclassified.

REFERENCE 1
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
McSwiggan,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Wolf,T.
TITLE Method and reagent for inhibiting the expression of disease related
genes

JOURNAL Patent: EP 1260586-A 332 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES Location/Qualifiers
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/organism="unclassified"
/mol_type="unassigned RNA"
/db_xref="taxon:32644"

Query Match 0.9%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAA 1493
|:|||||
Db 15 AAAAAAAAAA 3

RESULT 362
AX810148/c
LOCUS 15 bp DNA linear PAT 25-NOV-2003
DEFINITION Sequence 113 from Patent EP1333094.
ACCESSION AX810148
VERSION AX810148.1 GI:38523876
KEYWORDS
SOURCE unclassified
ORGANISM unclassified.

REFERENCE 1
AUTHORS Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
Harley,C.B. and Andrews,W.H.
TITLE Human telomerase catalytic subunit
JOURNAL Patent: EP 1333094-A 113 06-AUG-2003;
Geron Corporation (US) ; University Technology Corporation (US)

FEATURES Location/Qualifiers
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/organism="unclassified"
/mol_type="unassigned DNA"
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1078 TTTTGGGTTTG 1090
|:|||||
Db 13 TTTTGGGTTTG 1

RESULT 363
BD011057/c
LOCUS 15 bp DNA linear PAT 31-JAN-2002
DEFINITION Human telomerase catalytic subunit.
ACCESSION BD011057
VERSION BD011057.1 GI:18639430
KEYWORDS JP 2001081042-A/14.
SOURCE unidentified
ORGANISM unidentified
unclassified.

REFERENCE 1 (bases 1 to 15)
AUTHORS Sechi,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Mori,G.B.,
Harley,C.B. and Andrews,W.H.
TITLE Human telomerase catalytic subunit
JOURNAL Patent: JP 2001081042-A 14 27-MAR-2001;
GERON CORP. UNIVERSITY TECHNOLOGY CORP
KEYWORDS OS Unidentified
COMMENT PN JP 2001081042-A/14

PF 27-MAR-2001
PD 27-JUL-2000 JP 2000227474
PR 01-OCT-1996 US 08/724643,18-APR-1997 US 08/844419 PR
25-APR-1997 US 08/846017,06-MAY-1997 US 08/851843 PR
09-MAY-1997 US 08/854050,14-AUG-1997 US 08/911312 PR
14-AUG-1997 US 08/912951,14-AUG-1997 US 08/915503 PI THOMAS
R SECHI,JOACHIM LINGNER,TORU NAKAMURA,KAREN B CHAPMAN, PI GREG B
MORIN,
PI CALVIN B HARLEY, WILLIAM H ANDREWS
PC A61K38/00,A61K31/7088,A61K39/00,A61K48/00,A61P35/00,A61P43/00,
PC C07K5/10,
PC C07K5/107,C07K5/117,C07K7/06,C07K7/08,C07K16/40,C12N9/12, PC
C12N15/09,
PC C12Q1/02,C12Q1/48,C12Q1/68,G01N33/15,G01N33/50,G01N33/53, PC
G01N33/53,
PC G01N33/56,G01N33/573//C12P21/08,A61K37/02,C12N15/00 CC
Strandedness: Single;
CC topology: Linear;
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FT /organism="Unidentified".
FT /organism="Unidentified".
FT /mol_type="genomic DNA"
FT /db_xref="taxon:32644"

FEATURES
source 1..15
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/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 0.9%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1078 TTTTGGGTTTG 1090
|:|||||
Db 13 TTTTGGGTTTG 1

Search completed: April 21, 2004, 10:38:31
Job time : 7 secs

XX 10-NOV-1999; 99US-0164596P.
XX (GLAX) GLAXO GROUP LTD.
XX (AFFY-) AFFYMETRIX INC.
XX Au K, Chen J, Patil N, Thomas D;
XX WPI; 2001-335945/35.
XX New polymorphic sites derived from the human genome are useful to
PT determine sites correlating with phenotypic traits, particularly disease,
PT and also in forensics and paternity testing.
XX PS Claim 37; Page 9; 43pp; English.
XX The present invention relates to human oligonucleotides comprising a
CC single nucleotide polymorphic site (SNP: AAH89797-AAH89219). The present
CC sequence is one such oligonucleotide. The oligonucleotides can be used in
CC forensics, paternity testing, correlation of polymorphisms with
CC phenotypic traits, genetic mapping of phenotypic traits and marker
CC assisted breeding of animals and crop plants
XX Sequence 21 BP; 4 A; 8 C; 5 G; 4 T; 0 U; 0 Other;
Query Match 1.4%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX 979 TGCAGTGCCCCCTAAGTGACC 999
Db 1 TGCAGTGCCCCCTAAGTGACC 21
RESULT 13
AAH8906
ID AAH8906 standard; DNA; 21 BP.
XX AC AAH8906;
XX DT 27-FEB-2002 (first entry)
XX DE Human polymorphic oligonucleotide AC003693 fragment #2.
XX Human; single nucleotide polymorphic; SNP; forensic science;
KW paternity testing; phenotypic trait; genetic mapping; animal breeding;
KW plant breeding; ds.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT Variation replace(11,t)
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"
XX PN W0200134840-A2.
XX PD 17-MAY-2001.
XX PF 10-NOV-2000; 2000WO-US030766.
XX PR 10-NOV-1999; 99US-0164596P.
XX (GLAX) GLAXO GROUP LTD.
XX PA (AFFY-) AFFYMETRIX INC.
XX Au K, Chen J, Patil N, Thomas D;
XX WPI; 2001-335945/35.
XX New polymorphic sites derived from the human genome are useful to
PT determine sites correlating with phenotypic traits, particularly disease,
PT and also in forensics and paternity testing.

XX Claim 37; Page 9; 43pp; English.
XX The present invention relates to human oligonucleotides comprising a
CC single nucleotide polymorphic site (SNP: AAH89797-AAH89219). The present
CC sequence is one such oligonucleotide. The oligonucleotides can be used in
CC forensics, paternity testing, correlation of polymorphisms with
CC phenotypic traits, genetic mapping of phenotypic traits and marker
CC assisted breeding of animals and crop plants
XX Sequence 21 BP; 5 A; 5 C; 3 G; 8 T; 0 U; 0 Other;
Query Match 1.4%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX 1036 ATAACGTTTCCGGTATTACTC 1056
Db 1 ATAACGTTTCCGGTATTACTC 21
RESULT 14
ACC78663
ID ACC78663 standard; DNA; 21 BP.
XX AC ACC78663;
XX DT 02-SEP-2003 (first entry)
XX DE Nucleotide sequence of a PCR primer CD81_F.
XX KW Cardiopathy; nucleic acid marker; therapy; human; PCR; primer; ss.
XX OS Homo sapiens.
XX PN W02003040407-A2.
XX PD 15-MAY-2003.
XX PF 08-NOV-2002; 2002WO-BF012522.
XX PR 09-NOV-2001; 2001EP-00126800.
XX (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX Ruiz P, Grzeskowiak R, Drungowski M, Witt H, Osterziel KJ;
PI Perrot A, Saleh A;
XX WPI; 2003-430678/40.
XX New diagnostic composition comprising at least one nucleic acid molecule
PT that is capable of specifically hybridizing to the mRNA of the gene,
PT useful for diagnosing cardiopathy, e.g. cardiomyopathy or dilated
PT cardiomyopathy.
XX Example 1; Page 21; 82pp; English.
XX The invention relates to a diagnostic composition comprising at least one
CC nucleic acid molecule listed in the specification that is capable of
CC specifically hybridizing to the mRNA of at least one of the genes given
CC in the specification. The diagnostic composition and nucleic acid
CC molecules are useful for diagnosing cardiopathy or a disposition to
CC cardiopathy, e.g. cardiomyopathy or dilated cardiomyopathy. The method
CC involves contacting a target sample with the nucleic acid molecule cited
CC above, and comparing the concentration of the individual mRNA(s) with the
CC concentration of the corresponding mRNAs from at least one of the healthy
CC donor. The nucleic acids are also useful for the isolation and
CC development of a compound useful for therapy or prevention of a
CC cardiopathy. Sequences ACC78653-700 represent primers used in real-time
CC quantitative PCR for amplifying human genes, during the course of the
XX invention
XX Sequence 21 BP; 5 A; 4 C; 7 G; 5 T; 0 U; 0 Other;

12/10/2001

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DT 05-FEB-2003 (first entry)
XX CD81 forward PCR primer.
DE
XX
KW CD81; tetraspanin; human; dendritic cell; cell culture; cancer;
KW immunotherapy; cell therapy; cytostatic; antitumour; vaccine; PCR;
KW primer; ss.
XX
XX Homo sapiens.
XX
XX WO200244338-A2.
XX
XX 06-JUN-2002.
XX
XX 30-NOV-2001; 2001WO-US045099.
XX
XX 30-NOV-2000; 2000US-00726883.
XX
XX (UYCO ) UNIV COLUMBIA NEW YORK.
XX
XX Harris PE, Hesdorffer C;
XX
XX WPI; 2003-058273/05.
XX
XX Reproducibly generating dendritic cells comprises loading blood
XX mononuclear cells into cell culture container containing microcarrier
XX beads, incubating the container, separating non-adherent cells and cells
XX adhered to beads.
XX
XX Example 2; Page 24; 79pp; English.
XX
XX The present sequence is that of a forward primer, designated CD81-F, for
XX the human tetraspanin molecule, CD81. Semi-quantitative PCR was used to
XX determine the level of expression of 4 genes (CD37, CD81, CD53 and BCL-6)
XX in mature and immature dendritic cells (DCs). Abundant accumulation of
XX CD81 mRNA was detected in immature DCs, whereas significantly lower
XX levels of CD81 transcripts were detected following DC maturation,
XX indicating differential expression. The invention provides good
XX manufacturing procedure (GMP)-compatible culture methods for the
XX production of DCs to be used in cancer immunotherapy. These involve
XX loading blood mononuclear cells into a cell culture container, e.g. a gas
XX permeable cell culture bag containing sterile plastic microcarrier
XX beads, incubating the tissue culture, and separating non-adherent cells
XX from cells adhered to the microcarrier beads. The method can be adapted
XX for growth of other adherence-dependent haematopoietic cells
XX
XX Sequence 24 BP; 5 A; 9 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 1.6%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 398 GCGCCCAACACCTTCTATGTAGGC 421
Db 1 GCGCCCAACACCTTCTATGTAGGC 24

RESULT 11
ABV75839/c
ID ABV75839 standard; DNA; 24 BP.
XX
XX
XX ABV75839;
XX
XX 05-FEB-2003 (first entry)
XX
XX CD81 reverse PCR primer.
XX
XX CD81; tetraspanin; human; dendritic cell; cell culture; cancer;
KW immunotherapy; cell therapy; cytostatic; antitumour; vaccine; PCR;
KW primer; ss.
XX
XX Homo sapiens.
XX
XX

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PN WO200244338-A2.
XX
XX 06-JUN-2002.
XX
XX 30-NOV-2001; 2001WO-US045099.
XX
XX 30-NOV-2000; 2000US-00726883.
XX
XX (UYCO ) UNIV COLUMBIA NEW YORK.
XX
XX Harris PE, Hesdorffer C;
XX
XX WPI; 2003-058273/05.
XX
XX Reproducibly generating dendritic cells comprises loading blood
XX mononuclear cells into cell culture container containing microcarrier
XX beads, incubating the container, separating non-adherent cells and cells
XX adhered to beads.
XX
XX Example 2; Page 24; 79pp; English.
XX
XX The present sequence is that of a reverse primer, designated CD81-R, for
XX the human tetraspanin molecule, CD81. Semi-quantitative PCR was used to
XX determine the level of expression of 4 genes (CD37, CD81, CD53 and BCL-6)
XX in mature and immature dendritic cells (DCs). Abundant accumulation of
XX CD81 mRNA was detected in immature DCs, whereas significantly lower
XX levels of CD81 transcripts were detected following DC maturation,
XX indicating differential expression. The invention provides good
XX manufacturing procedure (GMP)-compatible culture methods for the
XX production of DCs to be used in cancer immunotherapy. These involve
XX loading blood mononuclear cells into a cell culture container, e.g. a gas
XX permeable cell culture bag containing sterile plastic microcarrier
XX beads, incubating the tissue culture, and separating non-adherent cells
XX from cells adhered to the microcarrier beads. The method can be adapted
XX for growth of other adherence-dependent haematopoietic cells
XX
XX Sequence 24 BP; 6 A; 8 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 1.6%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 892 CGAGATGATCCTGAGCATGCTGCT 915
Db 24 CGAGATGATCCTGAGCATGCTGCT 1

RESULT 12
AAH88905
ID AAH88905 standard; DNA; 21 BP.
XX
XX AAH88905;
XX
XX 27-FEB-2002 (first entry)
XX
XX Human polymorphic oligonucleotide AC003693 fragment #1.
XX
XX Human; single nucleotide polymorphic; SNP; forensic science;
KW paternity testing; phenotypic trait; genetic mapping; animal breeding;
KW plant breeding; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Variation replace(11,g)
XX /*tag= a
XX /standard_name= "single nucleotide polymorphism"

WO200134840-A2.
XX
XX 17-MAY-2001.
XX
XX 10-NOV-2000; 2000WO-US030766.
XX

```

CC The invention relates to a novel method for screening substances
 CC inhibiting the binding of hepatitis C virus (HCV) E2/NS1 protein to an
 CC antibody having an affinity for the protein. The novel method comprises:
 CC contacting the protein with any of the antibodies selected, from those
 CC described in the specification, in the presence or absence of a test
 CC substance; and comparing the binding results. Compositions comprising the
 CC (recombinant) antibodies are useful as antivirals and are especially
 CC useful in preventing or treating HCV (hepatitis C) infections. This
 CC polynucleotide sequence represents a PCR primer relating to the novel HCV
 CC therapy method of the invention
 XX
 SQ Sequence 26 BP; 3 A; 7 C; 13 G; 3 T; 0 U; 0 Other;

Query Match 1.7%; Score 26; DB 1; Length 26;
 Best Local Similarity 100.0%; Pred. No. 3.7;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 231 GCGCCGCGCATGGAGTGGAGGGCTGC 256
 Db 1 GCGCCGCGCATGGAGTGGAGGGCTGC 26

RESULT 8

AAH74674/C
 ID AAH74674 standard; DNA; 24 BP.

XX AC AAH74674;

DT 29-OCT-2001 (first entry)

DE PCR primer used to amplify DNA encoding a HCV protein.

XX Complementarity determining region; CDR; single chain antibody; ScFv;
 KW hepatitis C virus; HCV; HCV infection; CD81; E2 protein; NS1 protein;
 KW envelope glycoprotein; PCR primer; ss.

OS Hepatitis C virus.

XX WO200158459-A1.

XX 16-AUG-2001.

PF 13-FEB-2001; 2001WO-JP000967.

PR 14-FEB-2000; 2000JP-00034906.

PA (MITS-) MITSUBISHI-TOKYO PHARM INC.

PI Itami S, Shibui T, Seki M, Yotsumoto Y, Matsuura Y, Miyamura T;

XX WPI; 2001-496986/54.

XX Remedies for hepatitis C containing substances with antiviral effects
 PT e.g. antibodies, proteins, sulfated polysaccharides and low-molecular
 PT compounds, by inhibiting binding of hepatitis C virus envelope
 PT glycoprotein or CD81.

XX Example 1; Page 27; 138pp; Japanese.

XX PCR primers AAH74673-74 were used to amplify DNA encoding a hepatitis C
 CC virus (HCV) protein. The amplified fragment was used in the course of the
 CC invention. The specification describes a substance which inhibits the
 CC binding between hepatitis C virus (HCV) and cells with potential HCV
 CC infection, cells with expression of CD81, or CD81. This substance is
 CC especially an antibody with affinity towards HCV E2/NS1 protein,
 CC containing amino acid sequences based on the complementarity determining
 CC region (CDR) 1, CDR2 and CDR3 of the H and L chain variable regions. The
 CC antibody inhibits the viral envelope glycoprotein. It is also a CD81
 CC inhibitor. The antibodies and drugs are used for treatment and/or
 CC prevention of hepatitis C, or for diagnosis of hepatitis C

XX Sequence 24 BP; 5 A; 7 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 1.6%; Score 24; DB 1; Length 24;
 Best Local Similarity 100.0%; Pred. No. 7.9;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 927 TCCGGAACAGCTCCGTGTACTGAG 950
 Db 24 TCCGGAACAGCTCCGTGTACTGAG 1

RESULT 9

ABT34329/C
 ID ABT34329 standard; DNA; 24 BP.

XX AC ABT34329;

XX 12-JUN-2003 (first entry)

DE Hepatitis C virus treatment related PCR primer SEQ ID No 41.

XX Virucide; inhibit; binding; hepatitis C virus; HCV; E2/NS1 protein;
 KW antibody; recombinant; antiviral; infection; PCR; primer; ss.

OS Unidentified.

PN WO2003014728-A1.

XX 20-FEB-2003.

PF 09-AUG-2002; 2002WO-JP008175.

PR 10-AUG-2001; 2001JP-00243947.

XX (MITS-) MITSUBISHI PHARMA CORP.

PA (NINA-) JAPAN AGENCY NAT INST HEALTH.

PI Itami S, Seki M, Kito M, Matsuura Y, Miyamura T;

XX WPI; 2003-248334/24.

XX Pharmaceutical compositions for hepatitis C containing screened
 PT inhibitors of binding between hepatitis virus (HCV) E2/NS1 protein and
 PT antibody, useful in preventing or treating HCV infections.

PS Example 2; Page 24; 136pp; Japanese.

XX The invention relates to a novel method for screening substances
 CC inhibiting the binding of hepatitis C virus (HCV) E2/NS1 protein to an
 CC antibody having an affinity for the protein. The novel method comprises:
 CC contacting the protein with any of the antibodies selected, from those
 CC described in the specification, in the presence or absence of a test
 CC substance; and comparing the binding results. Compositions comprising the
 CC (recombinant) antibodies are useful as antivirals and are especially
 CC useful in preventing or treating HCV (hepatitis C) infections. This
 CC polynucleotide sequence represents a PCR primer relating to the novel HCV
 CC therapy method of the invention

XX Sequence 24 BP; 5 A; 7 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 1.6%; Score 24; DB 1; Length 24;
 Best Local Similarity 100.0%; Pred. No. 7.9;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 927 TCCGGAACAGCTCCGTGTACTGAG 950
 Db 24 TCCGGAACAGCTCCGTGTACTGAG 1

RESULT 10

ABV75838
 ID ABV75838 standard; DNA; 24 BP.

XX AC ABV75838;

XX

QY 1385 GCCTTCATGACCTGTCCTTTCTAAACAGTCGCGCTTCAACTGTATATCACA 1434
 |||||
 Db 1 GCCTTCATGACCTGTCCTTTCTAAACAGTCGCGCTTCAACTGTATATCACA 50

RESULT 3
 ACD44032
 ID ACD44032 standard; DNA; 31 BP.
 XX
 AC ACD44032;
 XX
 DT 09-SEP-2003 (first entry)
 XX
 DE Human gene single nucleotide polymorphism region #466.
 XX
 KW Human; single nucleotide polymorphism; SNP; forensic; paternity testing;
 KW genetic mapping of phenotypic trait; ds.
 XX
 OS Homo sapiens.
 XX
 PN US2003039973-A1.
 XX
 PD 27-FEB-2003.
 XX
 PF 24-JUL-2001; 2001US-00912263.
 XX
 PR 24-JUL-2000; 2000US-0220315P.
 XX
 PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
 XX
 PI Cargill M, Ireland JS, Lander ES;
 XX
 DR WPI; 2003-492161/46.
 XX
 PF New nucleic acids comprising single nucleotide polymorphisms, useful in
 XX forensics (e.g. to identify an individual), paternity testing,
 PT correlating polymorphisms with phenotypic traits, and genetic mapping of
 PT phenotypic traits.
 XX
 PS Example; Page 40; 48pp; English.

XX The invention describes a nucleic acid molecule comprising one of 525 31
 CC nucleotide sequences, given in the specification, or at least 10
 CC nucleotides in length, and comprising a polymorphic site, where the
 CC nucleotide at the polymorphic site is different from a nucleotide at the
 CC polymorphic site in a corresponding reference allele. The nucleic acids
 CC comprising a single nucleotide polymorphism are useful in forensics (e.g.
 CC to identify an individual), in paternity testing, in correlating
 CC polymorphisms with phenotypic traits, and in genetic mapping of
 CC of a gene and a phenotype can be used in the diagnosis of that phenotype,
 CC as well as in the development of treatments for the phenotype. This
 CC sequence represents a fragment of a human gene found to containing a
 CC single nucleotide polymorphism following re-sequencing. The regions can
 CC be used to develop primers and probes for use in detect the SNP regions
 CC in individuals
 XX
 SQ Sequence 31 BP; 5 A; 10 C; 7 G; 8 T; 0 U; 1 Other;

Query Match 2.0%; Score 30.6; DB 1; Length 31;
 Best Local Similarity 96.8%; Pred. No. 0.65;
 Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 820 CGATGACCTTCTTCGGGAAGCTGTACCTC 850
 |||||
 Db 1 CGATGACCTTCTTCGGGAAGCTGTACCTC 31

RESULT 4
 ACD44033
 ID ACD44033 standard; DNA; 31 BP.
 XX
 AC ACD44033;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human CD81/TAPA-1 RT-PCR probe.
 XX
 KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
 KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
 KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
 KW bacterial infection; PCR; probe; RT-PCR; reverse transcriptase PCR;

Query Match 2.0%; Score 30.6; DB 1; Length 31;
 Best Local Similarity 96.8%; Pred. No. 0.65;
 Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 820 CGATGACCTTCTTCGGGAAGCTGTACCTC 850
 |||||
 Db 1 CGATGACCTTCTTCGGGAAGCTGTACCTC 31

RESULT 5
 ACD35534
 ID ACD35534 standard; DNA; 28 BP.
 XX
 AC ACD35534;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human CD81/TAPA-1 RT-PCR probe.

Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
 cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
 virucide; antiparasitic; inflammatory disorder; parasitic infection;
 bacterial infection; PCR; probe; RT-PCR; reverse transcriptase PCR;

AC ACD44033;
 XX
 DT 09-SEP-2003 (first entry)
 XX
 DE Human gene single nucleotide polymorphism region #467.
 XX
 KW Human; single nucleotide polymorphism; SNP; forensic; paternity testing;
 KW genetic mapping of phenotypic trait; ds.
 XX
 OS Homo sapiens.
 XX
 PN US2003039973-A1.
 XX
 PD 27-FEB-2003.
 XX
 PF 24-JUL-2001; 2001US-00912263.
 XX
 PR 24-JUL-2000; 2000US-0220315P.
 XX
 PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
 XX
 PI Cargill M, Ireland JS, Lander ES;
 XX
 DR WPI; 2003-492161/46.

New nucleic acids comprising single nucleotide polymorphisms, useful in
 forensics (e.g. to identify an individual), paternity testing,
 correlating polymorphisms with phenotypic traits, and genetic mapping of
 phenotypic traits.

Example; Page 40; 48pp; English.
 The invention describes a nucleic acid molecule comprising one of 525 31
 nucleotide sequences, given in the specification, or at least 10
 nucleotides in length, and comprising a polymorphic site, where the
 nucleotide at the polymorphic site is different from a nucleotide at the
 polymorphic site in a corresponding reference allele. The nucleic acids
 comprising a single nucleotide polymorphism are useful in forensics (e.g.
 to identify an individual), in paternity testing, in correlating
 polymorphisms with phenotypic traits, and in genetic mapping of
 of a gene and a phenotype can be used in the diagnosis of that phenotype,
 as well as in the development of treatments for the phenotype. This
 sequence represents a fragment of a human gene found to containing a
 single nucleotide polymorphism following re-sequencing. The regions can
 be used to develop primers and probes for use in detect the SNP regions
 in individuals
 Sequence 31 BP; 4 A; 8 C; 8 G; 10 T; 0 U; 1 Other;

Query Match 2.0%; Score 30.6; DB 1; Length 31;
 Best Local Similarity 96.8%; Pred. No. 0.65;
 Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 862 TGCCATCGTGGTCGCTGTATCATGATCTTC 892
 |||||
 Db 1 TGCCATCGTGGTCGCTGTATCATGATCTTC 31

RESULT 5
 ACD35534
 ID ACD35534 standard; DNA; 28 BP.
 XX
 AC ACD35534;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human CD81/TAPA-1 RT-PCR probe.
 XX
 KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
 KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
 KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
 KW bacterial infection; PCR; probe; RT-PCR; reverse transcriptase PCR;

Query Match 2.0%; Score 30.6; DB 1; Length 31;
 Best Local Similarity 96.8%; Pred. No. 0.65;
 Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 862 TGCCATCGTGGTCGCTGTATCATGATCTTC 892
 |||||
 Db 1 TGCCATCGTGGTCGCTGTATCATGATCTTC 31

RESULT 5
 ACD35534
 ID ACD35534 standard; DNA; 28 BP.
 XX
 AC ACD35534;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human CD81/TAPA-1 RT-PCR probe.

Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
 cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
 virucide; antiparasitic; inflammatory disorder; parasitic infection;
 bacterial infection; PCR; probe; RT-PCR; reverse transcriptase PCR;

545 13.4 0.9 15 1 AAF52139 IGF-I oligonucleot
546 13.4 0.9 15 1 AAF51849 IGF-I oligonucleot
547 13.4 0.9 15 1 AAF53315 IGF-I oligonucleot
548 13.4 0.9 15 1 AAF46582 IGFβ3 oligonucleo
549 13.4 0.9 15 1 AAF49043 IGF-I oligonucleot
550 13.4 0.9 15 1 AAF49042 IGF-I oligonucleot
551 13.4 0.9 15 1 AAF80919 PTGS2 allele speci
552 13.4 0.9 15 1 AAF69483 Human IL4Ralpha ge
553 13.4 0.9 15 1 ABA97405 Nucleotide sequenc
554 13.4 0.9 15 1 ABK98166 Triple helix formi
555 13.4 0.9 15 1 ABK98185 Triple helix formi
556 13.4 0.9 15 1 ABZ95518 Human chymase anti
557 13.4 0.9 15 1 ABX79839 EST polymorphic DN
558 13.4 0.9 15 1 ADB68522 Single-base mismat
559 13.2 0.9 14 1 AAV48216 3' poly-A-anchorin
560 13.2 0.9 14 1 AAZ51049 3' poly-A-anchorin
561 13.2 0.9 14 1 AAZ36741 Anchored oligo(dT)
562 13.2 0.9 14 1 AAD44142 Oligo-dT PCR prime
563 13.2 0.9 14 1 AAD44148 Oligo-dT PCR prime
564 13.2 0.9 14 1 ADC51416 Rat LIRF protein-r
565 13.2 0.9 15 1 AAX18386 RT-PCR primer of t

ALIGNMENTS

RESULT 1
ABZ04679
ID ABZ04679 standard; DNA; 50 BP.
XX
AC ABZ04679;
XX
DT 09-JAN-2003 (first entry)
XX
DE Human leukocyte gene expression profiling probe SEQ ID NO 4670.

XX T7; leukocyte; gene expression profiling; allograft rejection;
KW atherosclerosis; congestive heart failure; systemic lupus erythematosus;
KW rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
KW ss.
XX
OS Homo sapiens.
XX
PN WO200257414-A2.
XX
PD 25-JUL-2002.

XX 22-OCT-2001; 2001WO-US047856.
XX
PR 20-OCT-2000; 2000US-0241994P.
PR 08-JUN-2001; 2001US-0296764P.
XX
PA (BIOC-) BIOCARDIA INC.
XX
PI Wohlgemuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;
PI Ly N, Woodward R, Quertermous T, Johnson F;
XX
XX WPI; 2002-636525/68.

XX New system for leukocyte expression profiling, diagnosing a disease, or
PT monitoring (the rate of) progression of a disease, e.g. atherosclerosis
PT or congestive heart failure, comprises diagnostic oligonucleotides.

XX Claim 1; Page 477; Opp; English.
XX The invention relates to a system for detecting gene expression, which
CC comprises one or two isolated DNA molecules that detect expression of a
CC gene, where the gene corresponds to any of 8143 oligonucleotides
CC (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful
CC for leukocyte expression profiling. It is particularly useful for
CC diagnosing a disease, monitoring (rate of) progression of a disease,
CC predicting therapeutic outcome, determining prognosis for a patient,
CC predicting disease complications in an individual or monitoring response

CC to treatment in an individual. The diseases include cardiac allograft
CC rejection, kidney allograft rejection, liver allograft rejection,
CC atherosclerosis, congestive heart failure, systemic lupus erythematosus,
CC rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
XX
SQ Sequence 50 BP; 13 A; 17 C; 5 G; 15 T; 0 U; 0 Other;
Query Match 3.3%; Score 50; DB 1; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.00024;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1404 TTCTAACAGTCGCTTCAACTGTAATCAACATCCTGACTCGTCATT 1453
Db 1 TTCTAACAGTCGCTTCAACTGTAATCAACATCCTGACTCGTCATT 50
|||||

RESULT 2
ABZ00175
ID ABZ00175 standard; DNA; 50 BP.
XX
AC ABZ00175;
XX
DT 09-JAN-2003 (first entry)

XX Human leukocyte gene expression profiling probe SEQ ID NO 166.
XX
DE
XX
XX T7; leukocyte; gene expression profiling; allograft rejection;
KW atherosclerosis; congestive heart failure; systemic lupus erythematosus;
KW rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
KW ss.
XX
OS Homo sapiens.
XX
PN WO200257414-A2.

XX 25-JUL-2002.
XX 22-OCT-2001; 2001WO-US047856.
XX
PR 20-OCT-2000; 2000US-0241994P.
PR 08-JUN-2001; 2001US-0296764P.
XX
XX (BIOC-) BIOCARDIA INC.
XX
PI Wohlgemuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;
PI Ly N, Woodward R, Quertermous T, Johnson F;
XX
XX WPI; 2002-636525/68.

XX New system for leukocyte expression profiling, diagnosing a disease, or
PT monitoring (the rate of) progression of a disease, e.g. atherosclerosis
PT or congestive heart failure, comprises diagnostic oligonucleotides.

XX Claim 1; Page 332; Opp; English.

XX The invention relates to a system for detecting gene expression, which
CC comprises one or two isolated DNA molecules that detect expression of a
CC gene, where the gene corresponds to any of 8143 oligonucleotides
CC (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful
CC for leukocyte expression profiling. It is particularly useful for
CC diagnosing a disease, monitoring (rate of) progression of a disease,
CC predicting therapeutic outcome, determining prognosis for a patient,
CC predicting disease complications in an individual or monitoring response
CC to treatment in an individual. The diseases include cardiac allograft
CC rejection, kidney allograft rejection, liver allograft rejection,
CC atherosclerosis, congestive heart failure, systemic lupus erythematosus,
CC rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
XX
SQ Sequence 50 BP; 11 A; 18 C; 6 G; 15 T; 0 U; 0 Other;

Query Match 3.3%; Score 50; DB 1; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.00024;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

C 399	1.0	15	1	ABL57056	Hydrazide phosphor	C 472	14.4	1.0	16	1	AA18367	RT-PCR primer of t	
C 400	1.0	15	1	ABL57060	Hydrazide precuroso	C 473	14.4	1.0	16	1	AA18363	RT-PCR primer of t	
C 401	1.0	15	1	ABK98141	Triple helix formi	C 474	14.4	1.0	16	1	AAH27758	Primer used in hum	
C 402	1.0	15	1	ABK98184	Triple helix formi	C 475	14.4	1.0	16	1	AAD44143	Oligo-dT PCR prime	
C 403	1.0	15	1	ABK97501	Oligonucleotide SE	C 476	14.4	1.0	16	1	AD866353	Human pTPN11 PCR p	
C 404	1.0	15	1	ABV74142	5' End of CDNA lib	C 477	14.2	0.9	15	1	AA47676	Oligo d(T) primer	
C 405	1.0	15	1	ABV74141	Oligonucleotide us	C 478	14.2	0.9	15	1	AAD44150	Oligo-AT PCR prime	
C 406	1.0	15	1	ABV75865	Oligonucleotide T1	C 479	14.2	0.9	16	1	AA18387	RT-PCR primer of t	
C 407	1.0	15	1	ADA14836	Hairpin target seq	C 480	14	0.9	14	1	AAQ33508	Sequence of micros	
C 408	1.0	15	1	ADB68520	Single-base mismat	C 481	14	0.9	14	1	AAT36896	Candida albicans 1	
C 409	1.0	15	1	ADC18592	Annealing control	C 482	14	0.9	14	1	AAT75017	Breast tumour cDNA	
C 410	1.0	16	1	AA18369	RT-PCR primer of t	C 483	14	0.9	14	1	AAH83329	Breast cancer tumo	
C 411	1.0	16	1	AB57075	Molecular beacon t	C 484	14	0.9	14	1	AAV09229	3' poly(T) primer	
C 412	1.0	16	1	ABQ94572	Tumour suppression	C 485	14	0.9	14	1	AAV12221	Poly(T) oligonucle	
C 413	1.0	16	1	ABD57845	Target oligonucleo	C 486	14	0.9	14	1	AAV69039	Human breast tumou	
C 414	1.0	16	1	ADB68508	PNA-HypNA hybridis	C 487	14	0.9	14	1	AAQ02695	Barley HPPD primer	
C 415	1.0	17	1	AAK69799	Human flt1 VEGF re	C 488	14	0.9	14	1	AAH14689	Triple helix third	
C 416	1.0	17	1	AAK69802	Human flt1 VEGF re	C 489	14	0.9	14	1	AAH14688	Triple helix formi	
C 417	1.0	17	1	AAV37934	Primer of the spec	C 490	14	0.9	14	1	AAH57019	WO9293258 oligonuc	
C 418	1.0	17	1	AAA30181	PCR primer GT15G u	C 491	14	0.9	14	1	AAH19468	Human senescence f	
C 419	1.0	17	1	AAA30180	PCR primer GT15C u	C 492	14	0.9	14	1	AAZ08326	Human lung tumour	
C 420	1.0	17	1	AAZ35714	Murine gene anchor	C 493	14	0.9	14	1	AAH08852	Human B18A1 cDNA	
C 421	1.0	17	1	AAH82722	Human IGA nephropa	C 494	14	0.9	14	1	AAH79077	(dT)12AG primer.	
C 422	1.0	17	1	AAH82721	Human IGA nephropa	C 495	14	0.9	14	1	AAH62349	Oligonucleotide #1	
C 423	1.0	17	1	AAZ36740	Anchored oligo(dT)	C 496	14	0.9	14	1	AAH23152	Human lung tumour-	
C 424	1.0	17	1	AAZ25448	Oestrogen receptor	C 497	14	0.9	14	1	AAH84160	Oligonucleotide #2	
C 425	1.0	17	1	AAZ25452	Oestrogen receptor	C 498	14	0.9	14	1	AAH83821	RNA oligonucleotid	
C 426	1.0	17	1	AAH64203	PCR anchor primer,	C 499	14	0.9	14	1	AAH99698	Breast tumour-spec	
C 427	1.0	17	1	AAH64204	PCR anchor primer,	C 500	14	0.9	14	1	ABK46742	Human breast tumou	
C 428	1.0	17	1	AAH64183	PCR anchor primer,	C 501	14	0.9	14	1	ABQ83278	EG1 cDNA tag relat	
C 429	1.0	17	1	AAH64182	PCR anchor primer,	C 502	14	0.9	14	1	ABQ83275	EG1 cDNA tag relat	
C 430	1.0	17	1	AAH64173	PCR anchor primer,	C 503	14	0.9	14	1	ABQ83269	EG1 cDNA tag relat	
C 431	1.0	17	1	AAH64172	PCR anchor primer,	C 504	14	0.9	14	1	ABH54141	Oligo-dT primer #2	
C 432	1.0	17	1	AAH64163	PCR anchor primer,	C 505	14	0.9	14	1	AAH24491	Retinoid-regulated	
C 433	1.0	17	1	AAH64162	PCR anchor primer,	C 506	14	0.9	14	1	ABA93701	Light responsive o	
C 434	1.0	17	1	AAH64215	PCR anchor primer,	C 507	14	0.9	14	1	AAH23321	Reverse transcript	
C 435	1.0	17	1	AAH64214	PCR anchor primer,	C 508	14	0.9	14	1	AAH11209	Differential displ	
C 436	1.0	17	1	AAH64231	PCR anchor primer,	C 509	14	0.9	14	1	ADC15182	Human breast tumou	
C 437	1.0	17	1	AAH64232	PCR anchor primer,	C 510	14	0.9	14	1	ADD66355	Human lung tumour-	
C 438	1.0	17	1	AAH92294	Human pollinosis-a	C 511	14	0.9	14	1	ADH87609	Human lung tumour	
C 439	1.0	17	1	AAH92293	Human pollinosis-a	C 512	14	0.9	15	1	AAH52140	Human ICAM hammerh	
C 440	1.0	17	1	AAH91720	PCR anchor primer,	C 513	14	0.9	15	1	AAH52134	Human ICAM hammerh	
C 441	1.0	17	1	AAH91721	PCR anchor primer,	C 514	14	0.9	15	1	AAH49041	IGF-I oligonucleot	
C 442	1.0	17	1	AAH82876	Human pollinosis-a	C 515	14	0.9	15	1	ABK98169	Triple helix formi	
C 443	1.0	17	1	AAH82875	Human pollinosis-a	C 516	14	0.9	15	1	ABK98187	Triple helix formi	
C 444	1.0	17	1	AAH47128	Nucleotide sequenc	C 517	14	0.9	15	1	ABK98168	Triple helix formi	
C 445	1.0	17	1	AAH47127	Nucleotide sequenc	C 518	14	0.9	15	1	ABK98167	Triple helix formi	
C 446	1.0	17	1	ABK49636	Human Acetyltransf	C 519	14	0.9	15	1	ABK98186	EST polymorphic DN	
C 447	1.0	17	1	ABK49635	Human Acetyltransf	C 520	14	0.9	15	1	ABK79833	Oligo-dT PCR prime	
C 448	1.0	17	1	ABL59040	Nucleotide sequenc	C 521	14	0.9	16	1	AAD44145	Oligo-dT PCR prime	
C 449	1.0	17	1	ABL59039	Nucleotide sequenc	C 522	14	0.9	16	1	AAD44147	Oligo-dT PCR prime	
C 450	1.0	17	1	ABN98831	Human allergic dis	C 523	14	0.9	16	1	AAD44149	RNA intron region	
C 451	1.0	17	1	ABN99830	Human allergic dis	C 524	14	0.9	16	1	AAH54153	Multiple repeated	
C 452	1.0	17	1	AAH49950	Human B153 expres	C 525	13.8	0.9	18	1	AAH85699	Human APPBP1 gene,	
C 453	1.0	17	1	AAH49949	Human B153 expres	C 526	13.6	0.9	15	1	ABZ04679	Human leukocyte ge	
C 454	1.0	17	1	AAH47236	Allergic disease e	C 527	13.6	0.9	50	1	ABZ04679	Human ICAM hammerh	
C 455	1.0	17	1	AAH47235	Allergic disease e	C 528	13.4	0.9	15	1	AAH52144	Mouse TNF-a hammer	
C 456	1.0	17	1	ABK49757	Human atopic derma	C 529	13.4	0.9	15	1	AAH56307	Human ICAM hammerh	
C 457	1.0	17	1	ABK49758	Human atopic derma	C 530	13.4	0.9	15	1	AAH52142	Chymase antisense	
C 458	1.0	17	1	AAH44151	Oligo-AT PCR prime	C 531	13.4	0.9	15	1	AAH76466	Trinucleotide simp	
C 459	1.0	17	1	AAH79793	EST polymorphic DN	C 532	13.4	0.9	15	1	AAH86420	Oligonucleotide se	
C 460	1.0	17	1	ADB04270	Human MD27 scanlin	C 533	13.4	0.9	15	1	AAH86603	Chymase antisense	
C 461	1.0	17	1	ABZ61566	Human H-Ras DNazym	C 534	13.4	0.9	15	1	AAH54258	Oligonucleotide se	
C 462	1.0	17	1	ABZ64568	Human HER2 DNazym	C 535	13.4	0.9	15	1	AAH18364	RT-PCR primer of t	
C 463	1.0	17	1	ADC84469	PCR primer for amp	C 536	13.4	0.9	15	1	AAH33702	Low adenosine anti	
C 464	1.0	17	1	ADC84470	PCR primer for amp	C 537	13.4	0.9	15	1	AAH11718	Human MIF gene DSK	
C 465	1.0	17	1	ADH77745	DNA oligo (Seqid 5	C 538	13.4	0.9	15	1	AAH19824	Human chymase poly	
C 466	14.6	1.0	15	1	ABN87920	Human GSK allele s	C 539	13.4	0.9	15	1	AAH46644	IGFBP3 oligonucleo
C 467	14.4	1.0	16	1	AAT44591	Cryptosporidium pa	C 540	13.4	0.9	15	1	AAH52137	IGF-I oligonucleot
C 468	14.4	1.0	16	1	AAH18365	RT-PCR primer of t	C 541	13.4	0.9	15	1	AAH52138	IGF-I oligonucleot
C 469	14.4	1.0	16	1	AAH18366	RT-PCR primer of t	C 542	13.4	0.9	15	1	AAH49438	IGF-I oligonucleot
C 470	14.4	1.0	16	1	AAH18362	RT-PCR primer of t	C 543	13.4	0.9	15	1	AAH46581	IGFBP3 oligonucleo
C 471	14.4	1.0	16	1	AAH18366	RT-PCR primer of t	C 544	13.4	0.9	15	1	AAH49440	IGF-I oligonucleot

C 253	1.1	17	1	ACF36345	Nucleotide sequenc	C 326	15.4	1.0	18	1	AA290641	Human adipose tiss
C 254	1.1	17	1	ACF36370	Nucleotide sequenc	C 327	15.4	1.0	18	1	AA290650	Human adipose tiss
C 255	1.1	17	1	ADC84468	PCR primer for amp	C 328	15.4	1.0	18	1	AA290647	Human adipose tiss
C 256	1.1	18	1	AAQ34110	Sequence of a micr	C 329	15.4	1.0	18	1	AAF85699	Multiple repeated
C 257	1.1	18	1	AAQ75025	PCR primer. Synth	C 330	15.4	1.0	18	1	ADA27361	Human microsatelli
C 258	1.1	18	1	AAT94668	Anchored poly(T) o	C 331	15.4	1.0	18	1	ADC26385	NOV protein-relate
C 259	1.1	18	1	AAV541173	Nucleotide sequenc	C 332	15.2	1.0	16	1	AAF82119	Human TSA7005 gene
C 260	1.1	18	1	AAV541164	Nucleotide sequenc	C 333	15.2	1.0	17	1	AA18388	RT-PCR primer of t
C 261	1.1	18	1	AAV54167	Nucleotide sequenc	C 334	15.2	1.0	17	1	AA14174	Modified Poly-T Pr
C 262	1.1	18	1	AAV37712	Human protein AQ2	C 335	15	1.0	15	1	AAQ79185	Nuclease resistant
C 263	1.1	18	1	AAV07750	Phosphorothioate o	C 336	15	1.0	15	1	AAQ79184	Nuclease resistant
C 264	1.1	18	1	AAV21970	Nuclease resistant	C 337	15	1.0	15	1	AAT52136	Human ICAM hammerh
C 265	1.1	18	1	AAV19943	Primer SEQ ID NO:3	C 338	15	1.0	15	1	AAT52138	Human ICAM hammerh
C 266	1.1	18	1	AAV19942	Primer SEQ ID NO:2	C 339	15	1.0	15	1	AAV01604	Oligonucleotide co
C 267	1.1	18	1	AAA40563	Human adult ovary	C 340	15	1.0	15	1	AAV01603	Oligonucleotide co
C 268	1.1	18	1	AAZ90643	Human adipose tiss	C 341	15	1.0	15	1	AAV07431	Synthetic peptide-
C 269	1.1	18	1	AAZ90646	Human adipose tiss	C 342	15	1.0	15	1	AAT86675	Oligonucleotide li
C 270	1.1	18	1	AAZ90643	Human adipose tiss	C 343	15	1.0	15	1	AAT86605	Oligonucleotide se
C 271	1.1	18	1	AAZ87161	Oligoarabinonucleo	C 344	15	1.0	15	1	AAZ87161	Transcript tag seq
C 272	1.1	18	1	AAZ87162	Deoxyarabinonucleo	C 345	15	1.0	15	1	AAZ87162	Tag sequence of a
C 273	1.1	18	1	AAZ87166	Deoxyarabinonucleo	C 346	15	1.0	15	1	AAZ87166	Tag sequence of a
C 274	1.1	18	1	AAZ87167	Deoxyarabinonucleo	C 347	15	1.0	15	1	AAZ87167	N3-P5 phosphoramid
C 275	1.1	18	1	AAZ87167	Oligonucleotide #6	C 348	15	1.0	15	1	AAZ87167	N3-P5 phosphoramid
C 276	1.1	18	1	AAZ87167	Oligonucleotide A1	C 349	15	1.0	15	1	AAZ87167	HCV 3', non core re
C 277	1.1	18	1	AAZ87167	Binary encoded seq	C 350	15	1.0	15	1	AAZ87167	Substrate for HH r
C 278	1.1	18	1	AAZ87167	Binary encoded seq	C 351	15	1.0	15	1	AAZ87167	PCR primer used to
C 279	1.1	18	1	AAZ87167	mRNA fragment used	C 352	15	1.0	15	1	AAZ87167	Primer used to rev
C 280	1.1	18	1	AAZ87167	Immunostimulatory	C 353	15	1.0	15	1	AAZ87167	Nucleic acid sequ
C 281	1.1	18	1	AAZ87167	Immunostimulatory	C 354	15	1.0	15	1	AAZ87167	Nucleic acid sequ
C 282	1.1	18	1	AAZ87167	Immunostimulatory	C 355	15	1.0	15	1	AAZ87167	Nucleic acid sequ
C 283	1.1	18	1	AAZ87167	Immunostimulatory	C 356	15	1.0	15	1	AAZ87167	Nucleic acid sequ
C 284	1.1	18	1	AAZ87167	Immunostimulatory	C 357	15	1.0	15	1	AAZ87167	Nucleic acid sequ
C 285	1.1	18	1	AAZ87167	Immunostimulatory	C 358	15	1.0	15	1	AAZ87167	Nucleic acid sequ
C 286	1.1	18	1	AAZ87167	Immunostimulatory	C 359	15	1.0	15	1	AAZ87167	Nucleic acid sequ
C 287	1.1	18	1	AAZ87167	Immunostimulatory	C 360	15	1.0	15	1	AAZ87167	Nucleic acid sequ
C 288	1.1	18	1	AAZ87167	Immunostimulatory	C 361	15	1.0	15	1	AAZ87167	Nucleic acid sequ
C 289	1.1	18	1	AAZ87167	Immunostimulatory	C 362	15	1.0	15	1	AAZ87167	Nucleic acid sequ
C 290	1.1	18	1	AAZ87167	Immunostimulatory	C 363	15	1.0	15	1	AAZ87167	Nucleic acid sequ
C 291	1.1	18	1	AAZ87167	Immunostimulatory	C 364	15	1.0	15	1	AAZ87167	Nucleic acid sequ
C 292	1.1	18	1	AAZ87167	Immunostimulatory	C 365	15	1.0	15	1	AAZ87167	Nucleic acid sequ
C 293	1.1	18	1	AAZ87167	Immunostimulatory	C 366	15	1.0	15	1	AAZ87167	Nucleic acid sequ
C 294	1.1	18	1	AAZ87167	Immunostimulatory	C 367	15	1.0	15	1	AAZ87167	Nucleic acid sequ
C 295	1.1	18	1	AAZ87167	Immunostimulatory	C 368	15	1.0	15	1	AAZ87167	Nucleic acid sequ
C 296	1.1	18	1	AAZ87167	Immunostimulatory	C 369	15	1.0	15	1	AAZ87167	Nucleic acid sequ
C 297	1.1	18	1	AAZ87167	Immunostimulatory	C 370	15	1.0	15	1	AAZ87167	Nucleic acid sequ
C 298	1.1	18	1	AAZ87167	Immunostimulatory	C 371	15	1.0	15	1	AAZ87167	Nucleic acid sequ
C 299	1.1	18	1	AAZ87167	Immunostimulatory	C 372	15	1.0	15	1	AAZ87167	Nucleic acid sequ
C 300	1.1	18	1	AAZ87167	Immunostimulatory	C 373	15	1.0	15	1	AAZ87167	Nucleic acid sequ
C 301	1.1	18	1	AAZ87167	Immunostimulatory	C 374	15	1.0	15	1	AAZ87167	Nucleic acid sequ
C 302	1.1	18	1	AAZ87167	Immunostimulatory	C 375	15	1.0	15	1	AAZ87167	Nucleic acid sequ
C 303	1.1	18	1	AAZ87167	Immunostimulatory	C 376	15	1.0	15	1	AAZ87167	Nucleic acid sequ
C 304	1.1	18	1	AAZ87167	Immunostimulatory	C 377	15	1.0	15	1	AAZ87167	Nucleic acid sequ
C 305	1.1	18	1	AAZ87167	Immunostimulatory	C 378	15	1.0	15	1	AAZ87167	Nucleic acid sequ
C 306	1.1	18	1	AAZ87167	Immunostimulatory	C 379	15	1.0	15	1	AAZ87167	Nucleic acid sequ
C 307	1.1	18	1	AAZ87167	Immunostimulatory	C 380	15	1.0	15	1	AAZ87167	Nucleic acid sequ
C 308	1.1	18	1	AAZ87167	Immunostimulatory	C 381	15	1.0	15	1	AAZ87167	Nucleic acid sequ
C 309	1.1	18	1	AAZ87167	Immunostimulatory	C 382	15	1.0	15	1	AAZ87167	Nucleic acid sequ
C 310	1.1	18	1	AAZ87167	Immunostimulatory	C 383	15	1.0	15	1	AAZ87167	Nucleic acid sequ
C 311	1.1	18	1	AAZ87167	Immunostimulatory	C 384	15	1.0	15	1	AAZ87167	Nucleic acid sequ
C 312	1.1	18	1	AAZ87167	Immunostimulatory	C 385	15	1.0	15	1	AAZ87167	Nucleic acid sequ
C 313	1.1	18	1	AAZ87167	Immunostimulatory	C 386	15	1.0	15	1	AAZ87167	Nucleic acid sequ
C 314	1.1	18	1	AAZ87167	Immunostimulatory	C 387	15	1.0	15	1	AAZ87167	Nucleic acid sequ
C 315	1.1	18	1	AAZ87167	Immunostimulatory	C 388	15	1.0	15	1	AAZ87167	Nucleic acid sequ
C 316	1.1	18	1	AAZ87167	Immunostimulatory	C 389	15	1.0	15	1	AAZ87167	Nucleic acid sequ
C 317	1.1	18	1	AAZ87167	Immunostimulatory	C 390	15	1.0	15	1	AAZ87167	Nucleic acid sequ
C 318	1.1	18	1	AAZ87167	Immunostimulatory	C 391	15	1.0	15	1	AAZ87167	Nucleic acid sequ
C 319	1.1	18	1	AAZ87167	Immunostimulatory	C 392	15	1.0	15	1	AAZ87167	Nucleic acid sequ
C 320	1.1	18	1	AAZ87167	Immunostimulatory	C 393	15	1.0	15	1	AAZ87167	Nucleic acid sequ
C 321	1.1	18	1	AAZ87167	Immunostimulatory	C 394	15	1.0	15	1	AAZ87167	Nucleic acid sequ
C 322	1.1	18	1	AAZ87167	Immunostimulatory	C 395	15	1.0	15	1	AAZ87167	Nucleic acid sequ
C 323	1.1	18	1	AAZ87167	Immunostimulatory	C 396	15	1.0	15	1	AAZ87167	Nucleic acid sequ
C 324	1.1	18	1	AAZ87167	Immunostimulatory	C 397	15	1.0	15	1	AAZ87167	Nucleic acid sequ
C 325	1.1	18	1	AAZ87167	Immunostimulatory	C 398	15	1.0	15	1	AAZ87167	Nucleic acid sequ

C 107	18	1.2	19	1	AAQ75551	Reverse transcript	C 180	16.4	1.1	18	1	ACF36339	Nucleotide sequenc
C 108	18	1.2	20	1	AAQ75557	Reverse transcript	C 181	16.4	1.1	18	1	ACF36364	Nucleotide sequenc
C 109	18	1.2	20	1	AAQ75575	Reverse transcript	C 182	16.4	1.1	19	1	AAQ75549	Reverse transcript
C 110	18	1.2	20	1	AAQ75576	Reverse transcript	C 183	16.4	1.1	19	1	AAQ75548	Reverse transcript
C 111	18	1.2	20	1	AAQ74916	Mammalian stem cel	C 184	16.4	1.1	19	1	AAQ75547	Reverse transcript
C 112	18	1.2	20	1	AAAL3753	Stem cell factor u	C 185	16.4	1.1	19	1	AAQ75555	Reverse transcript
C 113	18	1.2	20	1	AAH41332	Universal stem cel	C 186	16.2	1.1	18	1	AAQ18389	RT-PCR primer of t
C 114	18	1.2	20	1	AAQ04112	Human SCF (stem ce	C 187	16.2	1.1	19	1	AAQ18389	Template mRNA poly
C 115	18	1.2	20	1	AAH89092	Mammalian stem cel	C 188	16.2	1.1	19	1	AAQ18390	RT-PCR primer of t
C 116	18	1.2	20	1	AAH23890	Human SCF (stem ce	C 189	16.2	1.1	19	1	AAQ18390	(-)-limonene-6-hyd
C 117	18	1.2	20	1	AAQ04213	Human SCF (stem ce	C 190	16.2	1.1	19	1	AAQ299489	Primer HOOK for CD
C 118	18	1.2	20	1	AAQ10448	Human stem cell fa	C 191	16.2	1.1	19	1	AAQ15201	3' sequencing prim
C 119	18	1.2	20	1	AAQ35465	Rat SCF 5' cDNA am	C 192	16.2	1.1	19	1	AAQ21968	Mouse total gene è
C 120	18	1.2	20	1	ABQ73849	SCF universal olig	C 193	16.2	1.1	19	1	AAQ76617	Spearmint (-)-limo
C 121	18	1.2	20	1	ABQ05917	Hepatitis B virus	C 194	16.2	1.1	19	1	AAQ06525	Mouse microglia an
C 122	18	1.2	20	1	ABQ89240	Human oligonucleot	C 195	16.2	1.1	19	1	ABQ71509	CNS related 3' seq
C 123	18	1.2	20	1	ADBS2461	Stem cell factor (C 196	16.2	1.1	19	1	ABQ73231	Rabbit atheroscler
C 124	18	1.2	21	1	AAQ75713	Reverse transcript	C 197	16.2	1.1	19	1	AAQ34663	PCR primer #4 used
C 125	18	1.2	21	1	AAQ75703	Reverse transcript	C 198	16.2	1.1	19	1	AAQ40279	HOOK PCR primer us
C 126	18	1.2	21	1	AAQ75714	Reverse transcript	C 199	16.2	1.1	19	1	ABQ268389	Reverse transcript
C 127	18	1.2	21	1	AAQ75705	Reverse transcript	C 200	16.2	1.1	19	1	ACC79402	M13 sequencing pri
C 128	18	1.2	21	1	AAQ75706	Reverse transcript	C 201	16.2	1.1	19	1	AAQ49149	3' sequencing prim
C 129	18	1.2	21	1	AAQ75707	Reverse transcript	C 202	16.2	1.1	19	1	ADQ50267	3' sequencing prim
C 130	18	1.2	21	1	AAQ75710	Reverse transcript	C 203	16.2	1.1	19	1	ADQ21495	Human PRDI-BF1 RT-
C 131	18	1.2	21	1	AAQ75709	Reverse transcript	C 204	16	1.1	16	1	AAQ18368	RT-PCR primer of t
C 132	18	1.2	21	1	AAQ75711	Reverse transcript	C 205	16	1.1	16	1	AAQ07568	Homo sapiens fetal
C 133	17.4	1.2	19	1	AAQ75550	Reverse transcript	C 206	16	1.1	16	1	AAQ606068	DNA chip primer #4
C 134	17.4	1.2	20	1	AAQ75574	Reverse transcript	C 207	16	1.1	16	1	ABA04585	Oligonucleotide #5
C 135	17.4	1.2	20	1	AAQ75586	Reverse transcript	C 208	16	1.1	16	1	AAQ30895	Oligonucleotide-mi
C 136	17.4	1.2	20	1	AAQ75594	Reverse transcript	C 209	16	1.1	16	1	AAQ30880	Oligonucleotide po
C 137	17.4	1.2	20	1	AAQ75582	Reverse transcript	C 210	16	1.1	16	1	AAQ42481	Oligonucleotide us
C 138	17.4	1.2	20	1	AAQ75583	Reverse transcript	C 211	16	1.1	16	1	ABA97402	Nucleotide sequenc
C 139	17.4	1.2	20	1	AAQ75590	Reverse transcript	C 212	16	1.1	16	1	AAQ56451	2'-F-ANA antisense
C 140	17.4	1.2	20	1	AAQ75592	Reverse transcript	C 213	16	1.1	16	1	AAQ54078	Oligo-homodeoxyrib
C 141	17.4	1.2	20	1	AAQ75571	Cell cycle regulat	C 214	16	1.1	16	1	ADQ68519	DNA hybridisation
C 142	17.4	1.2	20	1	AAQ83128	Hepatitis E virus	C 215	16	1.1	17	1	AAQ69800	Human fit1 VEGF re
C 143	17.4	1.2	20	1	AAQ69679	Hepatitis E virus	C 216	16	1.1	17	1	AAQ69801	Human fit1 VEGF re
C 144	17.4	1.2	20	1	AAQ69675	Hepatitis E virus	C 217	16	1.1	17	1	AAQ49503	Human eosinophil c
C 145	17.4	1.2	20	1	ABZ85532	Human oligonucleot	C 218	16	1.1	17	1	AAQ18371	RT-PCR primer of t
C 146	17	1.1	18	1	AAQ94667	Anchored poly(T) o	C 219	16	1.1	17	1	AAQ18370	RT-PCR primer of t
C 147	17	1.1	18	1	AAQ54170	Nucleotide sequenc	C 220	16	1.1	17	1	AAQ30179	PCR primer GT15A u
C 148	17	1.1	18	1	AAQ16008	PCR primer D-R use	C 221	16	1.1	17	1	AAQ82720	Human Iga nephropa
C 149	17	1.1	18	1	AAQ18373	RT-PCR primer of t	C 222	16	1.1	17	1	AAQ26739	Anchored oligo(dT)
C 150	17	1.1	18	1	AAQ18372	RT-PCR primer of t	C 223	16	1.1	17	1	AAQ25450	Oestrogen receptor
C 151	17	1.1	18	1	AAQ290640	Human adipose tiss	C 224	16	1.1	17	1	AAQ25449	Oestrogen receptor
C 152	17	1.1	18	1	AAQ243267	Murine Sox3 Gene P	C 225	16	1.1	17	1	AAQ25451	Oestrogen receptor
C 153	17	1.1	18	1	AAQ05252	PCR primer D-R use	C 226	16	1.1	17	1	AAQ98232	Human retrovirus H
C 154	17	1.1	19	1	AAQ75552	Reverse transcript	C 227	16	1.1	17	1	AAQ50197	2'-Methoxyethoxy-m
C 155	17	1.1	19	1	AAQ75553	Reverse transcript	C 228	16	1.1	17	1	AAQ50197	PCR anchor primer,
C 156	17	1.1	19	1	AAQ75554	Reverse transcript	C 229	16	1.1	17	1	AAQ64181	PCR anchor primer,
C 157	17	1.1	20	1	AAQ75584	Reverse transcript	C 230	16	1.1	17	1	AAQ64171	PCR anchor primer,
C 158	17	1.1	20	1	AAQ75585	Reverse transcript	C 231	16	1.1	17	1	AAQ64161	PCR anchor primer,
C 159	17	1.1	20	1	AAQ75579	Reverse transcript	C 232	16	1.1	17	1	AAQ64213	PCR anchor primer,
C 160	17	1.1	20	1	AAQ75589	Reverse transcript	C 233	16	1.1	17	1	AAQ64230	Human pollinosis-a
C 161	17	1.1	20	1	AAQ75588	Reverse transcript	C 234	16	1.1	17	1	AAQ92292	PCR anchor primer,
C 162	17	1.1	20	1	AAQ75581	Reverse transcript	C 235	16	1.1	17	1	AAQ91719	Human pollinosis-a
C 163	17	1.1	20	1	AAQ75583	Reverse transcript	C 236	16	1.1	17	1	AAQ82874	Human pollinosis-a
C 164	17	1.1	20	1	AAQ75580	Reverse transcript	C 237	16	1.1	17	1	AAQ47126	Nucleotide sequenc
C 165	17	1.1	20	1	AAQ75587	Reverse transcript	C 238	16	1.1	17	1	ABQ13941	5'-PCR primer used
C 166	17	1.1	20	1	AAQ77752	Phosphorothioate o	C 239	16	1.1	17	1	ABQ13941	Human acetyltransf
C 167	17	1.1	20	1	ABZ89546	Human oligonucleot	C 240	16	1.1	17	1	ABQ59038	Nucleotide sequenc
C 168	17	1.1	20	1	ABZ88880	Human oligonucleot	C 241	16	1.1	17	1	ABQ99829	Human allergic dis
C 169	17	1.1	20	1	ABZ89179	Human oligonucleot	C 242	16	1.1	17	1	AAQ49948	Human B153 expres
C 170	17	1.1	20	1	ABZ92865	Human oligonucleot	C 243	16	1.1	17	1	AAQ47234	Allergic disease e
C 171	17	1.1	20	1	ABZ89703	Human oligonucleot	C 244	16	1.1	17	1	ABQ49756	Human atopic derma
C 172	17	1.1	20	1	ABZ88694	Human oligonucleot	C 245	16	1.1	17	1	ADQ04271	Human MDZ7 scannin
C 173	17	1.1	20	1	ABZ89014	Human oligonucleot	C 246	16	1.1	17	1	ADQ04272	Human MDZ7 scannin
C 174	16.6	1.1	18	1	AAQ44128	PCR primer #3 desi	C 247	16	1.1	17	1	ABQ70578	Primer. Synthetic
C 175	16.6	1.1	19	1	AAQ69640	Telomerase Oligo-d	C 248	16	1.1	17	1	AAQ56441	Antisense oligo #2
C 176	16.4	1.1	18	1	AAQ30173	Sequence derived f	C 249	16	1.1	17	1	AAQ56448	2'-F-ANA antisense
C 177	16.4	1.1	18	1	AAQ34669	Anchored poly(T) o	C 250	16	1.1	17	1	AAQ56449	2'-F-ANA antisense
C 178	16.4	1.1	18	1	AAQ75596	Binary encoded seq	C 251	16	1.1	17	1	AAQ56447	2'-F-ANA antisense
C 179	16.4	1.1	18	1	ABQ13935	5'-PCR primer used	C 252	16	1.1	17	1	AAQ56450	2'-F-ANA antisense

Query Match 1.4%; Score 21; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 668 AAGCTGTGTGTAAGACCTTC 688
 DB 1 AAGCTGTGTGTAAGACCTTC 21

RESULT 15

ACC78664/c

ID ACC78664 standard; DNA; 20 BP.

XX AC ACC78664;

XX DT 02-SRP-2003 (first entry)

XX DE Nucleotide sequence of a PCR primer CD81_R.

XX KW Cardiopathy; nucleic acid marker; therapy; human; PCR; primer; ss.

XX OS Homo sapiens.

XX PN WO2003040407-A2.

XX PD 15-MAY-2003.

XX PF 08-NOV-2002; 2002WO-EP012522.

XX PR 09-NOV-2001; 2001EP-00126800.

XX PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.

XX PI Ruiz P, Grzeskowiak R, Drungowski M, Witt H, Osterziel KJ;

XX PI Perrot A, Saleh A;

XX WPI; 2003-430678/40.

XX New diagnostic composition comprising at least one nucleic acid molecule that is capable of specifically hybridizing to the mRNA of the gene, useful for diagnosing cardiopathy, e.g. cardiomyopathy or dilated cardiomyopathy.

PS Example 1; Page 21; 82pp; English.

CC The invention relates to a diagnostic composition comprising at least one nucleic acid molecule listed in the specification that is capable of specifically hybridizing to the mRNA of at least one of the genes given in the specification. The diagnostic composition and nucleic acid molecules are useful for diagnosing cardiopathy or a disposition to cardiopathy, e.g. cardiomyopathy or dilated cardiomyopathy. The method involves contacting a target sample with the nucleic acid molecule cited above, and comparing the concentration of the individual mRNA(s) with the concentration of the corresponding mRNAs from at least one of the healthy donor. The nucleic acids are also useful for the isolation and development of a compound useful for therapy or prevention of a cardiopathy. Sequences ACC78653-700 represent primers used in real-time quantitative PCR for amplifying human genes, during the course of the invention

SQ Sequence 20 BP; 4 A; 6 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 1.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 931 GAACAGCTCGTGTACTGAG 950

DB 20 GAACAGCTCGTGTACTGAG 1

RESULT 16

QY 1221 GCTCTGCTGCTCAGCCAGG 1240

DB 20 GCTCTGCTGCTCAGCCAGG 1

ADC35543/c

ID ADC35543 standard; DNA; 20 BP.

XX AC ADC35543;

XX DT 18-DEC-2003 (first entry)

XX DE Human CD81/TAPA-1 antisense oligonucleotide #3.

XX KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection; cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial; virucide; antiparasitic; inflammatory disorder; parasitic infection; bacterial infection.

XX OS Homo sapiens.

XX Key Location/Qualifiers

XX modified_base 1..20

XX /tag= b

XX /mod_base= OTHER

XX /note= "Phosphorothioate backbone and all cytidines are 5-methyl cytidines"

XX modified_base 1..5

XX /tag= a

XX /mod_base= OTHER

XX /note= "2'-methoxyethyl nucleotide"

XX modified_base 16..20

XX /tag= c

XX /mod_base= OTHER

XX /note= "2'-methoxyethyl nucleotide"

XX US2003113914-A1.

XX 19-JUN-2003.

XX 10-DEC-2001; 2001US-00006430.

XX 10-DEC-2001; 2001US-00006430.

XX (ISIS-) ISIS PHARM INC.

XX Graham MJ, Dobie K;

XX WPI; 2003-810907/76.

XX Novel compound hybridizing with nucleic acid molecule encoding CD81 and inhibiting the expression of CD81, useful for treating infections and disease associated with expression of CD81 such as inflammation disorder.

PS Claim 3; SEQ ID NO 15; 55pp; English.

CC The invention relates to a compound (antisense oligonucleotide) hybridizing with the eighth nucleobase portion of an active site on a nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin) and inhibiting the expression of CD81. Also included is a composition comprising the antisense oligonucleotide and a carrier or a diluent. The antisense oligonucleotide is useful for inhibiting the expression of CD81 in cells or tissues. The antisense oligonucleotide is also useful for treating infections preferably viral, bacterial and parasitic and diseases such as inflammatory disorders and autoimmune disorders. The disease or condition is characterised by chemical dependency (e.g. cocaine addiction). The present sequence is a CD81 antisense oligonucleotide of the invention.

SQ Sequence 20 BP; 4 A; 6 C; 8 G; 2 T; 0 U; 0 Other;

Query Match 1.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 17
ADC35564/c
ID ADC35564 standard; DNA; 20 BP.
XX
AC ADC35564;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human CD81/TAPA-1 antisense oligonucleotide #24.
XX
KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
KW viricide; antiparasitic; inflammatory disorder; parasitic infection;
bacterial infection.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
modified_base 1..20
FT /tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
modified_base 1..5
FT /tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
XX
US2003113914-A1.
PN
XX
19-JUN-2003.
PD
XX
10-DEC-2001; 2001US-00006430.
PF
XX
10-DEC-2001; 2001US-00006430.
PR
XX
(ISIS-) ISIS PHARM INC.
PA
XX
Graham MJ, Dobie K;
PI
XX
WPI; 2003-810907/76.
DR
XX
Novel compound hybridizing with nucleic acid molecule encoding CD81 and
inhibiting the expression of CD81, useful for treating infections and
disease associated with expression of CD81 such as inflammation disorder.
PS
Claim 3; SEQ ID NO 36; 55pp; English.
XX
The invention relates to a compound (antisense oligonucleotide)
CC hybridizing with the eighth nucleobase portion of an active site on a
CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
CC and inhibiting the expression of CD81. Also included is a composition
CC comprising the antisense oligonucleotide and a carrier or a diluent. The
CC antisense oligonucleotide is useful for inhibiting the expression of CD81
CC in cells or tissues. The antisense oligonucleotide is also useful for
CC treating infections preferably viral, bacterial and parasitic and
CC diseases such as inflammatory disorders and autoimmune disorders. The
CC disease or condition is characterised by chemical dependency (e.g.
CC cocaine addiction). The present sequence is a CD81 antisense
CC oligonucleotide of the invention.
XX
Sequence 20 BP; 3 A; 5 C; 6 G; 6 T; 0 U; 0 Other;
Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 678 TGAAGACCTTCACGAGCG 697
Db 20 TGAAGACCTTCACGAGCG 1
RESULT 18
ADC35567/c
ID ADC35567 standard; DNA; 20 BP.
XX
AC ADC35567;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human CD81/TAPA-1 antisense oligonucleotide #27.
XX
KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
KW viricide; antiparasitic; inflammatory disorder; parasitic infection;
bacterial infection.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
modified_base 1..20
FT /tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
modified_base 1..5
FT /tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
XX
US2003113914-A1.
PN
XX
19-JUN-2003.
PD
XX
10-DEC-2001; 2001US-00006430.
PF
XX
10-DEC-2001; 2001US-00006430.
PR
XX
(ISIS-) ISIS PHARM INC.
PA
XX
Graham MJ, Dobie K;
PI
XX
WPI; 2003-810907/76.
DR
XX
Novel compound hybridizing with nucleic acid molecule encoding CD81 and
inhibiting the expression of CD81, useful for treating infections and
disease associated with expression of CD81 such as inflammation disorder.
PS
Claim 3; SEQ ID NO 39; 55pp; English.
XX
The invention relates to a compound (antisense oligonucleotide)
CC hybridizing with the eighth nucleobase portion of an active site on a
CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
CC and inhibiting the expression of CD81. Also included is a composition
CC comprising the antisense oligonucleotide and a carrier or a diluent. The
CC antisense oligonucleotide is useful for inhibiting the expression of CD81
CC in cells or tissues. The antisense oligonucleotide is also useful for
CC treating infections preferably viral, bacterial and parasitic and
CC diseases such as inflammatory disorders and autoimmune disorders. The
CC disease or condition is characterised by chemical dependency (e.g.
CC cocaine addiction). The present sequence is a CD81 antisense
CC oligonucleotide of the invention.
XX
Sequence 20 BP; 4 A; 3 C; 7 G; 6 T; 0 U; 0 Other;
Query Match 1.3%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 781 CATCAGCAACCTCTTCAGG 800
Db 20 CATCAGCAACCTCTTCAGG 1

RESULT 19
ADC35571/c
ID ADC35571 standard; DNA; 20 BP.
AC ADC35571;
DT 18-DEC-2003 (first entry)
XX Human CD81/TAPA-1 antisense oligonucleotide #31.
XX Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.
XX Homo sapiens.
XX Key Location/Qualifiers
FH modified_base 1..20
FT /tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT modified_base 1..5
FT /tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
XX US2003113914-A1.
XX 19-JUN-2003.
XX 10-DEC-2001; 2001US-00006430.
XX PF
XX 10-DEC-2001; 2001US-00006430.
XX PR
XX (ISIS-) ISIS PHARM INC.
XX PA
XX Graham MJ, Dobie K;
XX WPI; 2003-810907/76.
XX Novel compound hybridizing with nucleic acid molecule encoding CD81 and
PT inhibiting the expression of CD81, useful for treating infections and
PT disease associated with expression of CD81 such as inflammation disorder.
XX Claim 3; SEQ ID NO 43; 55pp; English.
XX The invention relates to a compound (antisense oligonucleotide)
CC hybridizing with the eighth nucleobase portion of an active site on a
CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
CC and inhibiting the expression of CD81. Also included is a composition
CC comprising the antisense oligonucleotide and a carrier or a diluent. The
CC antisense oligonucleotide is useful for inhibiting the expression of CD81
CC in cells or tissues. The antisense oligonucleotide is also useful for
CC treating infections preferably viral, bacterial and parasitic and
CC diseases such as inflammatory disorders and autoimmune disorders. The
CC disease or condition is characterised by chemical dependency (e.g.
CC cocaine addiction). The present sequence is a CD81 antisense
CC oligonucleotide of the invention.
XX

SQ Sequence 20 BP; 6 A; 5 C; 6 G; 3 T; 0 U; 0 Other;
Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 841 GCTGTACCTCATCGCATTTG 860
Db 20 GCTGTACCTCATCGCATTTG 1

RESULT 20
ADC35574/c
ID ADC35574 standard; DNA; 20 BP.
XX AC ADC35574;
XX DT 18-DEC-2003 (first entry)
XX Human CD81/TAPA-1 antisense oligonucleotide #34.
XX Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.
XX Homo sapiens.
XX Key Location/Qualifiers
FH modified_base 1..20
FT /tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT modified_base 1..5
FT /tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
XX US2003113914-A1.
XX 19-JUN-2003.
XX 10-DEC-2001; 2001US-00006430.
XX PF
XX 10-DEC-2001; 2001US-00006430.
XX PR
XX (ISIS-) ISIS PHARM INC.
XX PA
XX Graham MJ, Dobie K;
XX WPI; 2003-810907/76.
XX Novel compound hybridizing with nucleic acid molecule encoding CD81 and
PT inhibiting the expression of CD81, useful for treating infections and
PT disease associated with expression of CD81 such as inflammation disorder.
XX Claim 3; SEQ ID NO 46; 55pp; English.
XX The invention relates to a compound (antisense oligonucleotide)
CC hybridizing with the eighth nucleobase portion of an active site on a
CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
CC and inhibiting the expression of CD81. Also included is a composition
CC comprising the antisense oligonucleotide and a carrier or a diluent. The
CC antisense oligonucleotide is useful for inhibiting the expression of CD81
CC in cells or tissues. The antisense oligonucleotide is also useful for
CC treating infections preferably viral, bacterial and parasitic and
CC diseases such as inflammatory disorders and autoimmune disorders. The
CC disease or condition is characterised by chemical dependency (e.g.
CC cocaine addiction). The present sequence is a CD81 antisense
CC oligonucleotide of the invention.
XX

```
CC cocaine addiction). The present sequence is a CD81 antisense
CC oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 6 A; 6 C; 6 G; 2 T; 0 U; 0 Other;
Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 864 CCATCGTGCCTGCTGATC 883
DB 20 CCATCGTGCCTGCTGATC 1
RESULT 21
ADC35584/c
ID ADC35584 standard; DNA; 20 BP.
XX
AC ADC35584;
DT 18-DEC-2003 (first entry)
XX
DE Human CD81/TAPA-1 antisense oligonucleotide #44.
XX
KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
XX
US2003113914-A1.
19-JUN-2003.
XX
PF 10-DEC-2001; 2001US-00006430.
XX
PR 10-DEC-2001; 2001US-00006430.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Graham MJ, Dobie K;
XX
DR WPI; 2003-810907/76.
XX
XX
Novel compound hybridizing with nucleic acid molecule encoding CD81 and
inhibiting the expression of CD81, useful for treating infections and
disease associated with expression of CD81 such as inflammation disorder.
XX
PS Claim 3; SEQ ID NO 56; 55pp; English.
XX
The invention relates to a compound (antisense oligonucleotide)
hybridising with the eighth nucleobase portion of an active site on a
nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
and inhibiting the expression of CD81. Also included is a composition
comprising the antisense oligonucleotide and a carrier or a diluent. The
antisense oligonucleotide is useful for inhibiting the expression of CD81
in cells or tissues. The antisense oligonucleotide is also useful for
CC
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CC treating infections preferably viral, bacterial and parasitic and
CC diseases such as inflammatory disorders and autoimmune disorders. The
CC disease or condition is characterised by chemical dependency (e.g.
CC cocaine addiction). The present sequence is a CD81 antisense
CC oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 3 A; 6 C; 8 G; 3 T; 0 U; 0 Other;
Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 962 CTGGCCACAGGACCTCTGC 981
DB 20 CTGGCCACAGGACCTCTGC 1
RESULT 22
ADC35585/c
ID ADC35585 standard; DNA; 20 BP.
XX
AC ADC35585;
DT 18-DEC-2003 (first entry)
XX
DE Human CD81/TAPA-1 antisense oligonucleotide #45.
XX
KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
XX
US2003113914-A1.
19-JUN-2003.
XX
PF 10-DEC-2001; 2001US-00006430.
XX
PR 10-DEC-2001; 2001US-00006430.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Graham MJ, Dobie K;
XX
DR WPI; 2003-810907/76.
XX
XX
Novel compound hybridizing with nucleic acid molecule encoding CD81 and
inhibiting the expression of CD81, useful for treating infections and
disease associated with expression of CD81 such as inflammation disorder.
XX
PS Claim 3; SEQ ID NO 57; 55pp; English.
XX
The invention relates to a compound (antisense oligonucleotide)
hybridising with the eighth nucleobase portion of an active site on a
nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
and inhibiting the expression of CD81. Also included is a composition
comprising the antisense oligonucleotide and a carrier or a diluent. The
antisense oligonucleotide is useful for inhibiting the expression of CD81
in cells or tissues. The antisense oligonucleotide is also useful for
CC
```

CC comprising the antisense oligonucleotide and a carrier or a diluent. The
 CC antisense oligonucleotide is useful for inhibiting the expression of CD81
 CC in cells or tissues. The antisense oligonucleotide is also useful for
 CC treating infections preferably viral, bacterial and parasitic and
 CC diseases such as inflammatory disorders and autoimmune disorders. The
 CC disease or condition is characterised by chemical dependency (e.g.
 CC cocaine addiction). The present sequence is a CD81 antisense
 CC oligonucleotide of the invention.

XX
 SQ Sequence 20 BP; 4 A; 6 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 1.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1015 GGGCCATCACC GGCTGTGTA 1034
 |||||
 Db 20 GGGCCATCACC GGCTGTGTA 1

RESULT 23
 ADC35591/c
 ID ADC35591 standard; DNA; 20 BP.
 XX
 AC ADC35591;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human CD81/TAPA-1 antisense oligonucleotide #51.
 XX
 KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
 KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
 KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
 KW bacterial infection.
 XX
 OS Homo sapiens.
 XX

Key Location/Qualifiers
 modified_base 1..20
 /*tag= b
 /mod_base= OTHER
 /note= "Phosphorothioate backbone and all cytidines are 5
 -methyl cytidines"
 modified_base 1..5
 /*tag= a
 /mod_base= OTHER
 /note= "2'-methoxyethyl nucleotide"
 modified_base 16..20
 /*tag= c
 /mod_base= OTHER
 /note= "2'-methoxyethyl nucleotide"

US2003113914-A1.
 19-JUN-2003.
 10-DEC-2001; 2001US-00006430.
 10-DEC-2001; 2001US-00006430.
 (ISIS-) ISIS PHARM INC.
 Graham MJ, Dobie K;
 WPI; 2003-810907/76.
 Novel compound hybridizing with nucleic acid molecule encoding CD81 and
 inhibiting the expression of CD81, useful for treating infections and
 disease associated with expression of CD81 such as inflammation disorder.
 Claim 3; SEQ ID NO 63; 55pp; English.
 The invention relates to a compound (antisense oligonucleotide)

CC hybridising with the eighth nucleobase portion of an active site on a
 CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
 CC and inhibiting the expression of CD81. Also included is a composition
 CC comprising the antisense oligonucleotide and a carrier or a diluent. The
 CC antisense oligonucleotide is useful for inhibiting the expression of CD81
 CC in cells or tissues. The antisense oligonucleotide is also useful for
 CC treating infections preferably viral, bacterial and parasitic and
 CC diseases such as inflammatory disorders and autoimmune disorders. The
 CC disease or condition is characterised by chemical dependency (e.g.
 CC cocaine addiction). The present sequence is a CD81 antisense
 CC oligonucleotide of the invention.

XX
 SQ Sequence 20 BP; 4 A; 9 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 1.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1184 GAGGGCAGGGGTCCTTCGC 1203
 |||||
 Db 20 GAGGGCAGGGGTCCTTCGC 1

RESULT 24
 ADC35595/c
 ID ADC35595 standard; DNA; 20 BP.
 XX
 AC ADC35595;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human CD81/TAPA-1 antisense oligonucleotide #55.
 XX
 KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
 KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
 KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
 KW bacterial infection.
 XX
 OS Homo sapiens.
 XX

Key Location/Qualifiers
 modified_base 1..20
 /*tag= b
 /mod_base= OTHER
 /note= "Phosphorothioate backbone and all cytidines are 5
 -methyl cytidines"
 modified_base 1..5
 /*tag= a
 /mod_base= OTHER
 /note= "2'-methoxyethyl nucleotide"
 modified_base 16..20
 /*tag= c
 /mod_base= OTHER
 /note= "2'-methoxyethyl nucleotide"

US2003113914-A1.
 19-JUN-2003.
 10-DEC-2001; 2001US-00006430.
 10-DEC-2001; 2001US-00006430.
 (ISIS-) ISIS PHARM INC.
 Graham MJ, Dobie K;
 WPI; 2003-810907/76.
 Novel compound hybridizing with nucleic acid molecule encoding CD81 and
 inhibiting the expression of CD81, useful for treating infections and
 disease associated with expression of CD81 such as inflammation disorder.
 Claim 3; SEQ ID NO 63; 55pp; English.
 The invention relates to a compound (antisense oligonucleotide)

```
PS Claim 3; SEQ ID NO 67; 55pp; English.
XX
CC The invention relates to a compound (antisense oligonucleotide)
CC hybridizing with the eighth nucleobase portion of an active site on a
CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
CC and inhibiting the expression of CD81. Also included is a composition
CC comprising the antisense oligonucleotide and a carrier or a diluent. The
CC antisense oligonucleotide is useful for inhibiting the expression of CD81
CC in cells or tissues. The antisense oligonucleotide is also useful for
CC treating infections preferably viral, bacterial and parasitic and
CC diseases such as inflammatory disorders and autoimmune disorders. The
CC disease or condition is characterised by chemical dependency (e.g.
CC cocaine addiction). The present sequence is a CD81 antisense
CC oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 3 A; 5 C; 8 G; 4 T; 0 U; 0 Other;
    Query Match      1.3%; Score 20; DB 1; Length 20;
    Best Local Similarity 100.0%; Pred. No. 33;
    Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1261 CCCAGAGACTCAGCTGGCC 1280
Db 20 CCCAGAGACTCAGCTGGCC 1

RESULT 25
ADC35599/c
ID ADC35599 standard; DNA; 20 BP.
XX
AC ADC35599;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human CD81/TAPA-1 antisense oligonucleotide #59.
XX
KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20 /*tag= b
FT /*mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT modified_base 1..5 -methyl cytidines"
FT /*tag= a
FT /*mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT modified_base 16..20 /*tag= c
FT /*mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
XX
PN US2003113914-A1.
XX
PD 19-JUN-2003.
XX
PF 10-DEC-2001; 2001US-00006430.
XX
PR 10-DEC-2001; 2001US-00006430.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Graham MJ, Dobie K;
XX
DR WPI; 2003-810907/76.
XX
PT Novel compound hybridizing with nucleic acid molecule encoding CD81 and
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```
PT inhibiting the expression of CD81, useful for treating infections and
PT disease associated with expression of CD81 such as inflammation disorder.
XX
PS Claim 3; SEQ ID NO 71; 55pp; English.
XX
CC The invention relates to a compound (antisense oligonucleotide)
CC hybridizing with the eighth nucleobase portion of an active site on a
CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
CC and inhibiting the expression of CD81. Also included is a composition
CC comprising the antisense oligonucleotide and a carrier or a diluent. The
CC antisense oligonucleotide is useful for inhibiting the expression of CD81
CC in cells or tissues. The antisense oligonucleotide is also useful for
CC treating infections preferably viral, bacterial and parasitic and
CC diseases such as inflammatory disorders and autoimmune disorders. The
CC disease or condition is characterised by chemical dependency (e.g.
CC cocaine addiction). The present sequence is a CD81 antisense
CC oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 7 A; 5 C; 7 G; 1 T; 0 U; 0 Other;
    Query Match      1.3%; Score 20; DB 1; Length 20;
    Best Local Similarity 100.0%; Pred. No. 33;
    Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1369 TCTGTGGGCACCTCTGTGCT 1388
Db 20 TCTGTGGGCACCTCTGTGCT 1

RESULT 26
ADC35616/c
ID ADC35616 standard; DNA; 20 BP.
XX
AC ADC35616;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human CD81/TAPA-1 antisense oligonucleotide #76.
XX
KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20 /*tag= b
FT /*mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT modified_base 1..5 -methyl cytidines"
FT /*tag= a
FT /*mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT modified_base 16..20 /*tag= c
FT /*mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
XX
PN US2003113914-A1.
XX
PD 19-JUN-2003.
XX
PF 10-DEC-2001; 2001US-00006430.
XX
PR 10-DEC-2001; 2001US-00006430.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Graham MJ, Dobie K;
XX
```

DR WPI; 2003-810907/76.
 XX Novel compound hybridizing with nucleic acid molecule encoding CD81 and
 PT inhibiting the expression of CD81, useful for treating infections and
 PT disease associated with expression of CD81 such as inflammation disorder.
 XX Claim 3; SEQ ID NO 88; 55pp; English.
 XX The invention relates to a compound (antisense oligonucleotide)
 CC hybridizing with the eighth nucleobase portion of an active site on a
 CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
 CC and inhibiting the expression of CD81. Also included is a composition
 CC comprising the antisense oligonucleotide and a carrier or a diluent. The
 CC antisense oligonucleotide is useful for inhibiting the expression of CD81
 CC in cells or tissues. The antisense oligonucleotide is also useful for
 CC treating infections preferably viral, bacterial and parasitic and
 CC diseases such as inflammatory disorders and autoimmune disorders. The
 CC disease or condition is characterised by chemical dependency (e.g.
 CC cocaine addiction). The present sequence is a CD81 antisense
 CC oligonucleotide of the invention.
 XX Sequence 20 BP; 9 A; 3 C; 5 G; 3 T; 0 U; 0 Other;
 SQ
 Query Match 1.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1096 GTTCTGAACCTTCTCTTAC 1115
 DB 20 GTTCTGAACCTTCTCTTAC 1
 RESULT 27
 ADC35545/c
 ID ADC35545 standard; DNA; 20 BP.
 AC ADC35545;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human CD81/TAPA-1 antisense oligonucleotide #5.
 XX
 KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
 KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
 KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
 KW bacterial infection.
 XX Homo sapiens.
 OS
 PH Key Location/Qualifiers
 FT modified_base 1..20 /*tag= b
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate backbone and all cytidines are 5
 FT -methyl cytidines"
 FT modified_base 1..5
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl nucleotide"
 FT modified_base 16..20
 FT /*tag= c
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl nucleotide"
 XX
 XX US2003113914-A1.
 PN 19-JUN-2003.
 PD
 XX 10-DEC-2001; 2001US-00006430.
 PF
 XX 10-DEC-2001; 2001US-00006430.
 XX
 XX (ISIS-) ISIS PHARM INC.

XX Graham MJ, Dobie K;
 PI WPI; 2003-810907/76.
 XX Novel compound hybridizing with nucleic acid molecule encoding CD81 and
 PT inhibiting the expression of CD81, useful for treating infections and
 PT disease associated with expression of CD81 such as inflammation disorder.
 XX Claim 3; SEQ ID NO 17; 55pp; English.
 XX The invention relates to a compound (antisense oligonucleotide)
 CC hybridizing with the eighth nucleobase portion of an active site on a
 CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
 CC and inhibiting the expression of CD81. Also included is a composition
 CC comprising the antisense oligonucleotide and a carrier or a diluent. The
 CC antisense oligonucleotide is useful for inhibiting the expression of CD81
 CC in cells or tissues. The antisense oligonucleotide is also useful for
 CC treating infections preferably viral, bacterial and parasitic and
 CC diseases such as inflammatory disorders and autoimmune disorders. The
 CC disease or condition is characterised by chemical dependency (e.g.
 CC cocaine addiction). The present sequence is a CD81 antisense
 CC oligonucleotide of the invention.
 XX Sequence 20 BP; 8 A; 2 C; 7 G; 3 T; 0 U; 0 Other;
 SQ
 Query Match 1.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 272 TACCTGCTCTTCTGCTTCAA 291
 DB 20 TACCTGCTCTTCTGCTTCAA 1
 RESULT 28
 ADC35548/c
 ID ADC35548 standard; DNA; 20 BP.
 AC ADC35548;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human CD81/TAPA-1 antisense oligonucleotide #8.
 XX
 KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
 KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
 KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
 KW bacterial infection.
 XX Homo sapiens.
 OS
 PH Key Location/Qualifiers
 FT modified_base 1..20 /*tag= b
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate backbone and all cytidines are 5
 FT -methyl cytidines"
 FT modified_base 1..5
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl nucleotide"
 FT modified_base 16..20
 FT /*tag= c
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl nucleotide"
 XX
 XX US2003113914-A1.
 PN 19-JUN-2003.
 PD
 XX 10-DEC-2001; 2001US-00006430.
 PF
 XX

```
PR 10-DEC-2001; 2001US-00006430.
XX (ISIS-) ISIS PHARM INC.
PA Graham MJ, Dobie K;
PI WPI; 2003-810907/76.
XX
DR Novel compound hybridizing with nucleic acid molecule encoding CD81 and
PT inhibiting the expression of CD81, useful for treating infections and
PT disease associated with expression of CD81 such as inflammation disorder.
PS Claim 3; SEQ ID NO 20; 55pp; English.
XX
CC The invention relates to a compound (antisense oligonucleotide)
CC hybridizing with the eighth nucleobase portion of an active site on a
CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
CC and inhibiting the expression of CD81. Also included is a composition
CC comprising the antisense oligonucleotide and a carrier or a diluent. The
CC antisense oligonucleotide is useful for inhibiting the expression of CD81
CC in cells or tissues. The antisense oligonucleotide is also useful for
CC treating infections preferably viral, bacterial and parasitic and
CC diseases such as inflammatory disorders and autoimmune disorders. The
CC disease or condition is characterised by chemical dependency (e.g.
CC cocaine addiction). The present sequence is a CD81 antisense
CC oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 6 A; 9 C; 4 G; 1 T; 0 U; 0 Other;
Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 296 GTCCTCTGCTGCTGGAGG 315
DB 20 GTCCTCTGCTGCTGGAGG 1
RESULT 29
ADC35556/c
ID ADC35556 standard; DNA; 20 BP.
XX
AC ADC35556;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human CD81/TAPA-1 antisense oligonucleotide #16.
XX
KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT -methyl cytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
XX
PN US2003113914-A1.
PD 19-JUN-2003.
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XX 10-DEC-2001; 2001US-00006430.
XX
PR 10-DEC-2001; 2001US-00006430.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Graham MJ, Dobie K;
XX
DR WPI; 2003-810907/76.
XX
PT Novel compound hybridizing with nucleic acid molecule encoding CD81 and
PT inhibiting the expression of CD81, useful for treating infections and
PT disease associated with expression of CD81 such as inflammation disorder.
XX
PS Example 15; SEQ ID NO 28; 55pp; English.
XX
CC The invention relates to a compound (antisense oligonucleotide)
CC hybridizing with the eighth nucleobase portion of an active site on a
CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
CC and inhibiting the expression of CD81. Also included is a composition
CC comprising the antisense oligonucleotide and a carrier or a diluent. The
CC antisense oligonucleotide is useful for inhibiting the expression of CD81
CC in cells or tissues. The antisense oligonucleotide is also useful for
CC treating infections preferably viral, bacterial and parasitic and
CC diseases such as inflammatory disorders and autoimmune disorders. The
CC disease or condition is characterised by chemical dependency (e.g.
CC cocaine addiction). The present sequence is a CD81 antisense
CC oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 8 A; 6 C; 4 G; 2 T; 0 U; 0 Other;
Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 536 ATCCCTGTTTCCTGTGAGGT 555
DB 20 ATCCCTGTTTCCTGTGAGGT 1
RESULT 30
ADC35556/c
ID ADC35556 standard; DNA; 20 BP.
XX
AC ADC35556;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human CD81/TAPA-1 antisense oligonucleotide #28.
XX
KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT -methyl cytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
XX
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PN US2003113914-A1.
XX
PD 19-JUN-2003.
XX
PF 10-DEC-2001; 2001US-00006430.
XX
PR 10-DEC-2001; 2001US-00006430.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Graham MJ, Dobie K;
XX
DR WPI; 2003-810907/76.
XX
PT Novel compound hybridizing with nucleic acid molecule encoding CD81 and
XX inhibiting the expression of CD81, useful for treating infections and
XX disease associated with expression of CD81 such as inflammation disorder.
XX
PS Claim 3; SEQ ID NO 40; 55pp; English.
XX
CC The invention relates to a compound (antisense oligonucleotide)
CC hybridizing with the eighth nucleobase portion of an active site on a
CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
CC and inhibiting the expression of CD81. Also included is a composition
CC comprising the antisense oligonucleotide and a carrier or a diluent. The
CC antisense oligonucleotide is useful for inhibiting the expression of CD81
CC in cells or tissues. The antisense oligonucleotide is also useful for
CC treating infections preferably viral, bacterial and parasitic and
CC diseases such as inflammatory disorders and autoimmune disorders. The
CC disease or condition is characterised by chemical dependency (e.g.
CC cocaine addiction). The present sequence is a CD81 antisense
CC oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 4 A; 5 C; 7 G; 4 T; 0 U; 0 Other;
Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 790 CCTCTTCAAGGAGGACTGCC 809
Db 20 CCTCTTCAAGGAGGACTGCC 1

RESULT 31
ADC35551/c
ID ADC35551 standard; DNA; 20 BP.
XX
AC ADC35551;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human CD81/TAPA-1 antisense oligonucleotide #11.
XX
KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT -methyl cytidines"
FT modified_base 1..5
FT /tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT modified_base 16..20
FT /tag= c
FT

US2003113914-A1.
XX
PD 19-JUN-2003.
XX
PF 10-DEC-2001; 2001US-00006430.
XX
PR 10-DEC-2001; 2001US-00006430.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Graham MJ, Dobie K;
XX
DR WPI; 2003-810907/76.
XX
PT Novel compound hybridizing with nucleic acid molecule encoding CD81 and
XX inhibiting the expression of CD81, useful for treating infections and
XX disease associated with expression of CD81 such as inflammation disorder.
XX
PS Claim 3; SEQ ID NO 40; 55pp; English.
XX
CC The invention relates to a compound (antisense oligonucleotide)
CC hybridizing with the eighth nucleobase portion of an active site on a
CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
CC and inhibiting the expression of CD81. Also included is a composition
CC comprising the antisense oligonucleotide and a carrier or a diluent. The
CC antisense oligonucleotide is useful for inhibiting the expression of CD81
CC in cells or tissues. The antisense oligonucleotide is also useful for
CC treating infections preferably viral, bacterial and parasitic and
CC diseases such as inflammatory disorders and autoimmune disorders. The
CC disease or condition is characterised by chemical dependency (e.g.
CC cocaine addiction). The present sequence is a CD81 antisense
CC oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 4 A; 5 C; 7 G; 4 T; 0 U; 0 Other;
Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 375 ATCTGGAGCTGGGAGACAG 194
Db 20 ATCTGGAGCTGGGAGACAG 1

RESULT 32
ADC35557/c
ID ADC35557 standard; DNA; 20 BP.
XX
AC ADC35557;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human CD81/TAPA-1 antisense oligonucleotide #17.
XX
KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT -methyl cytidines"
FT modified_base 1..5
FT /tag= a
FT /mod_base= OTHER
FT

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```
FT      /note= "2'-methoxyethyl nucleotide"  
FT      16..20  
FT      /tag= c  
FT      /mod_base= OTHER  
FT      /note= "2'-methoxyethyl nucleotide"  
XX  
PN      US2003113914-A1.  
XX  
PD      19-JUN-2003.  
XX  
PF      10-DEC-2001; 2001US-00006430.  
XX  
PR      10-DEC-2001; 2001US-00006430.  
XX  
PA      (ISIS-) ISIS PHARM INC.  
XX  
PI      Graham MJ, Dobie K;  
XX      WPI; 2003-810907/76.  
DR  
XX      Novel compound hybridizing with nucleic acid molecule encoding CD81 and  
PT      inhibiting the expression of CD81, useful for treating infections and  
PT      disease associated with expression of CD81 such as inflammation disorder.  
XX  
PS      Claim 3; SEQ ID NO 29; 55pp; English.  
XX  
CC      The invention relates to a compound (antisense oligonucleotide)  
CC      hybridizing with the eighth nucleobase portion of an active site on a  
CC      nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)  
CC      and inhibiting the expression of CD81. Also included is a composition  
CC      comprising the antisense oligonucleotide and a carrier or a diluent. The  
CC      antisense oligonucleotide is useful for inhibiting the expression of CD81  
CC      in cells or tissues. The antisense oligonucleotide is also useful for  
CC      treating infections preferably viral, bacterial and parasitic and  
CC      diseases such as inflammatory disorders and autoimmune disorders. The  
CC      disease or condition is characterised by chemical dependency (e.g.  
CC      cocaine addiction). The present sequence is a CD81 antisense  
CC      oligonucleotide of the invention.  
XX  
SQ      Sequence 20 BP; 6 A; 6 C; 5 G; 3 T; 0 U; 0 Other;  
  
Query Match      1.3%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 33;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY      564 GCATCTGGGGCTTGTCAAC 593  
Db      |||||  
        20 GCATCTGGGGCTTGTCAAC 1  
  
RESULT 33  
ADC35586/c  
ID      ADC35586 standard; DNA; 20 BP.  
XX  
AC      ADC35586;  
XX  
DT      18-DEC-2003 (first entry)  
XX  
DE      Human CD81/TAPA-1 antisense oligonucleotide #46.  
XX  
KW      Antisense; ss; human; CD81; tetraspanin; viral infection;  
KW      cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;  
KW      virucide; antiparasitic; inflammatory disorder; parasitic infection;  
KW      bacterial infection.  
XX  
OS      Homo sapiens.  
XX  
FH      Key      Location/Qualifiers  
FT      modified_base 1..20  
FT      /tag= b  
FT      /mod_base= OTHER  
FT      /note= "Phosphorothioate backbone and all cytidines are 5  
FT      -methyl cytidines"
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FT      modified_base 1..5  
FT      /tag= a  
FT      /mod_base= OTHER  
FT      /note= "2'-methoxyethyl nucleotide"  
FT      modified_base 16..20  
FT      /tag= c  
FT      /mod_base= OTHER  
FT      /note= "2'-methoxyethyl nucleotide"  
XX  
PN      US2003113914-A1.  
XX  
PD      19-JUN-2003.  
XX  
PF      10-DEC-2001; 2001US-00006430.  
XX  
PR      10-DEC-2001; 2001US-00006430.  
XX  
PA      (ISIS-) ISIS PHARM INC.  
XX  
PI      Graham MJ, Dobie K;  
XX      WPI; 2003-810907/76.  
DR  
XX      Novel compound hybridizing with nucleic acid molecule encoding CD81 and  
PT      inhibiting the expression of CD81, useful for treating infections and  
PT      disease associated with expression of CD81 such as inflammation disorder.  
XX  
PS      Claim 3; SEQ ID NO 59; 55pp; English.  
XX  
CC      The invention relates to a compound (antisense oligonucleotide)  
CC      hybridising with the eighth nucleobase portion of an active site on a  
CC      nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)  
CC      and inhibiting the expression of CD81. Also included is a composition  
CC      comprising the expression of CD81. Also included is a composition  
CC      comprising the antisense oligonucleotide and a carrier or a diluent. The  
CC      antisense oligonucleotide is useful for inhibiting the expression of CD81  
CC      in cells or tissues. The antisense oligonucleotide is also useful for  
CC      treating infections preferably viral, bacterial and parasitic and  
CC      diseases such as inflammatory disorders and autoimmune disorders. The  
CC      disease or condition is characterised by chemical dependency (e.g.  
CC      cocaine addiction). The present sequence is a CD81 antisense  
CC      oligonucleotide of the invention.  
XX  
SQ      Sequence 20 BP; 7 A; 3 C; 5 G; 5 T; 0 U; 0 Other;  
  
Query Match      1.3%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 33;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY      1048 GTATTACTCTGCTACACGTA 1067  
Db      |||||  
        20 GTATTACTCTGCTACACGTA 1  
  
RESULT 34  
ADC35597/c  
ID      ADC35597 standard; DNA; 20 BP.  
XX  
AC      ADC35597;  
XX  
DT      18-DEC-2003 (first entry)  
XX  
DE      Human CD81/TAPA-1 antisense oligonucleotide #57.  
XX  
KW      Antisense; ss; human; CD81; tetraspanin; viral infection;  
KW      cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;  
KW      virucide; antiparasitic; inflammatory disorder; parasitic infection;  
KW      bacterial infection.  
XX  
OS      Homo sapiens.  
XX  
FH      Key      Location/Qualifiers  
FT      modified_base 1..20  
FT      /tag= b  
FT      /mod_base= OTHER  
FT      /note= "Phosphorothioate backbone and all cytidines are 5  
FT      -methyl cytidines"
```



```
FT FT /mod_base= OTHER
FT FT /note= "Phosphorothioate backbone and all cytidines are 5
FT FT -methyl cytidines"
FT FT 1. .5
FT FT /tag= a
FT FT /mod_base= OTHER
FT FT /note= "2'-methoxyethyl nucleotide"
FT FT 16. .20
FT FT /tag= c
FT FT /mod_base= OTHER
FT FT /note= "2'-methoxyethyl nucleotide"
XX XX US2003113914-A1.
XX PN 19-JUN-2003.
XX XX
XX PD 10-DEC-2001; 2001US-00006430.
XX XX
XX PR 10-DEC-2001; 2001US-00006430.
XX XX
XX PA (ISIS-) ISIS PHARM INC.
XX PI Graham MJ, Dobie K;
XX XX WPI; 2003-810907/76.
XX DR
XX XX
XX PT Novel compound hybridizing with nucleic acid molecule encoding CD81 and
XX PT inhibiting the expression of CD81, useful for treating infections and
XX PT disease associated with expression of CD81 such as inflammation disorder.
XX PS Example 15; SEQ ID NO 69; 55pp; English.
XX CC
XX CC The invention relates to a compound (antisense oligonucleotide)
XX CC hybridizing with the eighth nucleobase portion of an active site on a
XX CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
XX CC and inhibiting the expression of CD81. Also included is a composition
XX CC comprising the antisense oligonucleotide and a carrier or a diluent. The
XX CC antisense oligonucleotide is useful for inhibiting the expression of CD81
XX CC in cells or tissues. The antisense oligonucleotide is also useful for
XX CC treating infections preferably viral, bacterial and parasitic and
XX CC diseases such as inflammatory disorders and autoimmune disorders. The
XX CC disease or condition is characterised by chemical dependency (e.g.
XX CC cocaine addiction). The present sequence is a CD81 antisense
XX CC oligonucleotide of the invention.
XX SQ Sequence 20 BP; 6 A; 2 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1327 ACAGCTCACCTCTTCCTC 1346
Db |||||
20 ACAGCTCACCTCTTCCTC 1

RESULT 35
ADC35544/c
ID ADC35544 standard; DNA; 20 BP.
XX AC ADC35544;
XX DT
XX DT 18-DEC-2003 (first entry)
XX XX Human CD81/TAPA-1 antisense oligonucleotide #4.
XX XX Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.
XX XX Homo sapiens.
OS XX
```

```
PH Key Location/Qualifiers
FT modified_base 1. .20
FT FT /tag= b
FT FT /mod_base= OTHER
FT FT /note= "Phosphorothioate backbone and all cytidines are 5
FT FT -methyl cytidines"
FT FT 1. .5
FT FT /tag= a
FT FT /mod_base= OTHER
FT FT /note= "2'-methoxyethyl nucleotide"
FT FT 16. .20
FT FT /tag= c
FT FT /mod_base= OTHER
FT FT /note= "2'-methoxyethyl nucleotide"
XX XX US2003113914-A1.
XX PN 19-JUN-2003.
XX XX
XX PD 10-DEC-2001; 2001US-00006430.
XX XX
XX PR 10-DEC-2001; 2001US-00006430.
XX XX
XX PA (ISIS-) ISIS PHARM INC.
XX PI Graham MJ, Dobie K;
XX XX WPI; 2003-810907/76.
XX DR
XX XX
XX PT Novel compound hybridizing with nucleic acid molecule encoding CD81 and
XX PT inhibiting the expression of CD81, useful for treating infections and
XX PT disease associated with expression of CD81 such as inflammation disorder.
XX PS Claim 3; SEQ ID NO 16; 55pp; English.
XX CC
XX CC The invention relates to a compound (antisense oligonucleotide)
XX CC hybridizing with the eighth nucleobase portion of an active site on a
XX CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
XX CC and inhibiting the expression of CD81. Also included is a composition
XX CC comprising the antisense oligonucleotide and a carrier or a diluent. The
XX CC antisense oligonucleotide is useful for inhibiting the expression of CD81
XX CC in cells or tissues. The antisense oligonucleotide is also useful for
XX CC treating infections preferably viral, bacterial and parasitic and
XX CC diseases such as inflammatory disorders and autoimmune disorders. The
XX CC disease or condition is characterised by chemical dependency (e.g.
XX CC cocaine addiction). The present sequence is a CD81 antisense
XX CC oligonucleotide of the invention.
XX SQ Sequence 20 BP; 3 A; 8 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 TGGAGGGCTGCACCAAGTGC 265
Db |||||
20 TGGAGGGCTGCACCAAGTGC 1

RESULT 36
ADC35558/c
ID ADC35558 standard; DNA; 20 BP.
XX AC ADC35558;
XX DT
XX DT 18-DEC-2003 (first entry)
XX XX Human CD81/TAPA-1 antisense oligonucleotide #18.
XX XX Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.
OS XX
```

```
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT modified_base 1..20
XX FT /*tag= b
XX FT /mod_base= OTHER
XX FT /note= "Phosphorothioate backbone and all cytidines are 5
XX FT -methyl cytidines"
XX FT modified_base 1..5
XX FT /*tag= a
XX FT /mod_base= OTHER
XX FT modified_base 15..20
XX FT /*tag= c
XX FT /mod_base= OTHER
XX FT /note= "2'-methoxyethyl nucleotide"
XX FT modified_base 15..20
XX FT /*tag= c
XX FT /mod_base= OTHER
XX FT /note= "2'-methoxyethyl nucleotide"
XX PN US2003113914-A1.
XX PD 19-JUN-2003.
XX PF 10-DEC-2001; 2001US-00006430.
XX PR 10-DEC-2001; 2001US-00006430.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Graham MJ, Dobie K;
XX PI WPI; 2003-810907/76.
XX DR Novel compound hybridizing with nucleic acid molecule encoding CD81 and
XX PT inhibiting the expression of CD81, useful for treating infections and
XX PT disease associated with expression of CD81 such as inflammation disorder.
XX PS Claim 3; SEQ ID NO 30; 55pp; English.
XX CC The invention relates to a compound (antisense oligonucleotide)
XX CC hybridising with the eighth nucleobase portion of an active site on a
XX CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
XX CC and inhibiting the expression of CD81. Also included is a composition
XX CC comprising the antisense oligonucleotide and a carrier or a diluent. The
XX CC antisense oligonucleotide is useful for inhibiting the expression of CD81
XX CC in cells or tissues. The antisense oligonucleotide is also useful for
XX CC treating infections preferably viral, bacterial and parasitic and
XX CC diseases such as inflammatory disorders and autoimmune disorders. The
XX CC disease or condition is characterised by chemical dependency (e.g.
XX CC cocaine addiction). The present sequence is a CD81 antisense
XX CC oligonucleotide of the invention.
XX SQ Sequence 20 BP; 3 A; 6 C; 5 G; 6 T; 0 U; 0 Other;
Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 587 GACCAGATGCCAAGGATGT 606
Db 20 GACCAGATGCCAAGGATGT 1
RESULT 37
ADC35572/c
ID ADC35572 standard; DNA; 20 BP.
XX AC ADC35572;
XX DT 18-DEC-2003 (first entry)
XX DE Human CD81/TAPA-1 antisense oligonucleotide #32.
XX KW Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
```

```
KW cocaine addiction; autoimmune disorder; antinflammatory; antibacterial;
KW viricide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT modified_base 1..20
XX FT /*tag= b
XX FT /mod_base= OTHER
XX FT /note= "Phosphorothioate backbone and all cytidines are 5
XX FT -methyl cytidines"
XX FT modified_base 1..5
XX FT /*tag= a
XX FT /mod_base= OTHER
XX FT modified_base 15..20
XX FT /*tag= c
XX FT /mod_base= OTHER
XX FT /note= "2'-methoxyethyl nucleotide"
XX PN US2003113914-A1.
XX PD 19-JUN-2003.
XX PF 10-DEC-2001; 2001US-00006430.
XX PR 10-DEC-2001; 2001US-00006430.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Graham MJ, Dobie K;
XX PI WPI; 2003-810907/76.
XX DR Novel compound hybridizing with nucleic acid molecule encoding CD81 and
XX PT inhibiting the expression of CD81, useful for treating infections and
XX PT disease associated with expression of CD81 such as inflammation disorder.
XX PS Claim 3; SEQ ID NO 44; 55pp; English.
XX CC The invention relates to a compound (antisense oligonucleotide)
XX CC hybridising with the eighth nucleobase portion of an active site on a
XX CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
XX CC and inhibiting the expression of CD81. Also included is a composition
XX CC comprising the antisense oligonucleotide and a carrier or a diluent. The
XX CC antisense oligonucleotide is useful for inhibiting the expression of CD81
XX CC in cells or tissues. The antisense oligonucleotide is also useful for
XX CC treating infections preferably viral, bacterial and parasitic and
XX CC diseases such as inflammatory disorders and autoimmune disorders. The
XX CC disease or condition is characterised by chemical dependency (e.g.
XX CC cocaine addiction). The present sequence is a CD81 antisense
XX CC oligonucleotide of the invention.
XX SQ Sequence 20 BP; 6 A; 4 C; 7 G; 3 T; 0 U; 0 Other;
Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 848 CTCATCGGCATGTCGCAT 867
Db 20 CTCATCGGCATGTCGCAT 1
RESULT 38
ADC35617/c
ID ADC35617 standard; DNA; 20 BP.
XX AC ADC35617;
XX DT 18-DEC-2003 (first entry)
XX KW
```

```
DE Human CD81/TAPA-1 antisense oligonucleotide #77.
XX Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
KW viricide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
XX
XX US2003113914-A1.
XX
XX 19-JUN-2003.
XX
XX 10-DEC-2001; 2001US-00006430.
XX
XX 10-DEC-2001; 2001US-00006430.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Graham MJ, Dobie K;
XX WPI; 2003-810907/76.
XX
XX Novel compound hybridizing with nucleic acid molecule encoding CD81 and
PT inhibiting the expression of CD81, useful for treating infections and
PT disease associated with expression of CD81 such as inflammation disorder.
XX
XX Claim 3; SEQ ID NO 89; 55pp; English.
XX
XX The invention relates to a compound (antisense oligonucleotide)
CC hybridizing with the eighth nucleobase portion of an active site on a
CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
CC and inhibiting the expression of CD81. Also included is a composition
CC comprising the antisense oligonucleotide and a carrier or a diluent. The
CC antisense oligonucleotide is useful for inhibiting the expression of CD81
CC in cells or tissues. The antisense oligonucleotide is also useful for
CC treating infections preferably viral, bacterial and parasitic and
CC diseases such as inflammatory disorders and autoimmune disorders. The
CC disease or condition is characterised by chemical dependency (e.g.
CC cocaine addiction). The present sequence is a CD81 antisense
CC oligonucleotide of the invention.
XX
XX Sequence 20 BP; 8 A; 5 C; 4 G; 3 T; 0 U; 0 Other;
SQ
Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1110 TGTACCTTTTCAGGGCTGA 1129
Db 20 TGTACCTTTTCAGGGCTGA 1
RESULT 39
ADC35577/c
ID ADC35577 standard; DNA; 20 BP.
XX
AC ADC35577;
```

```
XX 19-DEC-2003 (first entry)
XX Human CD81/TAPA-1 antisense oligonucleotide #37.
XX Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
KW viricide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
XX
XX US2003113914-A1.
XX
XX 19-JUN-2003.
XX
XX 10-DEC-2001; 2001US-00006430.
XX
XX 10-DEC-2001; 2001US-00006430.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Graham MJ, Dobie K;
XX WPI; 2003-810907/76.
XX
XX Novel compound hybridizing with nucleic acid molecule encoding CD81 and
PT inhibiting the expression of CD81, useful for treating infections and
PT disease associated with expression of CD81 such as inflammation disorder.
XX
XX Claim 3; SEQ ID NO 49; 55pp; English.
XX
XX The invention relates to a compound (antisense oligonucleotide)
CC hybridizing with the eighth nucleobase portion of an active site on a
CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
CC and inhibiting the expression of CD81. Also included is a composition
CC comprising the antisense oligonucleotide and a carrier or a diluent. The
CC antisense oligonucleotide is useful for inhibiting the expression of CD81
CC in cells or tissues. The antisense oligonucleotide is also useful for
CC treating infections preferably viral, bacterial and parasitic and
CC diseases such as inflammatory disorders and autoimmune disorders. The
CC disease or condition is characterised by chemical dependency (e.g.
CC cocaine addiction). The present sequence is a CD81 antisense
CC oligonucleotide of the invention.
XX
XX Sequence 20 BP; 6 A; 8 C; 4 G; 2 T; 0 U; 0 Other;
SQ
Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 902 CTGACGATGCTGCTGCTG 921
Db 20 CTGACGATGCTGCTGCTG 1
RESULT 40
ADC35590/c
```

```
ID ADC35590 standard; DNA; 20 BP.
XX
AC ADC35590;
XX
DT 18-DEC-2003 (first entry)
XX
XX Human CD81/TAPA-1 antisense oligonucleotide #50.
XX
XX Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
KW cocaine addiction; autoimmune disorder; antinflammatory; antibacterial;
KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT -methyl cytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT modified_base 15..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
XX
XX US2003113914-A1.
XX
PD 19-JUN-2003.
XX
XX 10-DEC-2001; 2001US-00006430.
XX
XX 10-DEC-2001; 2001US-00006430.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Graham MJ, Dobie K;
XX WPI; 2003-810907/76.
XX
XX Novel compound hybridizing with nucleic acid molecule encoding CD81 and
XX inhibiting the expression of CD81, useful for treating infections and
XX disease associated with expression of CD81 such as inflammation disorder.
XX
XX Example 15; SEQ ID NO 62; 55pp; English.
XX
XX The invention relates to a compound (antisense oligonucleotide)
XX hybridising with the eighth nucleobase portion of an active site on a
XX nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
XX and inhibiting the expression of CD81. Also included is a composition
XX comprising the antisense oligonucleotide and a carrier or a diluent. The
XX antisense oligonucleotide is useful for inhibiting the expression of CD81
XX in cells or tissues. The antisense oligonucleotide is also useful for
XX treating infections preferably viral, bacterial and parasitic and
XX diseases such as inflammatory disorders and autoimmune disorders. The
XX disease or condition is characterised by chemical dependency (e.g.
XX cocaine addiction). The present sequence is a CD81 antisense
XX oligonucleotide of the invention.
XX
XX Sequence 20 BP; 6 A; 9 C; 1 G; 4 T; 0 U; 0 Other;
XX
Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1136 ATGTAGTGGCGGTGTATGAG 1155
DB 20 ATGTAGTGGCGGTGTATGAG 1
```

```
RESULT 41
ADC35605/c
ID ADC35605 standard; DNA; 20 BP.
XX
XX ADC35605;
XX
XX 18-DEC-2003 (first entry)
XX
XX Human CD81/TAPA-1 antisense oligonucleotide #65.
XX
XX Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection;
KW cocaine addiction; autoimmune disorder; antinflammatory; antibacterial;
KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
KW bacterial infection.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT -methyl cytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT modified_base 15..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotide"
XX
XX US2003113914-A1.
XX
PD 19-JUN-2003.
XX
XX 10-DEC-2001; 2001US-00006430.
XX
XX 10-DEC-2001; 2001US-00006430.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Graham MJ, Dobie K;
XX WPI; 2003-810907/76.
XX
XX Novel compound hybridizing with nucleic acid molecule encoding CD81 and
XX inhibiting the expression of CD81, useful for treating infections and
XX disease associated with expression of CD81 such as inflammation disorder.
XX
XX Example 15; SEQ ID NO 77; 55pp; English.
XX
XX The invention relates to a compound (antisense oligonucleotide)
XX hybridising with the eighth nucleobase portion of an active site on a
XX nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
XX and inhibiting the expression of CD81. Also included is a composition
XX comprising the antisense oligonucleotide and a carrier or a diluent. The
XX antisense oligonucleotide is useful for inhibiting the expression of CD81
XX in cells or tissues. The antisense oligonucleotide is also useful for
XX treating infections preferably viral, bacterial and parasitic and
XX diseases such as inflammatory disorders and autoimmune disorders. The
XX disease or condition is characterised by chemical dependency (e.g.
XX cocaine addiction). The present sequence is a CD81 antisense
XX oligonucleotide of the invention.
XX
XX Sequence 20 BP; 7 A; 2 C; 5 G; 6 T; 0 U; 0 Other;
XX
Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1440 CTGACTCCGTCATTAAATAA 1459
```

transcription; expression; reverse transcription; viral replication;
RNase H cleavage; triple helix formation; ss.
Synthetic.

Key Location/Qualifiers
modified_base 1..18
/*tag= a
/note= "Deoxyribose moiety replaced by 2'-deoxy-2'-fluoro-beta-D-arabinoose"

WO9967378-A1.
29-DEC-1999.
17-JUN-1999; 99WO-CA000571.
19-JUN-1998; 98CA-02241361.
(UYMC-) UNIV MCGILL.
Damha MJ, Parniak MA, Noronha AM, Wilds C, Borkow G, Arion D;
WPI; 2000-160584/14.
Therapeutic composition containing antisense oligonucleotides that
include arabinose sugars, particularly for inhibiting viral replication.
Example 2; Page 31; 91pp; English.

The invention relates to a new composition for selective, sequence-specific inhibition of gene transcription and expression in a host. The composition comprises oligonucleotides containing arabinose sugars that can hybridize to either a single-stranded (ss) RNA to induce RNase H cleavage activity, or to a DNA/DNA or DNA/RNA duplex to form a triple helix, thereby inhibiting DNA replication and/or transcription. The oligoarabinonucleotides are used for antisense inhibition of gene expression or to prevent DNA replication, or reverse transcription of RNA by retroviruses. The compositions are therefore particularly used to inhibit retroviral replication. The oligoarabinonucleotides can also be used, in combination with RNase H, as reagents for sequence-specific cleavage or RNA mapping, and additionally for the study and control of gene expression in cells. The oligoarabinonucleotides have excellent affinity for RNA, increased resistance to nucleases and show little if any non-specific binding to cellular or serum proteins. They target ss RNA, but not complementary ss DNA, so may be useful for targeting retroviral genomic RNA to inhibit the early stages of viral replication. Oligoarabinonucleotides containing pyrimidine bases form triple helices with significantly higher thermal stability than those produced by normal oligonucleotides. Sequences AAZ87165-287169 represent oligodeoxyarabinonucleotides containing 2'-deoxy-2'-fluoro-beta-D-arabinoose used in an exemplification of the present invention

Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
Query Match 1..18; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
DB 18 AAAAAAAAAAAAAA 3

RESULT 274
AAZ87167
ID AAZ87167 standard; DNA; 18 BP.
XX AC AAZ87167;
XX AC AAZ87167;
DT 08-MAY-2000 (first entry)
DE Deoxyarabinonucleotide SEQ ID NO:8.

2'-deoxy-2'-fluoro-beta-D-arabinoose; antisense; inhibition;
transcription; expression; reverse transcription; viral replication;
RNase H cleavage; triple helix formation; ss.
Synthetic.

Key Location/Qualifiers
modified_base 1..18
/*tag= a
/note= "Deoxyribose moiety replaced by 2'-deoxy-2'-fluoro-beta-D-arabinoose"

WO9967378-A1.
29-DEC-1999.
17-JUN-1999; 99WO-CA000571.
19-JUN-1998; 98CA-02241361.
(UYMC-) UNIV MCGILL.
Damha MJ, Parniak MA, Noronha AM, Wilds C, Borkow G, Arion D;
WPI; 2000-160584/14.
Therapeutic composition containing antisense oligonucleotides that
include arabinose sugars, particularly for inhibiting viral replication.
Example 2; Page 31; 91pp; English.

The invention relates to a new composition for selective, sequence-specific inhibition of gene transcription and expression in a host. The composition comprises oligonucleotides containing arabinose sugars that can hybridize to either a single-stranded (ss) RNA to induce RNase H cleavage activity, or to a DNA/DNA or DNA/RNA duplex to form a triple helix, thereby inhibiting DNA replication and/or transcription. The oligoarabinonucleotides are used for antisense inhibition of gene expression or to prevent DNA replication, or reverse transcription of RNA by retroviruses. The compositions are therefore particularly used to inhibit retroviral replication. The oligoarabinonucleotides can also be used, in combination with RNase H, as reagents for sequence-specific cleavage or RNA mapping, and additionally for the study and control of gene expression in cells. The oligoarabinonucleotides have excellent affinity for RNA, increased resistance to nucleases and show little if any non-specific binding to cellular or serum proteins. They target ss RNA, but not complementary ss DNA, so may be useful for targeting retroviral genomic RNA to inhibit the early stages of viral replication. Oligoarabinonucleotides containing pyrimidine bases form triple helices with significantly higher thermal stability than those produced by normal oligonucleotides. Sequences AAZ87165-287169 represent oligodeoxyarabinonucleotides containing 2'-deoxy-2'-fluoro-beta-D-arabinoose used in an exemplification of the present invention

Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 1..18; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
DB 1 AAAAAAAAAAAAAA 16

RESULT 275
AAD03565/c
ID AAD03565 standard; DNA; 18 BP.
XX AC AAD03565;
XX AC AAD03565;
DT 19-JUN-2001 (first entry)

```
XX DE Oligonucleotide #6 used for the preparation of normalised cDNA libraries.
XX KW Rat; secreted factor; clone P00188_D12; cardiant; antiinflammatory;
XX KW antiarrhythmic; antiarteriosclerotic; antiatherosclerotic; nephropathic;
XX KW antidiabetic; immunosuppressive; antiasthmatic; antirheumatoid;
XX KW antibacterial; osteoprotective; cerebroprotective; vasotropic; antilucer;
XX KW neutrophic; neuroprotective; congestive heart failure; myocarditis;
XX KW hypertrophic cardiomyopathy; angina pectoris; myocardial infarction;
XX KW kidney disease; acute renal failure; renal glucosuria; renal infarction;
XX KW polycystic kidney disease; hereditary nephritis; inflammatory disease;
XX KW tumour angiogenesis; osteoarthritis; toxic shock syndrome; psoriasis;
XX KW stroke; neural trauma; cerebral malaria; Crohn's disease; osteoporosis;
XX KW ulcerative colitis; Alzheimer's disease; gene therapy; ss.
XX OS Rattus norvegicus.
XX KW WO200123564-A1.
XX PN 05-APR-2001.
XX PD 27-SEP-2000; 2000WO-US026544.
XX PF 27-SEP-1999; 99US-0156280P.
XX PR (SCIO-) SCIOS INC.
XX PA Stanton LW, Kapoun AM;
XX PI WPI; 2001-266159/27.
XX DR
XX PT Novel secreted factor encoded by clone P00188D12 which is differentially
XX PT expressed in certain disease states, useful in diagnosing and treating
XX PT cardiac, renal or inflammatory diseases.
XX PS Example 1; Page 42; 71pp; English.
XX CC The patent discloses novel secreted factor protein encoded by clone
XX CC P00188_D12. The secreted factor is differentially expressed in certain
XX CC disease states. Secreted protein, its antibodies, antagonists or
XX CC compositions comprising them are useful in the diagnosis and treatment of
XX CC cardiac diseases such as congestive heart failure, myocarditis,
XX CC hypertrophic cardiomyopathy, angina pectoris, myocardial infarction,
XX CC cardiac arrhythmia, arteriosclerosis, kidney diseases such as acute renal
XX CC failure, renal glucosuria, renal infarction, nephrogenic diabetes
XX CC insipidus, polycystic kidney disease, hereditary nephritis and
XX CC inflammatory diseases such as asthma, autoimmune diabetes, tumour
XX CC angiogenesis, rheumatoid arthritis, osteoarthritis, toxic shock syndrome,
XX CC asthma, stroke, neural trauma, psoriasis, cerebral malaria, osteoporosis,
XX CC Crohn's disease, ulcerative colitis, Alzheimer's disease. Secreted
XX CC protein DNA is useful in antisense-mediated gene inhibition and in gene
XX CC therapy. An array comprising one or more oligonucleotides complementary
XX CC to reference RNA or DNA encoding the secreted factor is useful for
XX CC detecting cardiac, kidney and inflammatory disease. The present DNA
XX CC sequence is an oligonucleotide which is used in the preparation of a
XX CC normalised cDNA library containing secreted factor DNAs. The normalised
XX CC cDNA libraries are used in the identification of differentially expressed
XX CC rat secreted factor P00188_D12 gene
XX SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1496
Db 18 AAAAAAAAAAAAAA 3
RESULT 276
AAD17014
ID AAD17014 standard; DNA; 18 BP.
```

```
XX AAD17014;
XX AC 29-NOV-2001 (first entry)
XX DT Oligonucleotide A18-2PEG linker.
XX DE Scaffold protein; antibody mimic; fibronectin type III domain;
XX KW randomised loop; randomised beta-sheet; diagnostic purpose;
XX KW protein designing; ss.
XX OS Unidentified.
XX FT Key Location/Qualifiers
XX FT 18 misc_feature
XX FT /*tag= a
XX FT /note= "Linked to (PEG)2CCPuromycin"
XX PN WO200164942-A1.
XX PD 07-SEP-2001.
XX PF 28-FEB-2001; 2001WO-US006414.
XX PR 29-FEB-2000; 2000US-00515260.
XX PA (PHYL-) PHYLLOS INC.
XX PI Lipovsek D, Wagner RW, Kuimelis RG;
XX DR WPI; 2001-557782/62.
XX PT Fibronectin scaffold protein array for obtaining a protein/compound which
XX PT binds to a compound/protein, comprises a fibronectin type III domain
XX PT having a randomized loop, a randomized beta-sheet or their combination.
XX PS Disclosure; Page 25; 67pp; English.
XX CC The present invention relates to an array of proteins (antibody mimics)
XX CC comprising a fibronectin type III domain having a randomized loop, a
XX CC randomized beta-sheet, or their combination, and has the capacity to bind
XX CC to a compound that is not bound by a corresponding naturally-occurring
XX CC fibronectin, immobilised onto a solid support. The antibody mimics is
XX CC useful for detecting a compound preferably a protein, in a biological
XX CC sample. It is also useful to detect one or more different analytes
XX CC simultaneously in a sample. Hence is useful for diagnostic purposes. It
XX CC is also useful for the purpose of designing proteins capable of binding
XX CC to virtually any compound of interest. The present sequence is an
XX CC oligonucleotide A18-2PEG linker used in an exemplification of the
XX CC invention
XX SQ Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1496
Db 1 AAAAAAAAAAAAAA 16
RESULT 277
AAF75598/c
ID AAF75598 standard; DNA; 18 BP.
XX AC AAF75598;
XX DT 10-MAY-2001 (first entry)
XX DE Binary encoded sequence tag method anchored primer #3.
XX KW Binary encoded sequence tag; BEST; nucleic acid analysis;
```

```
KW gene expression; adaptor; PCR primer; ss.
OS Synthetic.
PN WO200112855-A2.
XX
XX 22-FEB-2001.
XX
XX 11-AUG-2000; 2000WO-US022164.
XX
XX 13-AUG-1999; 99US-0148870P.
PR 06-APR-2000; 2000US-00544713.
XX
XX (UYUA ) UNIV YALE.
XX
XX Kaufman JC, Roth ME, Lizardi PM, Feng L, Latimer DR;
XX WPI; 2001-202878/20.
XX
XX Producing binary sequence tags, useful for analyzing nucleic acid
XX sequence tags, gene expression or gene-expression patterns, involves
XX generating nucleic acid fragments, which are mixed with offset adaptors
XX and adaptor-indexers.
XX
XX Disclosure; Page 101; 101pp; English.
XX
XX The present invention describes a method of producing binary sequence
XX tags from nucleic acid fragments in a sample, involving incubating the
XX sample with cleaving reagents, mixing offset adaptors with the sample,
XX incubating with more cleaving reagents and mixing the sample with adaptor
XX -indexers where the adaptors are coupled to binary sequence tags. The
XX method is useful in sequence analysis, including analysis and comparison
XX of gene expression, nucleic acid samples and genomes
XX
XX Sequence 18 BP; 1 A; 1 C; 0 G; 16 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 16; DB 1; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 1.6e+02;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1481 AAAAAAAAAAAAAA 1496
XX |||||
XX 16 AAAAAAAAAAAAAA 1
XX
XX RESULT 278
XX AAF75597/C
XX ID AAF75597 standard; DNA; 18 BP.
XX AC AAF75597;
XX
XX 10-MAY-2001 (first entry)
XX
XX Binary encoded sequence tag method anchored primer #2.
XX
XX Binary encoded sequence tag; BEST; nucleic acid analysis;
XX gene expression; adaptor; PCR primer; ss.
XX Synthetic.
XX
XX WO200112855-A2.
XX
XX 22-FEB-2001.
XX
XX 11-AUG-2000; 2000WO-US022164.
XX
XX 13-AUG-1999; 99US-0148870P.
PR 06-APR-2000; 2000US-00544713.
XX
XX (UYUA ) UNIV YALE.
XX
XX Kaufman JC, Roth ME, Lizardi PM, Feng L, Latimer DR;
XX WPI; 2001-202878/20.
XX
XX Producing binary sequence tags, useful for analyzing nucleic acid
XX sequence tags, gene expression or gene-expression patterns, involves
XX generating nucleic acid fragments, which are mixed with offset adaptors
XX and adaptor-indexers.
XX
XX Disclosure; Page 101; 101pp; English.
XX
XX The present invention describes a method of producing binary sequence
XX tags from nucleic acid fragments in a sample, involving incubating the
XX sample with cleaving reagents, mixing offset adaptors with the sample,
XX incubating with more cleaving reagents and mixing the sample with adaptor
XX -indexers where the adaptors are coupled to binary sequence tags. The
XX method is useful in sequence analysis, including analysis and comparison
XX of gene expression, nucleic acid samples and genomes
XX
XX Sequence 18 BP; 1 A; 1 C; 0 G; 16 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 16; DB 1; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 1.6e+02;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1481 AAAAAAAAAAAAAA 1496
XX |||||
XX 16 AAAAAAAAAAAAAA 1
XX
XX RESULT 279
XX AAD20091
XX ID AAD20091 standard; mRNA; 18 BP.
XX AC AAD20091;
XX
XX 03-JAN-2002 (first entry)
XX
XX mRNA fragment used in 3' end PCR/IVT method of the invention.
XX
XX RNA polymerase; RNAP; RNA detection; IVT; in vitro transcription; ss.
XX Unidentified.
XX
XX US6271002-B1.
XX
XX 07-AUG-2001.
XX
XX 04-OCT-1999; 99US-00411074.
XX
XX 04-OCT-1999; 99US-00411074.
XX
XX (ROSE-) ROSETTA INPHARMATICS INC.
XX
XX Linsley PS, Schelter JM;
XX
XX WPI; 2001-624273/72.
XX
XX Amplifying and detecting RNA derived from a population of cells by
XX employing a primer that contains an RNA polymerase promoter in a
XX polymerase chain reaction.
XX
XX Example 3; Fig 1; 29pp; English.
XX
XX The invention relates to methods and kits for amplification of mRNA using
XX a primer in PCR that contains an RNA polymerase (RNAP) promoter. The
XX invention provides methods for amplification and detection of RNA derived
XX from a population of cells, preferably eukaryotic cells and most
XX preferably mammalian cells, which methods preserve fidelity with respect
XX to sequence and transcript representation and additionally enable
XX amplification of extremely small amounts of mRNA. The method and kit are
XX useful for amplifying and detecting RNA derived from a population of
XX cells, especially eukaryotic cells like mammals. The RNAs generated are
XX useful for profiling gene expression in different populations of cells.
XX The present sequence is a mRNA fragment used in 3' end PCR/IVT (in vitro
```

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CC transcription) method of the invention
XX
SQ Sequence 18 BP; 17 A; 0 C; 0 G; 0 T; 0 U; 1 Other;

Query Match      1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
DB 2 AAAAAAAAAAAAAA 17

RESULT 280
AAF99708/c
ID AAF99708 standard; DNA; 18 BP.
AC AAF99708;
XX
DT 12-JUN-2001 (first entry)
DE Immunostimulatory nucleic acid #824.
XX
KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW immunostimulatory; tumour; viral infection; bacterial infection;
KW fungal infection; parasitic infection; cancer; asthma;
KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS Synthetic.
XX
PN WO200122972-A2.
XX
PD 05-APR-2001.
XX
PF 25-SEP-2000; 2000WO-US026383.
XX
PR 25-SEP-1999; 99US-0156113P.
XX
PR 27-SEP-1999; 99US-0156135P.
XX
PR 23-AUG-2000; 2000US-0227436P.
XX
PA (IOWA ) UNIV IOWA RES FOUND.
PA (COLE-) COLEY PHARM GMBH.
XX
PI Krieg AM, Schetter C, Vollmer J;
XX
DR WPI; 2001-273485/28.
XX
PT Vaccinating against tumors, infectious diseases, allergies and asthma
PT using immunostimulatory Py-rich and TG nucleic acids.
XX
PS Claim 101; Page 56; 338pp; English.
XX
CC The present invention relates to a method for stimulating an immune
CC response. The method comprises administering an immunostimulatory nucleic
CC acid to a non-rodent subject in sufficient quantity to stimulate an
CC immune response. The present sequence is one such immunostimulatory
CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC also useful for preventing cancer, asthma, infectious disease, allergy or
CC immune deficiency. The present sequence can also be used to redirect a
CC Th2 to a Th1 immune response and to activate immune cells. Note: the
CC present sequence may have a phosphorothioate backbone
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match      1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
DB 18 AAAAAAAAAAAAAA 3

RESULT 282
AAF82472/c
ID AAF82472 standard; DNA; 18 BP.

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XX AC AAF82472;
XX DT 29-JUN-2001 (first entry)
XX DE Phagemid vector pCR2.1 polylinker oligonucleotide #6.
XX KW Phagemid vector; pCR2.1; rat; secreted factor; P00210D09; cardiant;
XX KW nephrotropic; antiinflammatory; gene therapy; cardiac disease;
XX KW renal disease; inflammatory disease; polylinker; ss.
XX OS Synthetic.
XX PN WO200123419-A2.
XX PD 05-APR-2001.
XX PF 27-SEP-2000; 2000WO-US026582.
XX PR 27-SEP-1999; 99US-0156277P.
XX PA (SCIO-) SCIOS INC.
XX PI Stanton LW, Kapoun AM;
XX DR WPI; 2001-328177/34.
XX PT Novel secreted factor encoded by clone P00210D09 useful for diagnosing,
XX PT treating and/or preventing various cardiac, renal and inflammatory
XX PT diseases.
XX PS Example 1; Page 41; 69pp; English.
XX CC The present sequence corresponds to polylinker DNA of the phagemid vector
XX CC pCR2.1. It was used in the construction of a normalised rat cDNA library,
XX CC which was used in an example demonstrating differential expression of a
XX CC rat gene referred to as clone P00210D09. The invention relates to a
XX CC polypeptide comprising a sequence of at least 80% identity to residues 22
XX CC -122 of the present sequence, or a sequence encoded by a nucleic acid
XX CC hybridising under stringent conditions to the complement of the coding
XX CC region comprising 1031 nucleotides, and having at least one biological
XX CC activity of the polypeptide encoded by clone P00210D09. The polypeptides
XX CC and polynucleotides of the invention are useful for the treatment of
XX CC cardiac, renal and inflammatory diseases. The polynucleotides are useful
XX CC in antisense mediated gene inhibition and in gene therapy. The
XX CC polypeptides are useful in assays for identifying lead compounds that may
XX CC be used as therapeutic agents in the treatment of cardiac, kidney or
XX CC inflammatory diseases
XX SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAAAAAA 1496
DB 18 AAAAAAAAAAAAAAAAAA 3

RESULT 283
ID ABK51158/c
AC ABK51158;
XX 30-JUL-2002 (first entry)
XX DE Human cytomegalovirus (HCMV) RT-PCR primer TXN.
XX KW Human cytomegalovirus; HCMV; virucide; cytomegalovirus infection; CMV;
XX KW cellular kinase; RICK; RIP; Nck-interacting kinase; MKK3; SRPK-2;
XX KW reverse transcriptase PCR; RT-PCR; primer; ss.

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XX OS Human cytomegalovirus.
XX FH Key Location/Qualifiers
XX FT misc_difference 17 /*tag= a
XX FT /label= n
XX FT /note= "n= dATP, dCTP or dGTP"
XX PN EPI201765-A2.
XX PD 02-MAY-2002.
XX PF 15-OCT-2001; 2001EP-00124604.
XX PR 16-OCT-2000; 2000US-0240750P.
XX PA (AXXI-) AXIIMA PHARM AG.
XX PI Schubart D, Habenberger P, Stein-Gerlach M, Bavec D;
XX DR WPI; 2002-373930/41.
XX PT Identifying agents for treatment or prevention of cytomegalovirus
XX PT infection, comprises contacting test compound with cellular kinase and
XX PT detecting change in cellular kinase activity.
XX PS Example 1; Page 13; 49pp; English.
XX CC The present invention relates to a new method for identifying compounds
XX CC for treating and/or preventing cytomegalovirus (CMV) infection and/or
XX CC related diseases. The method of the invention comprises contacting a test
XX CC compound with at least one of the cellular kinases RICK, RIP, Nck-
XX CC interacting kinase, MKK3 and SRPK-2 and detecting any change in kinase
XX CC activity. The method of the invention can be used to treat and/or prevent
XX CC CMV infections and related diseases. Oligonucleotides that can detect the
XX CC specified kinases can also be used for diagnosis of infection. The
XX CC present nucleic acid sequence represents human CMV reverse transcriptase
XX CC (RT)-PCR primer TXN that was used in the methods of the invention for
XX CC preparation of radioactively labelled cDNA probes
XX SQ Sequence 18 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 2 Other;

Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAAAAAA 1496
DB 16 AAAAAAAAAAAAAAAAAA 1

RESULT 284
AAS94743/c
XX ID AAS94743 standard; DNA; 18 BP.
XX AC AAS94743;
XX DT 12-MAR-2002 (first entry)
XX DE Rat secreted factor DNA oligonucleotide probe #6.
XX KW Rat; secreted factor polypeptide; cardiac disease; renal disease; kidney;
XX KW inflammatory disease; congestive heart failure; myocarditis; asthma; ss;
XX KW dilated congestive cardiomyopathy; angina pectoris; cardiac arrhythmia;
XX KW myocardial infarction; pulmonary hypertension; arteriosclerosis; stroke;
XX KW atherosclerosis; cardiac tumour; glomerulonephritis; nephrotic syndrome;
XX KW renal infarction; hereditary nephritis; polycystic kidney disease;
XX KW chronic renal failure; renal vein thrombosis; medullary sponge kidney;
XX KW rheumatoid arthritis; osteoarthritis; psoriasis; restenosis; PCR primer;
XX KW graft versus host reaction; Crohn's disease; ulcerative colitis; probe;
XX KW Alzheimer's disease; gene therapy.

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OS Synthetic.
PN WO200174901-A2.
XX
PD 11-OCT-2001.
XX
PF 23-MAR-2001; 2001WO-US009555.
XX
PR 31-MAR-2000; 2000US-0193548P.
XX
PR 14-MAR-2001; 2001US-00809545.
XX
XX (SCIO-) SCIOS INC.
PA
XX Stanton LW, White RT;
XX
XX WPI; 2002-010779/01.
DR
XX
XX Novel secreted factor polypeptide useful for treating cardiac diseases
PT such as arteriosclerosis, myocardial infarction, inflammatory diseases
PT such as asthma, stroke, and rheumatoid arthritis and renal diseases.
XX
PS Example 1; Page 51; 189pp; English.
XX
XX The invention relates to rat secreted factor polypeptides and the
CC polynucleotides encoding them. The sequences are useful for treating
CC cardiac, renal or inflammatory diseases. These include cardiac diseases
CC such as congestive heart failure, myocarditis, dilated congestive
CC cardiomyopathy, angina pectoris, myocardial infarction, cardiac
CC arrhythmia, pulmonary hypertension, arteriosclerosis, atherosclerosis and
CC cardiac tumours, renal diseases such as glomerulonephritis, nephrotic
CC syndrome, renal infarction, hereditary nephritis, polycystic kidney
CC disease, chronic renal failure, renal vein thrombosis and medullary
CC sponge kidney and inflammatory diseases such as asthma, rheumatoid
CC arthritis, osteoarthritis, stroke, psoriasis, stenosis, graft versus
CC host reaction, Crohn's disease, ulcerative colitis and Alzheimer's
CC disease. Sequences AAG94693-AAS94745 represent cDNA clones, which encode
CC the secreted factor polypeptides of the invention, and oligonucleotide
CC probes and PCR primers
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
XX
Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1496
DB 18 AAAAAAAAAAAAAA 3
RESULT 285
ABS78455/c
ID ABS78455 standard; DNA; 18 BP.
XX
AC ABS78455;
XX
DT 13-DEC-2002 (first entry)
XX
DE Angiogenesis inhibitory oligonucleotide #939.
XX
XX Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
XX tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
XX diabetic retinopathy; retinopathy of prematurity; macular degeneration;
XX corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
XX rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;
XX plaque neovascularisation; telangiectasia; haemophiliac joint;
XX angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
XX scleroderma; hypertrophic scar.
XX
OS Synthetic.
XX WO200253141-A2.
XX
XX 11-JUL-2002.
XX
XX 14-DEC-2001; 2001WO-US048458.
XX
XX 14-DEC-2000; 2000US-0255534P.
XX
XX (COLE-) COLEY PHARM GROUP INC.
PA

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PD 11-JUL-2002.
XX
XX 14-DEC-2001; 2001WO-US048458.
XX
XX 14-DEC-2000; 2000US-0255534P.
XX
XX (COLE-) COLEY PHARM GROUP INC.
PA
Bratzler RL;
XX
XX WPI; 2002-566690/60.
DR
XX
XX Inhibiting angiogenesis in a subject, involves administering at least one
PT antiangiogenic nucleic acid molecule to the subject.
PT
XX Claim 2; Page 36; 276pp; English.
XX
XX The invention relates to inhibiting angiogenesis in a subject, comprising
CC administering at least one antiangiogenic nucleic acid molecule. Also
CC included is a kit comprising a first container housing the antiangiogenic
CC nucleic acids, and instructions for administering them to a subject
CC having a condition characterised by unwanted angiogenesis. The method is
CC useful for inhibiting angiogenesis associated with solid tumour growth,
CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
CC neovascularisation, telangiectasia, haemophiliac joints, angiofibroma,
CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
CC hypertrophic scars. The present sequence is an antiangiogenic nucleic
XX acid of the invention
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
XX
Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1496
DB 18 AAAAAAAAAAAAAA 3
RESULT 286
ABS78429/c
ID ABS78429 standard; DNA; 18 BP.
XX
AC ABS78429;
XX
DT 13-DEC-2002 (first entry)
XX
DE Angiogenesis inhibitory oligonucleotide #913.
XX
XX Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
XX tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
XX diabetic retinopathy; retinopathy of prematurity; macular degeneration;
XX corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
XX rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;
XX plaque neovascularisation; telangiectasia; haemophiliac joint;
XX angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
XX scleroderma; hypertrophic scar.
XX
OS Synthetic.
XX WO200253141-A2.
XX
XX 11-JUL-2002.
XX
XX 14-DEC-2001; 2001WO-US048458.
XX
XX 14-DEC-2000; 2000US-0255534P.
XX
XX (COLE-) COLEY PHARM GROUP INC.
PA

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XX Bratzler RL;
 XX WPI; 2002-566690/60.
 XX Inhibiting angiogenesis in a subject, involves administering at least one
 PT antiangiogenic nucleic acid molecule to the subject.
 XX
 PS Claim 2; Page 35; 276pp; English.
 XX The invention relates to inhibiting angiogenesis in a subject, comprising
 CC administering at least one antiangiogenic nucleic acid molecule. Also
 CC included is a kit comprising a first container housing the antiangiogenic
 CC nucleic acids, and instructions for administering them to a subject
 CC having a condition characterised by unwanted angiogenesis. The method is
 CC useful for inhibiting angiogenesis associated with solid tumour growth,
 CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
 CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
 CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
 CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
 CC neovascularisation, telangiectasia, haemophilic joints, angiodermoma,
 CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
 CC hypertrophic scars. The present sequence is an antiangiogenic nucleic
 CC acid of the invention
 XX
 SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
 Query Match 1.1%; Score 16; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1481 AAAAAAAAAAAAAA 1496
 Db 18 AAAAAAAAAAAAAA 3
 RESULT 287
 ID ABL39401/c
 AC ABL39401;
 XX 16-APR-2002 (first entry)
 XX Immunostimulatory nucleic acid SEQ ID NO: 837.
 XX Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
 KW angiogenesis; metastasis; cytostatic; ss.
 XX Synthetic.
 XX Key Location/Qualifiers
 XX modified_base 1..18
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "phosphorothioate backbone"
 XX
 XX W0200197843-A2.
 XX
 XX 27-DEC-2001.
 XX
 XX 22-JUN-2001; 2001WO-US020154.
 XX
 XX 22-JUN-2000; 2000US-0213346P.
 XX
 XX (IOWA) UNIV IOWA RES FOUND.
 XX
 XX Weiner G, Hartmann G;
 XX WPI; 2002-154611/20.
 XX Treating or preventing cancer, such as basal cell carcinoma, comprises
 PT administering immunostimulatory nucleic acids that induce expression of

PT cell surface antigens and antibodies to a subject having or at risk of
 PT developing cancer.
 XX
 PS Disclosure; Page 308; 312pp; English.
 XX The present invention relates to methods for treating or preventing
 CC cancer, involving administering to a subject having or at risk of
 CC developing cancer immunostimulatory nucleic acids that induce expression
 CC of cell surface antigens and antibodies. The methods are useful for
 CC treating or preventing cancer such as basal cell carcinoma, bladder
 CC cancer, bone cancer, brain and central nervous system (CNS) cancer,
 CC breast cancer, cervical cancer, colon and rectum cancer, connective
 CC tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx
 CC cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-
 CC Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
 CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
 CC cancer, stomach cancer, testicular cancer, and uterine cancer. The
 CC present sequence is an immunostimulatory oligonucleotide described in the
 CC exemplification of the invention
 XX
 SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
 Query Match 1.1%; Score 16; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1481 AAAAAAAAAAAAAA 1496
 Db 18 AAAAAAAAAAAAAA 3
 RESULT 288
 ID AAD41497/c
 AC AAD41497;
 XX 30-OCT-2002 (first entry)
 XX Oligonucleotide used for amplifying sea hare cytoplasm L DNA.
 DE
 XX Apoptosis; ion channel modulator; hyperproliferative disease; tumour;
 KW therapy; leukaemia; carcinoma; sarcoma; degenerative disease; melanoma;
 KW Alzheimer's disease; Parkinson's disease; arteriosclerosis;
 KW heart disease; stroke; vascular disease; nootropic; neuroprotective;
 KW cerebroprotective; cardiant; cytotoxic protein; cytoplasm L; ss.
 XX Unidentified.
 XX W0200231144-A2.
 XX 18-APR-2002.
 XX 12-OCT-2001; 2001WO-EP011837.
 XX 13-OCT-2000; 2000EP-00122466.
 XX (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 XX Butzke D, Machuy N, Rudel T, Meyer TF;
 XX WPI; 2002-537205/57.
 XX Novel polypeptide having cytotoxic activity obtainable from Aplysia,
 PT useful for destroying tumors, for identifying novel targets for the
 PT development of anti-tumor agents, and as specific ion channel modulators.
 XX Example 5; Page 37; 87pp; English.
 XX The present invention relates to novel polypeptides having cytotoxic
 CC activity obtainable from sea hare Aplysia. Sequences of the invention are
 CC useful for the manufacture of cytotoxic agents against apoptosis-
 CC resistant cells, where the agents are useful for diagnosis, prevention,

CC treatment of disorders associated with dysfunctions of GAP-SH3 binding
 CC protein, factors for generating or detoxifying reactive oxygen species
 CC (ROS) and factors for blocking and/or by-passing of caspases. They are
 CC useful for tumour therapy. Cytotoxic proteins of the invention are useful
 CC for destroying tumours and/or selectively killing cells in tissues, for
 CC identifying novel targets for the development of pharmaceutical agents,
 CC preferably anti-tumour agents and as specific ion channel modulators,
 CC e.g., blockers or openers for therapy, diagnostic or research. They are
 CC useful for the diagnosis and therapy of hyperproliferative diseases,
 CC preferably tumours, e.g., leukaemia, carcinoma, sarcoma and melanoma.
 CC They are also useful for development of drugs for the treatment of
 CC degenerative diseases such as Alzheimer's disease, Parkinson's disease,
 CC arteriosclerosis, heart diseases, stroke and vascular diseases. The
 CC present sequence is an oligonucleotide which is used for amplifying sea
 CC hare cytoplasmic DNA. This sequence is used in the exemplification of the
 CC invention
 XX
 SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 16; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
 |||||
 Db 18 AAAAAAAAAAAAAA 3

RESULT 289
 ABS53437/c
 ID ABS53437 standard; DNA; 18 BP.

AC ABS53437;

XX 29-NOV-2002 (first entry)

XX Poly d(T) primer.

XX Terminal continuation; TC; ss; second strand cDNA synthesis; primer;
 KW poly d(T).

XX Synthetic.

XX WO200265093-A2.

XX 22-AUG-2002.

XX 14-FEB-2002; 2002WO-US005713.

XX 14-FEB-2001; 2001US-02686645P.

PR 14-FEB-2001; 2001US-02686645P.

PR 18-JUL-2001; 2001US-0306216P.

PR 07-NOV-2001; 2001US-0344557P.

PR 07-NOV-2001; 2001US-0348242P.

PR 09-NOV-2001; 2001US-0350176P.

XX (BAYU) BAYLOR COLLEGE MEDICINE.

PA (REME-) RES FOUND MENTAL HYGIENE INC.

XX Ginsberg SD, Che S;

XX WPI; 2002-567050/60.

XX Increasing efficiency of second strand cDNA synthesis using terminal

PT continuation model before performing further RNA amplification by RNA

PT transcription.

XX Example 7; Page 80; 128pp; English.

XX This invention relates to a novel method for increasing the efficiency of
 CC second strand cDNA synthesis through a mechanism of terminal
 CC continuation. In the method an RNA molecule is obtained and a first
 CC primer is added that comprises a region that hybridises to a

CC complementary region of the molecule before a second primer is added
 CC comprising at least one riboguanine at the 3' end of the primer. A first
 CC complementary nucleic acid molecule is synthesised, the RNA molecule and
 CC second primer are removed and a second complementary nucleic acid
 CC molecule is synthesised to form a second hybrid with an extension product
 CC of the third primer bound to the first complementary molecule. The method
 CC of the invention is useful for increasing the efficiency of second strand
 CC cDNA synthesis and may be used for linear amplification of genetic
 CC signals from histologically stained tissue. The present sequence
 CC represents a poly d(T) PCR primer used in the method of the invention
 XX

SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
 Query Match 1.1%; Score 16; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
 |||||
 Db 18 AAAAAAAAAAAAAA 3

RESULT 290
 ABA93239/c
 ID ABA93239 standard; DNA; 18 BP.

XX ABA93239;

XX 18-APR-2002 (first entry)

DE Adaptor oligonucleotide SEQ ID NO:2.

XX Detection; comparative detection; adaptor; ss.

XX Synthetic.

XX JP2001333800-A.

XX 04-DEC-2001.

XX 30-MAY-2000; 2000JP-00160324.

XX 30-MAY-2000; 2000JP-00160324.

XX (UNIT-) UNITECH CO LTD.

XX WPI; 2002-135950/18.

XX Comparative detection of the amounts of RNA and DNA.

XX Disclosure; Page 9; 9pp; Japanese.

XX The present invention describes a method for the comparative detection of
 CC the amount of an RNA. The method comprises: (a) cDNAs obtained by
 CC transcribing respectively from at least two tissue RNAs are respectively
 CC fragmented by using a same restriction enzyme; (b) each different adaptor
 CC and a common adaptor are added to each of the cDNA fragments derived from
 CC the same or different tissues by the step (a); (c) the resultant adaptor-
 CC added cDNAs are mixed together; (d) an adaptor primer having the common
 CC sequence to said different adaptor and a gene-specific adaptor are used
 CC to amplify said adaptor-added cDNAs containing no region derived from
 CC polyadenylic acid of the mRNA before the addition of the adaptor among
 CC the adaptor-added cDNAs prepared by the step (b); (e) the ratios of the
 CC cDNA amounts are measured between the tissues; (f) the RNA is detected
 CC from the measured result; (g) each different adaptor and a common adaptor
 CC are added to each of the genomic DNA fragments derived from a same or
 CC different individuals; (h) the resultant adaptor-added genomic DNAs are
 CC mixed together; (i) the adaptor-added genomic DNAs are amplified by using
 CC an adaptor primer having the common sequence to the different adaptor and
 CC a sequence-specific adaptor; and (j) the ratios of the amplified amounts
 CC of the genomic DNAs are measured between the individuals. The method is
 CC used for the detection of the amounts of RNA and DNA. The present
 CC sequence represents an oligonucleotide which is used in the

CC exemplification of the present invention
 XX Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
 SQ Query Match 1.1%; Score 16; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1496
 Db 18 AAAAAAAAAAAAAA 3

RESULT 291
 AAD52799/c
 ID AAD52799 standard; DNA; 18 BP.
 XX AC AAD52799;
 XX DT 14-MAY-2003 (first entry)
 XX DE Primer used to prepare radioactively labelled cDNA probes from RNA.
 XX KW Human; pyridylpyrimidine derivative; cellular protein kinase; Scrapie;
 KW cellular protein phosphatase; cellular signal transduction; prophylaxis;
 KW prion infection; chronic wasting disease; CWD; Creutzfeldt-Jacob disease;
 KW CJD; transmissible mink encephalopathy; bovine spongiform encephalopathy;
 KW TME; BSE; Gerstmann-Straussler-Scheinker syndrome; GSS; Alpers syndrome;
 KW fatal familial insomnia; FFI; kuru; neurodegenerative disease; neurotropic;
 KW Alzheimer's disease; primer; ss.
 XX OS Homo sapiens.
 XX PN WO200293164-A2.
 XX PD 21-NOV-2002.
 XX PF 16-MAY-2002; 2002WO-EP005420.
 XX PR 16-MAY-2001; 2001EP-00111858.
 PR 29-MAY-2001; 2001US-0293528P.
 PR 13-JUL-2001; 2001EP-00117113.
 PR 18-JUL-2001; 2001US-0305898P.
 XX PA (AXXI-) AXIWA PHARM AG.
 XX PI Stein-Gerlach M, Salaasidis K, Bacher G, Mueller S;
 XX WPI; 2003-120714/11.
 XX New pyridylpyrimidine derivatives useful in the treatment or prevention
 of infectious disease e.g. Kuru syndrome and Creutzfeldt-Jacob disease
 (CJD).

Example; Page 38; 96pp; English.

The invention relates to novel pyridylpyrimidine derivatives and methods
 of detecting prion infections and/or prion disease in an individual or in
 cells, cell cultures and/or cell lysates. The method involves adding at
 least one monoclonal or polyclonal antibody, oligonucleotide or pyridyl-
 pyrimidine derivative to the sample or in cells, cell cultures and/or
 cell lysates and detecting the activity of at least one human cellular
 protein kinases (e.g., FGF-R1 (also known as fig. Fl-1, Flt-2, b-FGFR),
 Trk (also known as CCK-2, DDR-2 or EDDR; EC number 2.7.1.112), Abl (also
 known as c-abl), c-kit, MKK7 (also known as SAPK1a, SAPKalpha), CDC2 (also
 known as CDK1), PRK), human cellular protein phosphatases such as PTP-SL
 (also known as MCP83) and PTP-zeta, the cellular signal transduction
 molecules HSP80 and GPR-1. The invention is useful for regulating the
 production of prions in cells and in the manufacture of pharmaceutical
 composition for prophylaxis and/or treatment of infectious disease (e.g.
 Scrapie, chronic wasting disease (CWD), transmissible mink encephalopathy
 (TME), Creutzfeldt-Jacob disease (CJD), bovine spongiform encephalopathy
 (BSE), variant CJD, Gerstmann-Straussler-Scheinker syndrome (GSS), fatal

CC familial insomnia (FFI), Kuru and Alpers syndrome, especially BSE, CJD,
 vCJD) or neurodegenerative diseases (e.g., Alzheimer's disease) in humans
 or ruminants. The present DNA sequence is a primer used to prepare
 CC radioactively labelled cDNA probes from RNA. This sequence is used in the
 CC exemplification of the invention
 XX Sequence 18 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 2 Other;
 SQ Query Match 1.1%; Score 16; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1496
 Db 16 AAAAAAAAAAAAAA 1

RESULT 292
 AAD56466
 ID AAD56466 standard; RNA; 18 BP.
 XX AC AAD56466;
 XX DT 07-AUG-2003 (first entry)
 XX DE Target RNA #1 used in the exemplification of the invention.
 XX KW Acyclic linker; gene expression; gene therapy; ss.
 XX OS Unidentified.
 XX PN WO2003037909-A1.
 XX PD 08-MAY-2003.
 XX PF 29-OCT-2002; 2002WO-CA001628.
 XX PR 29-OCT-2001; 2001US-0330719P.
 XX PA (UYMC-) UNIV MCGILL.
 XX PI Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;
 XX WPI; 2003-421516/39.
 XX Novel acyclic linker-containing oligonucleotide useful for preventing or
 decreasing translation, reverse transcription and/or replication of a
 target RNA in a system, comprises a modified deoxyribonucleotide.

Example 2; Fig 5; 104pp; English.

The invention relates to an acyclic linker-containing oligonucleotide
 comprising at least one modified deoxyribonucleotide. Oligonucleotides of
 the invention are useful for preventing or decreasing translation,
 reverse transcription and/or replication of a target RNA in a system.
 They are useful for selectively preventing gene expression in a sequence-
 specific manner, for hybridising to complementary RNA such as cellular
 mRNA or viral RNA, to hybridise to and induce cleavage of complementary
 RNA. They are also useful therapeutically in formulations or medicaments
 to prevent or treat a disease characterised by the expression of a
 particular target RNA. The invention is used in gene therapy. The present
 sequence is a target RNA, used in the exemplification of the invention

Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
 Query Match 1.1%; Score 16; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1496
 Db 1 AAAAAAAAAAAAAA 16

```
RESULT 293
AAD56440/c
ID AAD56440 standard; DNA; 18 BP.
XX
XX AAD56440;
AC
DT 07-AUG-2003 (first entry)
XX
DE Antisense oligo #1, to elicit RNase H degradation of target RNA.
XX
XX Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
KW antisense; ss.
XX
XX Unidentified.
XX
PN WO2003037909-A1.
XX
PD 08-MAY-2003.
XX
PF 29-OCT-2002; 2002WO-CA001628.
XX
PR 29-OCT-2001; 2001US-0330719P.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;
XX WPI; 2003-421516/39.
DR
XX
XX Novel acyclic linker-containing oligonucleotide useful for preventing or
PT decreasing translation, reverse transcription and/or replication of a
PT target RNA in a system, comprises a modified deoxyribonucleotide.
XX
XX Example 2; Fig 9; 104pp; English.
XX
XX The invention relates to an acyclic linker-containing oligonucleotide
CC comprising at least one modified deoxyribonucleotide. Oligonucleotides of
CC the invention are useful for preventing or decreasing translation,
CC reverse transcription and/or replication of a target RNA in a system.
CC They are useful for selectively preventing gene expression in a sequence-
CC specific manner, for hybridising to complementary RNA such as cellular
CC mRNA or viral RNA, to hybridise to and induce cleavage of complementary
CC RNA. They are also useful therapeutically in formulations or medicaments
CC to prevent or treat a disease characterised by the expression of a
CC particular target RNA. The invention is used in gene therapy. The present
CC sequence is an antisense oligo used to elicit human RNase (ribonuclease)
CC H degradation of target RNA. This sequence is used in the exemplification
CC of the invention
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
DB 18 AAAAAAAAAAAAAA 3

RESULT 294
AAD56446/c
ID AAD56446 standard; DNA; 18 BP.
XX
XX AAD56446;
AC
DT 07-AUG-2003 (first entry)
XX
DE 2' P-ANA antisense oligo #1, to elicit RNase H degradation of target RNA.
XX
XX Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
KW antisense; ss.
```

```
XX Unidentified.
OS
XX
PH Key Location/Qualifiers
FT modified_base 1..18
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-deoxy-2'-fluoroarabinothymidine"
XX
PN WO2003037909-A1.
XX
XX 08-MAY-2003.
XX
XX 29-OCT-2002; 2002WO-CA001628.
XX
XX 29-OCT-2001; 2001US-0330719P.
XX
XX (UYMC-) UNIV MCGILL.
XX
XX Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;
XX WPI; 2003-421516/39.
DR
XX
XX Novel acyclic linker-containing oligonucleotide useful for preventing or
PT decreasing translation, reverse transcription and/or replication of a
PT target RNA in a system, comprises a modified deoxyribonucleotide.
XX
XX Example 2; Fig 7; 104pp; English.
XX
XX The invention relates to an acyclic linker-containing oligonucleotide
CC comprising at least one modified deoxyribonucleotide. Oligonucleotides of
CC the invention are useful for preventing or decreasing translation,
CC reverse transcription and/or replication of a target RNA in a system.
CC They are useful for selectively preventing gene expression in a sequence-
CC specific manner, for hybridising to complementary RNA such as cellular
CC mRNA or viral RNA, to hybridise to and induce cleavage of complementary
CC RNA. They are also useful therapeutically in formulations or medicaments
CC to prevent or treat a disease characterised by the expression of a
CC particular target RNA. The invention is used in gene therapy. The present
CC sequence is an antisense oligo used to elicit human RNase (ribonuclease)
CC H degradation of target RNA. This sequence is used in the exemplification
CC of the invention
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
DB 18 AAAAAAAAAAAAAA 3

RESULT 295
ACH03247/c
ID ACH03247 standard; DNA; 18 BP.
XX
XX ACH03247;
AC
XX
XX 25-SEP-2003 (first entry)
XX
XX Immunostimulatory nucleic acid #882.
DE
XX
XX Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
KW antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;
KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
XX
XX Synthetic.
XX
XX US2003050268-A1.
XX
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PD 13-MAR-2003.
 XX
 PF 29-MAR-2002; 2002US-00112653.
 XX
 XX 29-MAR-2001; 2001US-0279642P.
 PR
 XX (KRIE/) KRIEG A M.
 XX (BERG/) BERG D J.
 PA
 XX Krieg AM, Berg DJ;
 XX WPI; 2003-521815/49.
 XX
 XX Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
 PT allergic contact dermatitis, latex dermatitis or inflammatory bowel
 PT disease by administering an immunostimulatory nucleic acid.
 XX
 PS Disclosure; Page 33; 229pp; English.
 XX
 CC The invention describes a method of treating non-allergic inflammatory
 CC disease comprising administering to a subject having or at risk of
 CC developing a non-allergic inflammatory disease an immunostimulatory
 CC nucleic acid for prevention or treatment of the disease. The method is
 CC useful for treating non-allergic inflammatory diseases, such as
 CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
 CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
 CC This sequence represents an immunostimulatory nucleic acid
 XX
 XX Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
 SQ

Query Match 1.1%; Score 16; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1481 AAAAAAAAAAAAAA 1496
 DB 18 AAAAAAAAAAAAAA 3

RESULT 296
 AAD57871/C
 ID AAD57871 standard; DNA; 18 BP.
 XX
 AC AAD57871;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Antisense oligo #1 used in the exemplification of the invention.
 XX
 KW Sugar-modified nucleoside; acquired immune deficiency syndrome; AIDS;
 KW hepatitis B; gene therapy; virucide; anti-HIV; antisense; ss.
 XX
 OS Unidentified.
 XX

Key Location/Qualifiers
 FH misc_RNA 1..3
 FT /*tag= a
 FT /label= RNA
 FT /note= "2'-O-methyl-D-uridine"
 FT 7..9
 FT misc_RNA
 FT /*tag= b
 FT /label= RNA
 FT /note= "2'-O-methyl-D-uridine"
 FT 13..15
 FT /*tag= c
 FT /label= RNA
 FT /note= "2'-O-methyl-D-uridine"
 PN WO2003064441-A2.
 XX
 PD 07-AUG-2003.
 XX
 PF 31-JAN-2003; 2003WO-CA000129.
 XX
 XX 01-FEB-2002; 2002US-0352873P.
 PR
 XX (UYMC-) UNIV MCGILL.
 XX
 XX Damha MJ, Parniak MA;
 XX WPI; 2003-689523/65.
 XX
 XX New oligonucleotide, useful for preventing or treating a disease related
 PT to a target RNA in a system, e.g., AIDS or hepatitis B.
 XX
 PS Example 2; Page 35; 73pp; English.
 XX

Query Match 1.1%; Score 16; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1481 AAAAAAAAAAAAAA 1496
 DB 18 AAAAAAAAAAAAAA 3

RESULT 296
 AAD57871/C
 ID AAD57871 standard; DNA; 18 BP.
 XX
 AC AAD57871;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Antisense DNA-RNA hybrid #2 used in the exemplification of the invention.
 XX
 KW Sugar-modified nucleoside; acquired immune deficiency syndrome; AIDS;
 KW hepatitis B; gene therapy; virucide; anti-HIV; antisense; DNA-RNA hybrid;
 ss.
 XX
 OS Unidentified.
 XX

Key Location/Qualifiers
 FH misc_RNA 1..3
 FT /*tag= a
 FT /label= RNA
 FT /note= "2'-O-methyl-D-uridine"
 FT 7..9
 FT misc_RNA
 FT /*tag= b
 FT /label= RNA
 FT /note= "2'-O-methyl-D-uridine"
 FT 13..15
 FT /*tag= c
 FT /label= RNA
 FT /note= "2'-O-methyl-D-uridine"
 PN WO2003064441-A2.
 XX
 PD 07-AUG-2003.
 XX
 PF 31-JAN-2003; 2003WO-CA000129.
 XX
 XX 01-FEB-2002; 2002US-0352873P.
 PR
 XX (UYMC-) UNIV MCGILL.
 XX
 XX Damha MJ, Parniak MA;
 XX WPI; 2003-689523/65.
 XX
 XX New oligonucleotide, useful for preventing or treating a disease related
 PT to a target RNA in a system, e.g., AIDS or hepatitis B.
 XX
 PS Example 2; Page 35; 73pp; English.
 XX

Query Match 1.1%; Score 16; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1481 AAAAAAAAAAAAAA 1496
 DB 18 AAAAAAAAAAAAAA 3

RESULT 297
 AAD57878/C
 ID AAD57878 standard; DNA; 18 BP.
 XX
 AC AAD57878;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Antisense DNA-RNA hybrid #2 used in the exemplification of the invention.
 XX
 KW Sugar-modified nucleoside; acquired immune deficiency syndrome; AIDS;
 KW hepatitis B; gene therapy; virucide; anti-HIV; antisense; DNA-RNA hybrid;
 ss.
 XX
 OS Unidentified.
 XX

Key Location/Qualifiers
 FH misc_RNA 1..3
 FT /*tag= a
 FT /label= RNA
 FT /note= "2'-O-methyl-D-uridine"
 FT 7..9
 FT misc_RNA
 FT /*tag= b
 FT /label= RNA
 FT /note= "2'-O-methyl-D-uridine"
 FT 13..15
 FT /*tag= c
 FT /label= RNA
 FT /note= "2'-O-methyl-D-uridine"
 PN WO2003064441-A2.
 XX
 PD 07-AUG-2003.
 XX
 PF 31-JAN-2003; 2003WO-CA000129.
 XX
 XX 01-FEB-2002; 2002US-0352873P.
 PR
 XX (UYMC-) UNIV MCGILL.
 XX
 XX Damha MJ, Parniak MA;
 XX WPI; 2003-689523/65.
 XX
 XX New oligonucleotide, useful for preventing or treating a disease related
 PT to a target RNA in a system, e.g., AIDS or hepatitis B.
 XX
 PS Example 2; Page 35; 73pp; English.
 XX

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XX Example 2; Page 35; 73pp; English.
XX
CC The present invention relates to a new oligonucleoside which comprises
CC alternating first and second segments. The first segment comprises at
CC least one sugar modified nucleoside. The second segment comprises at
CC least one 2'-deoxynucleoside. The oligonucleoside comprises at least 2 of
CC each of the first and second segments, so that it comprises at least 4
CC alternating segments. The oligonucleotide is useful for preparing a
CC composition for inducing RNase H-mediated cleavage of a target RNA in a
CC system, preventing or decreasing translation, transcription or
CC replication of a target RNA in a system, detecting the presence of a
CC target RNA in a system, validating a gene target corresponding to a
CC target RNA in a system or preventing or treating a disease related to a
CC target RNA in a system, e.g., acquired immune deficiency syndrome (AIDS)
CC or hepatitis B. The invention is useful in gene therapy. The present
CC sequence is an antisense DNA-RNA hybrid used in the exemplification of
CC the invention
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 9 T; 9 U; 0 Other;

Query Match      1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
Db 18 AAAAAAAAAAAAAA 3

RESULT 298
AAD57879/c
ID AAD57879 standard; DNA; 18 BP.
XX
AC AAD57879;
XX
DT 20-NOV-2003 (first entry)
XX
DE Antisense DNA-RNA hybrid #3 used in the exemplification of the invention.
XX
KW Sugar-modified nucleoside; acquired immune deficiency syndrome; AIDS;
KW hepatitis B; gene therapy; virucide; anti-HIV; antisense; DNA-RNA hybrid;
KW ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT misc_RNA 1.6
FT /*tag= a
FT /label= RNA
FT /note= "2'-O-methyl-D-uridine"
FT misc_RNA 13..18
FT /*tag= b
FT /label= RNA
FT /note= "2'-O-methyl-D-uridine"
XX
PN WO2003064441-A2.
XX
PD 07-AUG-2003.
XX
PF 31-JAN-2003; 2003WO-CA000129.
XX
PR 01-FEB-2002; 2002US-0352873P.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Damha MJ, Parniak MA;
XX
DR WPI; 2003-689523/65.
XX
PT New oligonucleotide, useful for preventing or treating a disease related
PT to a target RNA in a system, e.g., AIDS or hepatitis B.
XX
```

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PS Example 2; Page 35; 73pp; English.
XX
CC The present invention relates to a new oligonucleoside which comprises
CC alternating first and second segments. The first segment comprises at
CC least one sugar modified nucleoside. The second segment comprises at
CC least one 2'-deoxynucleoside. The oligonucleoside comprises at least 2 of
CC each of the first and second segments, so that it comprises at least 4
CC alternating segments. The oligonucleotide is useful for preparing a
CC composition for inducing RNase H-mediated cleavage of a target RNA in a
CC system, preventing or decreasing translation, transcription or
CC replication of a target RNA in a system, detecting the presence of a
CC target RNA in a system, validating a gene target corresponding to a
CC target RNA in a system or preventing or treating a disease related to a
CC target RNA in a system, e.g., acquired immune deficiency syndrome (AIDS)
CC or hepatitis B. The invention is useful in gene therapy. The present
CC sequence is an antisense DNA-RNA hybrid used in the exemplification of
CC the invention
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 6 T; 12 U; 0 Other;

Query Match      1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
Db 18 AAAAAAAAAAAAAA 3

RESULT 299
AAD57877/c
ID AAD57877 standard; DNA; 18 BP.
XX
AC AAD57877;
XX
DT 20-NOV-2003 (first entry)
XX
DE Antisense DNA-RNA hybrid #1 used in the exemplification of the invention.
XX
KW Sugar-modified nucleoside; acquired immune deficiency syndrome; AIDS;
KW hepatitis B; gene therapy; virucide; anti-HIV; antisense; DNA-RNA hybrid;
KW ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT misc_RNA 1
FT /*tag= a
FT /label= RNA
FT /note= "2'-O-methyl-D-uridine"
FT misc_RNA 3
FT /*tag= b
FT /label= RNA
FT /note= "2'-O-methyl-D-uridine"
FT misc_RNA 5
FT /*tag= c
FT /label= RNA
FT /note= "2'-O-methyl-D-uridine"
FT misc_RNA 7
FT /*tag= d
FT /label= RNA
FT /note= "2'-O-methyl-D-uridine"
FT misc_RNA 9
FT /*tag= e
FT /label= RNA
FT /note= "2'-O-methyl-D-uridine"
FT misc_RNA 11
FT /*tag= f
FT /label= RNA
FT /note= "2'-O-methyl-D-uridine"
FT misc_RNA 13
FT /*tag= g
FT /label= RNA
FT
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FT misc_RNA /note= "2'-O-methyl-D-uridine"
FT 15
FT FT /*tag= h
FT /label= RNA
FT /note= "2'-O-methyl-D-uridine"
FT 17
FT misc_RNA
FT /*tag= i
FT /label= RNA
FT /note= "2'-O-methyl-D-uridine"
FT 18
XX WO2003064441-A2.
XX PN
XX XX
XX PD
XX PF 07-AUG-2003.
XX PR 31-JAN-2003; 2003WO-CA000129.
XX PS
XX PA 01-FEB-2002; 2002US-0352873P.
XX (UYMC-) UNIV MCGILL.
XX Damha MJ, Parniak MA;
XX WPI; 2003-689523/65.
XX New oligonucleotide, useful for preventing or treating a disease related
XX to a target RNA in a system, e.g., AIDS or hepatitis B.
XX Example 2; Page 35; 73pp; English.
XX The present invention relates to a new oligonucleoside which comprises
XX alternating first and second segments. The first segment comprises at
XX least one sugar modified nucleoside. The second segment comprises at
XX least one 2'-deoxynucleoside. The oligonucleoside comprises at least 2 of
XX each of the first and second segments, so that it comprises at least 4
XX alternating segments. The oligonucleotide is useful for preparing a
XX composition for inducing RNase H-mediated cleavage of a target RNA in a
XX system, preventing or decreasing translation, transcription or
XX replication of a target RNA in a system, detecting the presence of a
XX target RNA in a system, validating a gene target corresponding to a
XX target RNA in a system or preventing or treating a disease related to a
XX target RNA in a system, e.g., acquired immune deficiency syndrome (AIDS)
XX or hepatitis B. The invention is useful in gene therapy. The present
XX sequence is an antisense DNA-RNA hybrid used in the exemplification of
XX the invention
XX SQ Sequence 18 BP; 0 A; 0 C; 0 G; 9 T; 9 U; 0 Other;
Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. NO. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1496
DB 18 AAAAAAAAAAAAAA 3
RESULT 300
AAD57890
ID AAD57890 standard; RNA; 18 BP.
AC AAD57890;
XX 20-NOV-2003 (first entry)
XX Target RNA #1 used in RNase H assay.
XX Sugar-modified nucleoside; acquired immune deficiency syndrome; AIDS;
XX hepatitis B; gene therapy; virucide; anti-HIV; ss.
XX Unidentified.
XX WO2003064441-A2.
XX

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PD 07-AUG-2003.
XX 31-JAN-2003; 2003WO-CA000129.
XX 01-FEB-2002; 2002US-0352873P.
XX (UYMC-) UNIV MCGILL.
XX Damha MJ, Parniak MA;
XX WPI; 2003-689523/65.
XX New oligonucleotide, useful for preventing or treating a disease related
XX to a target RNA in a system, e.g., AIDS or hepatitis B.
XX Example 4; Page 38; 73pp; English.
XX The present invention relates to a new oligonucleoside which comprises
XX alternating first and second segments. The first segment comprises at
XX least one sugar modified nucleoside. The second segment comprises at
XX least one 2'-deoxynucleoside. The oligonucleoside comprises at least 2 of
XX each of the first and second segments, so that it comprises at least 4
XX alternating segments. The oligonucleotide is useful for preparing a
XX composition for inducing RNase H-mediated cleavage of a target RNA in a
XX system, preventing or decreasing translation, transcription or
XX replication of a target RNA in a system, detecting the presence of a
XX target RNA in a system, validating a gene target corresponding to a
XX target RNA in a system or preventing or treating a disease related to a
XX target RNA in a system, e.g., acquired immune deficiency syndrome (AIDS)
XX or hepatitis B. The invention is useful in gene therapy. The present
XX sequence is a target RNA used in RNase H assay. This sequence is used in
XX the exemplification of the invention
XX SQ Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 1.1%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. NO. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1496
DB 1 AAAAAAAAAAAAAA 16
RESULT 301
ADB37210/c
ID ADB37210 standard; DNA; 18 BP.
XX ADB37210;
XX 04-DEC-2003 (first entry)
XX Immunostimulatory nucleic acid #824.
XX ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
XX hypo-responsive subject; immunostimulatory.
XX Synthetic.
XX US2003087848-A1.
XX 08-MAY-2003.
XX 02-FEB-2001; 2001US-00776479.
XX 03-FEB-2000; 2000US-0179991P.
XX (BRAT/) BRATZLER R L.
XX (PETE/) PETERSEN D M.
XX (FOUR/) FOURON Y.
XX Bratzler RL, Petersen DM, Fouron Y;
XX

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DR WPI; 2003-657977/62.
 XX Treating and/or preventing allergy or asthma using an immunostimulatory
 PT nucleic acid alone or in combination with an asthma/allergy medicament.
 XX
 PS Disclosure; Page 17; 221pp; English.
 XX
 CC The invention relates to a method of treating or preventing allergy or
 CC asthma which comprises administering to a subject a poly-G nucleic acid
 CC in an aerosol formulation. The methods and compositions of the present
 CC invention are useful for diagnosing and/or treating asthma and allergy
 CC especially in a hypo-responsive subject. The present sequence represents
 CC an immunostimulatory nucleic acid of the invention.
 XX
 XX Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
 SQ

Query Match 1.1%; Score 16; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
 DB 18 AAAAAAAAAAAAAA 3

RESULT 302
 ADB37236/C
 ID ADB37236 standard; DNA; 18 BP.
 XX
 AC ADB37236;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE Immunostimulatory nucleic acid #850.
 XX
 KW ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
 KW hypo-responsive subject; immunostimulatory.
 XX
 OS Synthetic.
 XX
 US2003087848-A1.
 XX
 PD 08-MAY-2003.
 XX
 PF 02-FEB-2001; 2001US-0076479.
 XX
 PR 03-FEB-2000; 2000US-0179991P.
 XX
 PA (BRAT/) BRATZLER R L.
 PA (PETE/) PETERSEN D M.
 PA (FOUR/) FOURON Y.
 XX
 PI Bratzler RL, Petersen DM, Fouron Y;
 XX
 XX WPI; 2003-657977/62.
 XX
 XX Treating and/or preventing allergy or asthma using an immunostimulatory
 PT nucleic acid alone or in combination with an asthma/allergy medicament.
 XX
 PS Disclosure; Page 18; 221pp; English.
 XX
 CC The invention relates to a method of treating or preventing allergy or
 CC asthma which comprises administering to a subject a poly-G nucleic acid
 CC in an aerosol formulation. The methods and compositions of the present
 CC invention are useful for diagnosing and/or treating asthma and allergy
 CC especially in a hypo-responsive subject. The present sequence represents
 CC an immunostimulatory nucleic acid of the invention.
 XX
 XX Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
 SQ

Query Match 1.1%; Score 16; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
 DB 18 AAAAAAAAAAAAAA 3

RESULT 303
 ADE77617
 ID ADE77617 standard; DNA; 18 BP.
 XX
 AC ADE77617;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Human probe NEG for elongation mediated multiplexed analysis of HLA-DR.
 XX
 KW probe; ss; negative control; CFTR; human leukocyte antigen; HLA;
 KW genetic testing; carrier screening; genotyping; profiling; polymorphic;
 KW multiplexed elongation assay; enzymatic recognition;
 KW cystic fibrosis conductance transmembrane regulator.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO2003034029-A2.
 XX
 PD 24-APR-2003.
 XX
 PF 15-OCT-2002; 2002WO-US033012.
 XX
 PR 15-OCT-2001; 2001US-0329427P.
 PR 15-OCT-2001; 2001US-0329428P.
 PR 15-OCT-2001; 2001US-0329619P.
 PR 15-OCT-2001; 2001US-0329620P.
 PR 14-MAR-2002; 2002US-0364416P.
 XX
 PA (BIOA-) BIOARRAY SOLUTIONS LTD.
 XX
 PI Li AX, Hashmi G, Seul M;
 XX
 WPI; 2003-393553/37.
 XX
 XX Concurrent interrogation of a number of polymorphic sites, useful for
 PT genetic testing, carrier screening, genetic profiling, and identity
 PT testing, comprises conducting a multiplexed elongation assay using
 PT probes.
 XX
 PS Example 9; Page 46; 143pp; English.
 XX
 CC This invention relates to a novel method for the concurrent interrogation
 CC of a number of polymorphic sites in the presence of, and without
 CC interference from, non-designated polymorphic sites. Specifically, it
 CC comprises conducting a multiplexed elongation assay by applying one or
 CC more temperature cycles to achieve linear amplification of the target or
 CC a combination of annealing and elongation steps under temperature-
 CC controlled conditions. Furthermore, this detection method uses probe
 CC extension or elongation and relies on enzymatic recognition, a superior
 CC technique that no longer depends on differential hybridisation. The
 CC present invention describes probes and methods useful for identifying or
 CC detecting polymorphisms at one or more designated sites, such that they
 CC can identify mutations within the cystic fibrosis conductance
 CC transmembrane regulator (CFTR) or the human leukocyte antigen (HLA)
 CC genes. In addition, concurrent interrogation of a multiplicity of
 CC polymorphic sites is useful for genetic testing, carrier screening,
 CC genotyping or genetic profiling, and identity testing. This
 CC oligonucleotide is the negative control probe used for the elongation
 CC mediated multiplexed analysis of HLA-DR, in an exemplification of the
 CC invention.
 XX
 SQ Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
 Query Match 1.1%; Score 16; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1496
 |||||
 Db 1 AAAAAAAAAAAAAA 16

RESULT 304
 AAD44129
 ID AAD44129 standard; DNA; 18 BP.
 AC AAD44129;
 XX
 XX 13-DEC-2002 (first entry)
 DT PCR primer #4 designed to bind human MMP PPR region.
 DE
 DE Sequential consensus region-directed amplification; gene expression;
 KW disease diagnosis; gene analysis; human; matrix metalloproteinase; MMP;
 KW propeptide region; PPR; PCR; primer; ss.
 XX Homo sapiens.
 XX US6277571-B1.
 PN 21-AUG-2001.
 PD
 XX 30-SEP-1998; 98US-00163485.
 XX 03-OCT-1997; 97US-00943162.
 PR 03-OCT-1997; 97US-0108152P.
 XX (UYVI-) UNIV VIRGINIA COMMONWEALTH INTELLECTUAL.
 PA Fillmore H, Broadus W, Gillies G;
 PI WPI; 2002-412824/44.
 DR
 XX Sequential consensus region-directed amplification for sorting mixture of
 PT DNAs into 2 or more subsets or distinguishing gene expression patterns in
 PT 2 samples, useful for disease diagnosis and gene analysis.
 XX Example; Col 12; 19pp; English.
 PS
 XX The invention relates to a method of sequential consensus region-directed
 CC amplification for sorting a mixture of DNAs into 2 or more subsets or
 CC distinguishing gene expression patterns in 2 samples. The methods, kits
 CC and oligonucleotides are useful for sorting a mixture of DNAs into 2 or
 CC more subsets or distinguishing gene expression patterns in 2 samples e.g.
 CC for disease diagnosis and gene analysis. The present sequence is a PCR
 CC primer designed to bind to human matrix metalloproteinase (MMP)
 CC propeptide region (PPR). This primer is used to illustrate the method of
 CC the invention
 XX
 XX Sequence 18 BP; 6 A; 2 C; 3 G; 3 T; 0 U; 4 Other;

Query Match 1.1%; Score 15.8; DB 1; Length 18;
 Best Local Similarity 77.8%; Pred. No. 1.7e+02;
 Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 599 AAGGATGTGAAGCAGTTC 616
 |||||
 Db 1 AARGAYGTNAACAGTTC 18

RESULT 305
 AAV19118/c
 ID AAV19118 standard; DNA; 17 BP.
 AC AAV19118;
 XX 28-AUG-1998 (first entry)
 DT
 XX

DE Anchored oligo(T) primer.
 XX Secreted apoptosis-related protein; SARP; mSARP1; mouse; prostate cancer;
 KW breast cancer; diagnosis; gene therapy; PCR; primer; ss.
 XX Synthetic.
 OS
 XX WO9813493-A2.
 PN 02-APR-1998.
 PD
 XX 24-SEP-1997; 97WO-US017154.
 PF
 XX 24-SEP-1996; 96US-0026603P.
 PR 11-OCT-1996; 96US-0028363P.
 XX (LXRB-) LXR BIOTECHNOLOGY INC.
 PA Umansky S, Melkonyan H;
 XX WPI; 1998-230704/20.
 DR
 XX New secreted apoptosis-related proteins - useful for modulating
 PT apoptosis, particularly for treatment of prostatic or breast cancer, also
 PT for diagnosis and monitoring of disease.
 XX Example 1; Page 30; 101pp; English.
 PS
 XX This oligo(T) synthetic oligonucleotide was used for first strand cDNA
 CC synthesis from total RNA isolated from either logarithmically growing or
 CC quiescent dN1/2 mouse fibroblast cells. It was also used with an
 CC arbitrary d(N10) primer in PCR. The PCR products were used in a
 CC differential display to identify the mSARP1 gene (see AAV19112) that
 CC codes for novel murine secreted apoptosis-related protein mSARP1 (see
 CC AAV37814). The invention relates to SARP polynucleotides (see also
 CC AAV19113-15) and polypeptides (see also AAV37815-17), antibodies specific
 CC for SARP, and use of such polynucleotides and antibodies in diagnostic
 CC and therapeutic methods, and methods for treating diseases related to the
 CC regulation of SARP expression in tissue and body fluid samples, including
 CC cancers
 XX
 XX Sequence 17 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 2 Other;

Query Match 1.0%; Score 15.6; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.7e+02;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1479 CTAAAAAAAAAAAAA 1495
 : |||||
 Db 17 SNAAAAAAAAAAAAAA 1

RESULT 306
 AAZ89372/c
 ID AAZ89372 standard; DNA; 17 BP.
 XX
 XX AAZ89372;
 AC
 XX 15-JUN-2000 (first entry)
 DT
 XX RNA detecting primer #2.
 DE
 XX Amplification; detection; gene expression; primer; ss.
 XX Unidentified.
 OS
 XX DE19840731-A1.
 PN 09-MAR-2000.
 PD
 XX 07-SEP-1998; 98DE-01040731.
 PF
 XX 07-SEP-1998; 98DE-01040731.
 PR

XX (HMRI) HOECHST MARION ROUSSEL DEUT GMBH.
XX WPI; 2000-257789/23.
XX
XX Analysis of RNA samples, useful for detection of differential gene
PT expression uses two differently labeled primers.
XX
XX Disclosure; Page 10; 10pp; German.
XX
XX This invention describes a novel method for analysis of an RNA sample
CC which comprises amplifying cDNA with first and second differentially labeled
CC primers and analysis of the amplified labeled cDNA. The method is useful
CC for analyzing differential gene expression, for identifying and/or
CC characterizing pharmacological activities or for identifying target
CC genes. The use of different primer combinations allow more cDNAs to be
CC amplified. The method also provides a more detailed analysis than prior
CC art methods. This sequence represents a primer used to illustrate the
CC method of the invention
XX
SQ Sequence 17 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 2 Other;

Query Match 1.0%; Score 15.6; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.7e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAAA 1495
Db 16 KAAAAAATAAAAAA 1

RESULT 307
AAAT76338/c
ID AAAT76338 standard; DNA; 17 BP.
XX
AC AAT76338;
XX
XX 15-SEP-1997 (first entry)
XX
XX Human fibronectin antisense oligonucleotide HUMFNA/HSFIB1A55.
XX
XX Asthma; airway epithelium; adenosine free; cystic fibrosis;
XX chronic obstructive pulmonary disease; bronchitis; ss.
XX
XX Synthetic.
XX
XX WO9640162-A1.
XX
XX 19-DEC-1996.
XX
XX 06-JUN-1996; 96WO-US009306.
XX
XX 07-JUN-1995; 95US-00474497.
XX
XX (UYEC-) UNIV EAST CAROLINA.
XX
XX Nyce JW, Metzger WJ;
XX
XX WPI; 1997-051871/05.
XX
XX Treatment of airway diseases such as asthma - by topically applying
PT adenosine-free antisense oligo:nucleotide to airway epithelium of
PT subject.
XX
XX Claim 5; Page 36; 71pp; English.
XX
XX A method for treating airway disease in a subject has been produced,
CC which involves the topical administration of an essentially adenosine
CC free antisense oligonucleotide (ON) to the airway epithelium of the
CC subject. The present sequence is an antisense oligonucleotide
CC HUMFNA/HSFIB1A55 specific for the human fibronectin. The method can be
CC used to treat airway diseases such as cystic fibrosis, asthma, chronic
CC obstructive pulmonary disease, bronchitis and other airway diseases

CC characterised by an inflammatory response. By eliminating adenosine from
CC the antisense ON, its liberation upon antisense degradation is prevented,
CC thereby preventing adenosine- induced bronchoconstriction in patients
CC with hyper-reactive airways
XX
SQ Sequence 17 BP; 0 A; 5 C; 12 G; 0 T; 0 U; 0 Other;

Query Match 1.0%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 89 CCCCCGCGCCCGCGCC 105
Db 17 CCCCCGCGCCCGCGCC 1

RESULT 308
AAAX54140/c
ID AAAX54140 standard; DNA; 17 BP.
XX
AC AAX54140;
XX
XX 05-JUL-1999 (first entry)
XX
XX Human fibronectin antisense oligonucleotide fragment.
XX
XX Antisense oligonucleotide; multiple target; antisense treatment;
KW impaired respiration; inflammation; lung disease;
KW pulmonary vasoconstriction; inflammation; allergic rhinitis;
KW acute asthma; allergy; asthma; impeded respiration;
KW respiratory distress syndrome; pain; cystic fibrosis;
KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;
KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KW colon cancer; breast cancer; lung cancer; pancreatic cancer;
KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
KW prostate cancer; ss.
XX
XX Synthetic.
XX
XX WO9913886-A1.
XX
XX 25-MAR-1999.
XX
XX 17-SEP-1998; 98WO-US019419.
XX
XX 17-SEP-1997; 97US-0059160P.
PR 09-JUN-1998; 98US-00093972.
XX
XX (UYEC-) UNIV EAST CAROLINA.
XX
XX Nyce JW;
XX
XX WPI; 1999-229400/19.
XX
XX New antisense oligonucleotides used in treatment of, e.g. pulmonary
PT vasoconstriction.
XX
XX Disclosure; Page 55; 120pp; English.
XX
XX The specification describes antisense oligonucleotides (AAX52869-X55271)
CC directed against at least 2 mRNAs selected from target genes, coding and
CC non-coding regions of RNAs corresponding to target genes, gene initiation
CC codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-
CC end and the juxta-section between coding and non-coding regions and all
CC segments of RNAs encoding proteins associated with one or more diseases,
CC conditions or mixtures. The antisense oligonucleotides may be derived
CC from sequences AAX55272-74. These multiple target oligonucleotides
CC (specifically AAX55180-271) can be used for the antisense treatment of
CC diseases and conditions. Typical diseases and conditions are those
CC associated with impaired respiration and inflammation, including lung
CC diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,
CC acute asthma, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, pulmonary hypertension,

CC pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary
 CC disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.
 CC colon cancer, breast cancer, lung cancer, pancreatic cancer,
 CC hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as
 CC well as all types of cancers which may metastasize or have metastasized
 CC to the lungs, including breast and prostate cancer
 XX
 SQ Sequence 17 BP; 0 A; 5 C; 12 G; 0 T; 0 U; 0 Other;
 Query Match 1.0%; Score 15.4; DB 1; Length 17;
 Best Local Similarity 94.1%; Pred. No. 1.8e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 89 CCCCCGCGCCCGCGCC 105
 DB 17 CCCCCGCGCCCGCGCC 1
 RESULT 309
 AAA33584/c
 ID AAA33584 standard; DNA; 17 BP.
 XX
 AC AAA33584;
 XX
 XX 28-JUL-2000 (first entry)
 DE
 XX Low adenosine antisense oligonucleotide SEQ ID NO:1273.
 XX Human; adenosine receptor; low adenosine antisense oligonucleotide;
 KW phosphorothioate; impaired respiration; inflammation; allergy;
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
 KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200009525-A2.
 XX
 XX 24-FEB-2000.
 XX
 XX 03-AUG-1999; 99WO-US017712.
 XX
 XX 03-AUG-1998; 98US-0095212P.
 XX
 XX (UYEC-) UNIV EAST CAROLINA.
 XX
 XX Nyce JW;
 XX
 XX WPI; 2000-205971/18.
 XX
 XX New antisense oligonucleotides useful for treating e.g. pulmonary
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
 PT cancers.
 XX
 XX Claim 18; Page 424; 1343pp; English.
 XX
 XX The present invention describes a new composition comprising an antisense
 CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
 CC nucleic acids involved in bronchoconstriction, allergies, and/or
 CC inflammation. The ON can have antiinflammatory, antiallergic,
 CC antiasthmatic, cytostatic and analgesic activities. The compositions are
 CC useful for the treatment of diseases associated with inflammation,
 CC impaired airways, including lung disease and diseases whose secondary
 CC effects afflict the lungs of a subject. They can be used for treating
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
 CC impaired respiration, respiratory distress syndrome, pain, cystic
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
 CC carcinomas, and cancers which may metastasize to the lungs, including

CC breast and prostate cancer. The reduction of the adenosine content of the
 CC ONs reduces side effects. The A-containing ONs break down with the
 CC release of deoxyadenosine which activates adenosine receptors causing
 CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
 CC nucleotide sequences given in the sequence listing from the present
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
 CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
 CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
 CC AAA33992) are specifically claimed ONs from the present invention. N.B.
 CC Sequences given in the disclosure of the present invention do not match
 CC up with their corresponding SEQ ID NO: sequences given in the sequence
 CC listing
 XX
 SQ Sequence 17 BP; 0 A; 5 C; 12 G; 0 T; 0 U; 0 Other;
 Query Match 1.0%; Score 15.4; DB 1; Length 17;
 Best Local Similarity 94.1%; Pred. No. 1.8e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 89 CCCCCGCGCCCGCGCC 105
 DB 17 CCCCCGCGCCCGCGCC 1
 RESULT 310
 AAF19706/c
 ID AAF19706 standard; DNA; 17 BP.
 XX
 AC AAF19706;
 XX
 XX 14-MAR-2001 (first entry)
 DT Human fibronectin polynucleotide fragment #1273.
 DE
 XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 KW human; airway disorder; bronchoconstriction; lung inflammation;
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KW cancer; ss.
 XX
 XX Homo sapiens.
 OS
 XX WO200062736-A2.
 XX
 XX 26-OCT-2000.
 XX
 XX 24-MAR-2000; 2000WO-US008020.
 XX
 XX 06-APR-1999; 99US-0127958P.
 XX
 XX (UYEC-) UNIV EAST CAROLINA.
 XX
 XX (NYCE/) NYCE J W.
 XX
 XX Nyce JW;
 XX
 XX WPI; 2000-679539/66.
 XX
 XX Low adenosine (A) content antisense oligonucleotides which do not trigger
 PT adenosine receptors during metabolism, useful e.g. for treating cancers
 PT and respiratory obstructions.
 XX
 XX Claim 14; Page 220; 1592pp; English.
 PS
 XX The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (1) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
 CC (1) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.

CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergies) and/or
CC surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention
XX
SQ Sequence 17 BP; 0 A; 5 C; 12 G; 0 T; 0 U; 0 Other;

Query Match 1.0%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 89 CCCCCCGCGCCGCGCC 105
Db 17 CCCCCCGCGCCGCGCC 1

RESULT 311
AAA25453/C
ID AAA25453 standard; DNA; 17 BP.
XX
AC AAA25453;
XX
DT 19-JUL-2000 (first entry)
XX
DE Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1951.
KW Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW gene expression modification; cancer; phosphorothioate; endonuclease;
KW anticancer; breast cancer; endometrium cancer; ss.
XX
OS Homo sapiens.
XX
PN WO954459-A2.
XX
PD 28-OCT-1999.
XX
PF 19-APR-1999; 99WO-US008547.
XX
PR 20-APR-1998; 98US-0082404P.
PR 23-JUN-1998; 98US-00103636.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Thompson JD, Beigelman L, Mcswiggen JA, Karpeisky A, Ballon L;
PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;
PI Matulic-Adamic J;
XX
DR WPI; 2000-013248/01.
XX
PT New nucleic acids that interact, and optionally cleave, target sequences,
PT used to treat cancer.

PS Claim 77; Page 79; 148pp; English.
XX
CC The present invention describes nucleic acids (A) that interact stably
CC with a target sequence and contain at least one phosphorodithioate
CC link, having endonuclease activity. (A), and more generally any catalytic
CC nucleic acid (A') that modulates expression of the oestrogen receptor
CC gene, are used to treat cancer (particularly of breast or endometrium),
CC in vivo or by transforming cells ex vivo and implanting treated cells, or
CC for other conditions associated with levels of oestrogen receptor.
CC Because of the high selectivity for targeted RNA, (A) can also be used to
CC correlate inhibition of gene expression with alterations in phenotype,
CC particularly for identification of therapeutic targets, and as research
CC reagents (for RNA, in the same way that restriction endonucleases are
CC used with DNA). The combination of modifications in (A) improves
CC resistance to nucleases, binding affinity and/or activity. AAA23503 to
CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
CC AAA24748 to AAA25992 represent their corresponding target sequences.
CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
CC sequences, and AAA26107 to AAA26218 represent their corresponding target
CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
CC antisense oligonucleotides used in the exemplification of the present
CC invention
XX
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1480 TAAAAAATAAAAAA 1496
Db 17 TACAAAAAATAAAAAA 1

RESULT 312
ABK18911
ID ABK18911 standard; RNA; 17 BP.
XX
AC ABK18911;
XX
DT 09-APR-2002 (first entry)
XX
DE Human ERG DNAzyme target sequence Seq ID No 1558.
XX
KW Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;
KW ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;
KW vulnary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;
KW tumour angiogenesis; diabetic retinopathy; macular degeneration;
KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;
KW angiofibroma of tuberosus sclerosis; port-wine stain; wound healing; ss;
KW Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;
KW Osler-Weber-rendu syndrome, leukaemia; osteoporosis; DNAzyme; inozyme;
amberzyme.
XX
OS Homo sapiens.
XX
PN WO20018124-A2.
XX
PD 22-NOV-2001.
XX
PF 16-MAY-2001; 2001WO-US015866.
XX
PR 16-MAY-2000; 2000US-00572021.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (GLAX) GLAXO GROUP LTD.
XX
PI Jarvis T, Von Carlowitz I, Mcswiggen JA, McLaughlin F, Randi AM;
XX WPI; 2002-082995/11.
XX
PT Novel polynucleotide which down regulates expression of Ets-related gene,
PT useful for treating cancer, diabetic retinopathy, macular degeneration,

PT arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.
 XX Claim 4; Page 105; 149pp; English.
 PS The invention relates to a nucleic acid molecule (I) which down regulates
 CC expression of an Ets-related gene (ERG). (I) is useful for treating
 CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,
 CC tumour angiogenesis, diabetic retinopathy, macular degeneration,
 CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca
 CC vulgaris, angiofibroma of tuberosus sclerosis, port-wine stains, Sturge
 CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-tendu
 CC syndrome, leukemia, osteoporosis and wound healing. (I) is useful for
 CC treating a patient having a condition associated with the level of ERG,
 CC by contacting cells of the patient with (I) under conditions suitable for
 CC the treatment. The method comprises the use of one or more therapies
 CC under conditions suitable for the treatment. Leukaemia or tumour
 CC angiogenesis is treated by administering (I) to the patient in
 CC conjunction with one or more of other therapies such as radiation or
 CC chemotherapy treatment. (I) is useful for reducing ERG activity in a
 CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of
 CC ERG gene, by contacting (I) with RNA, in the presence of a divalent
 CC cation such as Mg²⁺. (I) is useful for diagnosis of conditions and
 CC diseases related to the expression of ERG, and as diagnostic tool to
 CC examine genetic drift and mutations within diseased cells or to detect
 CC the presence of ERG RNA in a cell. (I) is useful for specifically
 CC targeting genes that share homology with ERG gene or ERG fusion genes.
 CC ABK17354-ABK22719 represent nucleic acids, including antisense and
 CC enzymatic nucleic acid molecules which regulate expression of ERG, and
 CC related PCR primers of the invention
 XX
 SQ Sequence 17 BP; 1 A; 7 C; 9 G; 0 T; 0 U; 0 Other;

Query Match 1.0%; Score 15.4; DB 1; Length 17;
 Best Local Similarity 94.1%; Pred. No. 1.8e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 25 CGGCGCGCGCGCGCG 41
 ||||| ||||| ||||| |||||
 Db 1 CGGCGCGCGCGCGCG 17

RESULT 313
 ABZ95400/c
 ID ABZ95400 standard; DNA; 17 BP.

XX AC ABZ95400;

XX DT 17-OCT-2003 (first entry)

XX DE Human fibronectin antisense fragment no.1264.

XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antisthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; lung; adenosine sensitivity;
 KW lung inflammation; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.

XX OS Homo sapiens.

XX PN W0200285308-A2.

XX PD 31-OCT-2002.

XX PF 23-APR-2002; 2002WO-US013135.

XX PR 24-APR-2001; 2001US-0286137P.

XX PA (SPIG-) EPIGENESIS PHARM INC.

XX PI Nvce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

PI Miller S, Tang L, Shahabuddin S;

XX

DR WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.

PS Disclosure; SEQ ID NO 10642; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antisthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 17 BP; 0 A; 5 C; 12 G; 0 T; 0 U; 0 Other;

Query Match 1.0%; Score 15.4; DB 1; Length 17;
 Best Local Similarity 94.1%; Pred. No. 1.8e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 89 CCCCCCGCGCGCGCGCC 105
 ||||| ||||| ||||| |||||
 Db 17 CCCCCCGCGCGCGCGCC 1

RESULT 314

ADB04273/c

ID ADB04273 standard; DNA; 17 BP.

XX AC ADB04273;

XX DT 20-NOV-2003 (first entry)

XX DE Human MD27 scanning oligonucleotide SEQ ID 5259.

XX KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
 KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
 KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
 KW developmental disorder; ss.

XX OS Homo sapiens.

XX PN EPI281758-A2.

XX PD 05-FEB-2003.

XX PF 30-JUL-2002; 2002EP-00016874.

XX PR 02-AUG-2001; 2001US-00922181.

XX PA (AEOM-) AEOMICA INC.

XX PI Shannon M, Gu Y, Nguyen C;

XX WPI; 2003-423107/40.

XX PT New zinc finger-containing proteins and nucleic acids, useful in

PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MD23,
PT MD24, MD27 or MD212, e.g. cancer.
XX
PS Example 8; SEQ ID NO 5259; 103pp; English.
XX
CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
CC encoded at chromosome 7q22.1. MD24 is encoded at chromosome 6p21.3-22.2.
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MD23,
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
Query Match 1.0%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1480 TAAAAAATAAAAAAAAAA 1496
Db 17 TCAAAAAAAAAAAAAAAAAA 1
RESULT 315
ADB04274/c
ID ADB04274 standard; DNA; 17 BP.
XX
AC ADB04274;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MD27 scanning oligonucleotide SEQ ID 5260.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MD23, MD24, MD27; MD212; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
OS Homo sapiens.
XX
PN EP1281758-A2.
XX
PD 05-FEB-2003.
XX
PF 30-JUL-2002; 2002EP-00016874.
XX
PR 02-AUG-2001; 2001US-00922181.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Shannon M, Gu Y, Nguyen C;
XX
DR WPI; 2003-423107/40.
XX
PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MD23,
PT MD24, MD27 or MD212, e.g. cancer.
XX
PS Example 8; SEQ ID NO 5260; 103pp; English.
XX
CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is

CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MD23,
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 17 BP; 1 A; 0 C; 2 G; 14 T; 0 U; 0 Other;
Query Match 1.0%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1479 CTAAAAAATAAAAAAAAAA 1495
Db 17 CTCAAAAAATAAAAAAAAAA 1
RESULT 316
ADB03682
ID ADB03682 standard; DNA; 17 BP.
XX
AC ADB03682;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MD27 scanning oligonucleotide SEQ ID 4668.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MD23, MD24, MD27; MD212; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
OS Homo sapiens.
XX
PN EP1281758-A2.
XX
PD 05-FEB-2003.
XX
PF 30-JUL-2002; 2002EP-00016874.
XX
PR 02-AUG-2001; 2001US-00922181.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Shannon M, Gu Y, Nguyen C;
XX
DR WPI; 2003-423107/40.
XX
PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MD23,
PT MD24, MD27 or MD212, e.g. cancer.
XX
PS Example 8; SEQ ID NO 4668; 103pp; English.
XX
CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MD23,
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic

CC acids can also be used as probes to detect and characterize gross
 CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
 CC useful in constructing microarrays for measuring gene expression. The
 CC proteins are useful as therapeutic agents for gene therapy or as
 CC vaccines. The present sequence was used to illustrate the invention.
 XX
 SQ Sequence 17 BP; 2 A; 8 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 1.0%; Score 15.4; DB 1; Length 17;
 Best Local Similarity 94.1%; Pred. No. 1.8e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 946 CTGAGGCCCGCAGCTC 962
 Db 1 CTGAGGCCCGCAGCTC 17

RESULT 317

ABZ61368
 ID ABZ61368 standard; RNA; 17 BP.

XX AC ABZ61368;

XX DT 21-MAR-2003 (first entry)

XX DE Human H-Ras DNase target #159.

XX KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
 KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosolic; anti-HIV;
 KW anti-rheumatic; cancer; AIDS; ss.

XX OS Homo sapiens.

XX PN WO200297114-A2.

XX PD 05-DEC-2002.

XX PF 29-MAY-2002; 2002WO-US016940.

XX PR 29-MAY-2001; 2001US-0294140P.

XX PR 06-JUN-2001; 2001US-0296249P.

XX PR 10-SEP-2001; 2001US-0318471P.

XX PA (RIBO-) RIBOZYME PHARM INC.

XX PI Mcswiggen J;

XX WPI; 2003-140484/13.

XX Novel short interfering RNA and enzymatic nucleic acid useful for
 PT treating cancer, modulates the expression of a nucleic acid encoding
 PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.

XX Claim 58; Page 114; 185pp; English.

XX The invention relates to a novel short interfering RNA (siRNA) nucleic
 CC acid molecule or an enzymatic nucleic acid molecule, that modulates
 CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
 CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
 CC acid molecule of the invention has cytostatic, anti-HIV, and anti-
 CC rheumatic activity. The nucleic acid molecules are useful for reducing
 CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
 CC also useful for treating breast, ovarian, colorectal, lung, prostate,
 CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
 CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ65520 - ABZ65524,
 CC ABZ66530 - ABZ66585 represent substrate/target sequences for the human
 CC ribozymes of the invention

SQ Sequence 17 BP; 0 A; 6 C; 11 G; 0 T; 0 U; 0 Other;

Query Match 1.0%; Score 15.4; DB 1; Length 17;
 Best Local Similarity 94.1%; Pred. No. 1.8e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 25 CGCGCGCGACGGCGCG 41
 Db 1 CGCGCGCGCGCGCGCG 17

RESULT 318

AAQ30446/C

ID AAQ30446 standard; DNA; 18 BP.

XX AC AAQ30446;

XX DT 25-MAR-2003 (revised)

XX DT 07-DEC-1992 (first entry)

XX DE Oligomer TNFR941 for forming triplex with HUMFR target duplex.

XX KW Human tumour necrosis factor receptor mRNA; AIDS; modified; HIV; RSV;
 KW HPV; malignancy; hepatitis; inflammation; ss.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT modified_base 5

XX FT /tag= a

XX FT /mod_base= m5c

XX FT modified_base 18

XX FT /tag= b

XX FT /mod_base= OTHER

XX FT /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"

XX PN WO9209705-A1.

XX PD 11-JUN-1992.

XX PF 25-NOV-1991; 91WO-US008811.

XX PR 23-NOV-1990; 90US-00617907.

XX PR 18-JAN-1991; 91US-00643382.

XX PR 08-APR-1991; 91US-00683420.

XX PR 17-APR-1991; 91US-00686544.

XX PR 17-APR-1991; 91US-00686546.

XX PR 17-APR-1991; 91US-00686547.

XX PR 27-SEP-1991; 91US-00766733.

XX PA (GILE-) GILEAD SCI INC.

XX PI Froehner B, Krawczyk S, Matteucci MD, Milligan J;

XX WPI; 1992-217083/26.

XX New oligomers contg. modified bases - which form a triplex with G-C
 PT doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis,
 PT herpes malignancy and inflammation.

XX Claim 12; Page 72; 77pp; English.

XX The synthetic oligomer is capable of forming a triplex at physiological
 CC pH with a purine rich target sequence by coupling into the major groove
 CC of the duplex. The specific target sequence of this oligomer is the human
 CC tumour necrosis factor receptor mRNA beginning at nucleotide 2354 contg.
 CC a purine rich sequence concd. on one strand of the duplex. The oligomer,
 CC and others like it are useful in diagnosis and therapy of diseases
 CC characterised by specific DNA duplex targets, e.g. HPV, HER, HIV,
 CC hepatitis B, herpes, malignant tumours and inflammation. The triple
 CC helices form under mild conditions thus assays may be carried out without
 CC subjecting the test specimen to harsh conditions. See also AAQ25452-25501
 CC and AAQ30226-448. (Updated on 25-MAR-2003 to correct PN field.) (Updated
 CC on 25-MAR-2003 to correct PD field.)

SQ Sequence 18 BP; 1 A; 1 C; 0 G; 16 T; 0 U; 0 Other;
 Query Match 1.0%; Score 15.4; DB 1; Length 18;

Best Local Similarity 94.1%; Pred. No. 2e+02; Mismatches 0; Indels 1; Gaps 0;
Matches 16; Conservative

QY 1480 TAAAAAAGAAAAA 1496
| | | | | | | | | | | | | | | | | |
DB 18 TAAAAAAGAAAAA 2

RESULT 319
AAV54174/C
ID AAV54174 standard; cDNA; 18 BP.

XX AC AAV54174;
XX DT 21-DEC-1998 (first entry)
XX DE Nucleotide sequence PCR primer 11.
XX KW PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
XX KW immunohistological staining.

XX OS Synthetic.

XX PN WO9839437-A1.

XX PD 11-SEP-1998.

XX PF 05-MAR-1998; 98WO-JP000905.

XX PR 05-MAR-1997; 97JP-00050302.

XX PA (KYOW) KYOWA HAKKO KOGYO KK.

XX PI Sakaki Y;

XX DR WPI; 1998-495844/42.

XX PT Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
treating diseases associated with apoptosis.

XX PS Example 1; Page 50; 70pp; Japanese.

XX CC This is the nucleotide sequence of a PCR primer used in the method of the
invention, involving the use of novel apoptosis-related DNAs and
proteins. The inventions can be used as diagnostic reagents for apoptosis
e.g. (monoclonal) antibodies for the protein, as a reagent in
immunohistological staining, as apoptosis inhibitors. It can also be used
for treatment of apoptosis-related diseases

XX SQ Sequence 18 BP; 0 A; 1 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1478 GCTAAAAAAGAAAAA 1494
| | | | | | | | | | | | | | | | | |
DB 18 GCAAAAAAAGAAAAA 2

RESULT 320
AAV54165/C
ID AAV54165 standard; cDNA; 18 BP.

XX AC AAV54165;

XX DT 21-DEC-1998 (first entry)

XX DE Nucleotide sequence PCR primer 2.

XX KW PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
XX KW immunohistological staining.

OS Synthetic.

XX PN WO9839437-A1.

XX PD 11-SEP-1998.

XX PF 05-MAR-1998; 98WO-JP000905.

XX PR 05-MAR-1997; 97JP-00050302.

XX PA (KYOW) KYOWA HAKKO KOGYO KK.

XX PI Sakaki Y;

XX DR WPI; 1998-495844/42.

XX PT Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
treating diseases associated with apoptosis.

XX PS Example 1; Page 47; 70pp; Japanese.

XX CC This is the nucleotide sequence of a PCR primer used in the method of the
invention, involving the use of novel apoptosis-related DNAs and
proteins. The inventions can be used as diagnostic reagents for apoptosis
e.g. (monoclonal) antibodies for the protein, as a reagent in
immunohistological staining, as apoptosis inhibitors. It can also be used
for treatment of apoptosis-related diseases

XX SQ Sequence 18 BP; 1 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 2e+02;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1480 TAAAAAAGAAAAA 1496
| | | | | | | | | | | | | | | | | |
DB 18 TCAAAAAAAGAAAAA 2

RESULT 321

AAV54166/C

ID AAV54166 standard; cDNA; 18 BP.

XX AC AAV54166;

XX DT 21-DEC-1998 (first entry)

XX DE Nucleotide sequence PCR primer 3.

XX KW PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
XX KW immunohistological staining.

XX OS Synthetic.

XX PN WO9839437-A1.

XX PD 11-SEP-1998.

XX PF 05-MAR-1998; 98WO-JP000905.

XX PR 05-MAR-1997; 97JP-00050302.

XX PA (KYOW) KYOWA HAKKO KOGYO KK.

XX PI Sakaki Y;

XX DR WPI; 1998-495844/42.

XX PT Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
treating diseases associated with apoptosis.

XX PS Example 1; Page 48; 70pp; Japanese.


```
XX PR 23-JUL-1998; 98JP-00225228.
XX PA (NISB ) JAPAN TOBACCO INC.
XX DR WPI; 2000-306578/27.
XX PT A physiologically active protein specifically derived from mammal tissue.
XX PS Example 2; Page 18; 50pp; Japanese.
XX CC The invention relates to identification of genes and proteins of adipose
CC tissue relating to obesity, particularly complications of visceral
CC obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
CC hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
CC proteins (AAV67598-Y67600) are used in the genetic diagnosis, prevention
CC and treatment of adipose tissue related diseases. Sequences AAZ90640-51
CC represent PCR primers amplifying the human adipose tissue genes
XX SQ Sequence 18 BP; 0 A; 1 C; 2 G; 15 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 15.4; DB 1; Length 18;
XX Best Local Similarity 94.1%; Pred. No. 2e+02;
XX Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1478 GCTAATAAAAAAAAAA 1494
DB 18 GCAAAAAAAAAAAAAA 2

RESULT 328
AAZ90647/C
ID AAZ90647 standard; DNA; 18 BP.
XX AC AAZ90647;
XX DT 13-JUN-2000 (first entry)
XX DE Human adipose tissue gene amplifying primer #8.
XX KW Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
XX KW arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX OS Homo sapiens.
XX PN JP2000037190-A.
XX PD 08-FEB-2000.
XX PF 23-JUL-1998; 98JP-00225228.
XX PR 23-JUL-1998; 98JP-00225228.
XX PA (NISB ) JAPAN TOBACCO INC.
XX DR WPI; 2000-306578/27.
XX PT A physiologically active protein specifically derived from mammal tissue.
XX PS Example 2; Page 18; 50pp; Japanese.
XX CC The invention relates to identification of genes and proteins of adipose
XX CC tissue relating to obesity, particularly complications of visceral
XX CC obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
XX CC hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
XX CC proteins (AAV67598-Y67600) are used in the genetic diagnosis, prevention
XX CC and treatment of adipose tissue related diseases. Sequences AAZ90640-51
XX CC represent PCR primers amplifying the human adipose tissue genes
XX SQ Sequence 18 BP; 1 A; 0 C; 2 G; 15 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 15.4; DB 1; Length 18;
XX Best Local Similarity 94.1%; Pred. No. 2e+02;
XX Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1478 TAAATAAAAAAAAAA 1496
DB 18 TCAAAAAAAAAAAAAA 2

RESULT 329
AAF85699
ID AAF85699 standard; DNA; 18 BP.
XX AC AAF85699;
XX DT 13-JUL-2001 (first entry)
XX DE Multiple repeated heat process PCR related oligonucleotide #3.
XX KW Multiple repeated heat circulation; polymerase chain reaction; PCR;
XX KW target DNA production; DNA synthesis; ds.
XX OS Unidentified.
XX PN CN1278558-A.
XX PD 03-JAN-2001.
XX PF 22-JUN-1999; 99CN-00114949.
XX PR 22-JUN-1999; 99CN-00114949.
XX PA (XIAQ/) XIA Q.
XX PI Xia Q;
XX DR WPI; 2001-245741/26.
XX PT Asynchronous chain-extending polymerase chain reaction for producing lots
XX PT of target DNA fragments, comprises a multiple repeated heat circulation
XX PS Disclosure; Page 3; 4pp; Chinese.
XX CC The present invention relates to a kind of two chains asynchronously-
XX CC elongated DNA amplification technology in vitro, which is characterized
XX CC by that firstly, a pair of specific primers is synthesized according to
XX CC the target DNA sequence to be amplified, then a repetitive sequence
XX CC complementary oligo-repetitive sequence of 3' target DNA chain whose tail
XX CC end is modified and elongation vitality is lost, then the oligo-
XX CC repetitive sequence, chain primer, heat-resisting DNA polymerase, dNTP
XX CC substrate, template DNA, magnesium ion, polymerase chain reaction (PCR)
XX CC buffer solution and ultra-pure water are mixed uniformly and made into a
XX CC reaction system. The reaction system then undergoes the processes of high
XX CC -temp., low-temp., medium-low temp., medium-temp, and repeated heat
XX CC circulation treatment in the heat-circulating instrument to obtain
XX CC million copies of specific target DNA fragments. The invention adopts a
XX CC multiple repeated heat circulation process, so that it can produce lots
XX CC of target DNA fragments. The present sequence was used in the
XX CC exemplification of the invention
XX SQ Sequence 18 BP; 0 A; 6 C; 12 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 15.4; DB 1; Length 18;
XX Best Local Similarity 94.1%; Pred. No. 2e+02;
XX Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 25 CGGCGCGCGACGCGGCG 41
DB 1 CGGCGCGCGCGCGGCG 17

RESULT 330
ADA27361
ID ADA27361 standard; DNA; 18 BP.
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XX AC ADA27361;
XX PD
XX DT 20-NOV-2003 (first entry)
XX DE
XX DE Human microsatellite repeat M2_3_8.
XX KW ds; HLA-related research; HLA class II-associated disease;
XX KW transplantation matching; recombination hot spot identification;
XX KW linkage disequilibrium study; human; microsatellite.
XX OS Homo sapiens.
XX XX
XX XX US2003108940-A1.
XX PD 12-JUN-2003.
XX XX
XX PF 06-DEC-2002; 2002US-00314405.
XX XX
XX PR 15-NOV-2000; 2000US-00713616.
XX XX
XX PA (INOK/) INOKO H.
XX XX
XX PI Inoko H, Tamiya G, Matsuzaka Y;
XX XX WPI; 2003-616782/58.
XX XX
XX PT New oligonucleotide primer capable of specifically hybridizing to a DNA
XX PT having the sequence of the flanking regions of a microsatellite (e.g.
XX PT M249), useful for HLA-related research, e.g. transplantation matching.
XX PS
XX PS Example 2; Page 5; 20pp; English.
XX XX
XX CC The invention relates to an oligonucleotide primer capable of
XX CC specifically hybridizing to a DNA having the sequence of the flanking
XX CC regions of a microsatellite selected from M2-4-9, M2-2-9, M2-2-12, M2-3-
XX CC 11, M2-2-20, M2-2-21, M2-2-22, M2-2-23, M2-2-24, M2-4-25, M2-4-26, M2-2-
XX CC 29, M2-2-32, M2-4-32, M2-4-33, M2-4-37, M2-3-22, M2-2-36, M2-5-11, M2-2-
XX CC 46, and M2-2-48. The primer is useful for determining the number of
XX CC repeat units of the microsatellite cited above. The primer is useful in
XX CC HLA-related research, such as genetic mapping of HLA class II-associated
XX CC diseases, transplantation matching, population genetics, and
XX CC identification of recombination hot spots as well as linkage
XX CC disequilibrium studies. The present sequence represents the human
XX CC microsatellite repeat M2_3_8.
XX XX
XX SQ Sequence 18 BP; 0 A; 6 C; 12 G; 0 T; 0 U; 0 Other;

Query Match 1.0%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 25 CGCGCGCGACGCGCGCG 41
Db 2 CGCGCGCGCGCGCGCG 18

RESULT 331
ADC26385
ID ADC26385 standard; DNA; 18 BP.
XX AC
XX AC ADC26385;
XX DT 18-DEC-2003 (first entry)
XX DE
XX DE NOV protein-related reverse PCR primer SEQ ID 210.
XX KW NOV; cytostatic; metabolic disorder; immune; neurodegenerative;
XX KW circulatory; haemopoietic; wasting; cancer; gene therapy; vaccine;
XX KW transgenic; human; ss; PCR; primer.
XX OS Homo sapiens.
XX XX

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PN WO2003004687-A2.
XX
XX PD 16-JAN-2003.
XX XX
XX PF 03-JUL-2002; 2002WO-US021361.
XX XX
XX PR 05-JUL-2001; 2001US-0303046P.
XX PR 09-JUL-2001; 2001US-0303828P.
XX PR 09-JUL-2001; 2001US-0304016P.
XX PR 11-JUL-2001; 2001US-0304502P.
XX PR 13-JUL-2001; 2001US-0305262P.
XX PR 16-JUL-2001; 2001US-0305673P.
XX PR 17-JUL-2001; 2001US-0306085P.
XX PR 24-JUL-2001; 2001US-0307536P.
XX PR 27-JUL-2001; 2001US-0308228P.
XX PR 30-JUL-2001; 2001US-0308677P.
XX PR 01-AUG-2001; 2001US-0309255P.
XX PR 17-AUG-2001; 2001US-031328P.
XX PR 12-SEP-2001; 2001US-0318711P.
XX PR 19-SEP-2001; 2001US-0323380P.
XX PR 21-SEP-2001; 2001US-0323969P.
XX PR 04-JAN-2002; 2002US-0345022P.
XX PR 28-FEB-2002; 2002US-0361172P.
XX PR 01-MAR-2002; 2002US-0360814P.
XX PR 01-MAR-2002; 2002US-0360830P.
XX PR 01-MAR-2002; 2002US-0361133P.
XX PR 01-MAR-2002; 2002US-0361147P.
XX PR 05-MAR-2002; 2002US-0361677P.
XX PR 02-APR-2002; 2002US-0363677P.
XX PR 12-APR-2002; 2002US-0372326P.
XX PR 16-APR-2002; 2002US-0372990P.
XX PR 19-APR-2002; 2002US-0373881P.
XX PR 19-APR-2002; 2002US-0373921P.
XX PR 02-JUL-2002; 2002US-00188186.
XX XX
XX PA (CURA-) CURAGEN CORP.
XX PI Anderson DW, Berghs C, Boldog FL, Burgess CE, Casman SJ;
XX PI Catterton E, Edinger S, Eisen AJ, Ellerman K, Gerlach V, Gorman L;
XX PI Guo X, Jeffers M, Kekuda R, Li L, Malyankar UM, Miller CE;
XX PI Padigaru M, Patturajan M, Pena CEA, Rastelli L, Shenoy S;
XX PI Shimkets RA, Spaderna SK, Spytek KA, Stone DJ, Taupier RJ;
XX PI Vernet CAM, Voss EZ, Zhong M;
XX WPI; 2003-221607/21.
XX XX
XX PT New isolated NOVX polypeptide, useful for determining the presence of, or
XX PT predisposition to a disease associated with altered levels of expression
XX PT of the polypeptide, and for treating or preventing cancer.
XX XX
XX PS Example C; SEQ ID NO 210; 478pp; English.
XX XX
XX CC The invention relates to a novel isolated NOV polypeptide. The
XX CC polypeptide of the invention demonstrates cytostatic activity and may be
XX CC used for determining the presence of, or predisposition to a disease
XX CC associated with altered levels of expression of the polypeptide,
XX CC including metabolic disorders, immune disorders, neurodegenerative
XX CC disorders, circulatory diseases, haemopoietic disorders, wasting diseases
XX CC and cancer. The polypeptide may also be utilised during gene therapy
XX CC procedures, vaccine development and transgenic animal production. The
XX CC current sequence is that of the PCR primer of the invention which was
XX CC used to analyse human NOV DNA.
XX XX
XX SQ Sequence 18 BP; 4 A; 7 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 1.0%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 714 CCAGCACACTGACTGCT 730
Db 2 CCAGGACACTGACTGCT 18

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RESULT 332
AAF82119/c
ID AAF82119 standard; DNA; 16 BP.
XX
AC AAF82119;
XX
DT 27-JUN-2001 (first entry)
XX
DE Human TSA7005 gene isolation related PCR primer SEQ ID NO:4.
XX
KW Human; TSA7005; Reg; pancreatic beta cell growth; hypoglycaemic;
KW diagnosis; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN JP2001025389-A.
XX
PD 30-JAN-2001.
XX
PF 15-JUL-1999; 99JP-00201279.
XX
PR 15-JUL-1999; 99JP-00201279.
XX
PA (SAKA ) OTSUKA PHARM CO LTD.
XX
DR WPI; 2001-303742/32.
XX
PT TSA7005 gene, encoding a polypeptide useful for the diagnosis and
PT treatment of diseases associated with its expression.
XX
PS Example 1; Page 24; 25pp; Japanese.
XX
CC The present sequence represents a PCR primer which is used in an example
CC from the present invention for the isolation of human TSA7005 gene. The
CC human TSA7005 protein shares 32% homology with human and mouse Reg
CC proteins, and 34% homology with the rat Reg protein. TSA7005 has
CC pancreatic beta cell growth activity and hypoglycaemic activity. The
CC TSA7005 protein can be used for the diagnosis and treatment of diseases
CC associated with the gene and its expression product
XX
SQ Sequence 16 BP; 1 A; 0 C; 0 G; 14 T; 0 U; 1 Other;
Query Match 1.0%; Score 15.2; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 1.8e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1480 TAAAAAATAAAAAA 1495
Db 16 TAAAAAATAAAAAA 1
RESULT 333
AAI18388/c
ID AAI18388 standard; DNA; 17 BP.
XX
AC AAI18388;
XX
DT 11-MAY-1999 (first entry)
XX
DE RT-PCR primer of the invention SEQ ID 29.
XX
KW RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
OS Synthetic.
XX
PN JP11032765-A.
XX
PD 09-FEB-1999.
XX
PF 18-JUL-1997; 97JP-00208312.
XX
PR 18-JUL-1997; 97JP-00208312.
XX
PA (TAKI ) TAKARA SHUZO CO LTD.
XX
DR WPI; 1999-183822/16.
XX
PT Peptides having at least two new nucleotides - useful as primers in RT-PCR.
XX
PS Example 1; Page 12; 19pp; Japanese.
XX
CC This sequence represents a primer of the invention. The invention relates
CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
CC a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC natural number indicating the repetition of alpha; beta, delta = V or N;
CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC repetition of gamma, in which thymine expressed by gamma is composed of
CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC useful as primers for RT-PCR and determination of base sequences. The new
CC sequences allow for reproductive and highly efficient analysis of gene
CC sequences
XX
SQ Sequence 17 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 2 Other;
Query Match 1.0%; Score 15.2; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1480 TAAAAAATAAAAAA 1495
Db 16 BAAAAAATAAAAAA 1
RESULT 334
AAS14174/c
ID AAS14174 standard; DNA; 17 BP.
XX
AC AAS14174;
XX
DT 18-DEC-2001 (first entry)
XX
DE Modified Poly-T Primer #1 used in construction of probe sets.
XX
KW WRAP-Probe; gene expression array; global amplification; RNA array; ss;
KW tissue microarray; drug discovery assay; reporter binding site; forensic;
KW diagnostic; genomic analysis; universal linker; poly-T primer.
XX
OS Synthetic.
XX
PN WO200166802-A1.
XX
PD 13-SEP-2001.
XX
PF 09-MAR-2001; 2001WO-US007508.
XX
PR 09-MAR-2000; 2000US-0187982P.
XX
PA (GENE-) GENETAG TECHNOLOGY INC.
XX
PI Shafer DA;
XX
PW WPI; 2001-596845/67.
XX
PT Novel probe sets with common universal linkers at one or both ends (WRAP
PT probes) for gene expression arrays to provide global amplification of
PT probe set and to provide common equivalent signaling regardless of
PT length.
XX
PS Disclosure; Page 88; 97pp; English.
XX
CC The invention relates to a probe set for gene expression arrays to

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CC provide common equivalent signalling per probe and global amplification
CC of the set. The probe set has a pool of modified cDNA probes, each probe
CC having a central target specific segment copied from a portion of a
CC single mRNA transcript and a universal linker (a WRAP-Probe) located on
CC one or both terminal ends. The universal linker has reporter binding
CC sites to join common reporters to the probes and primer binding sites to
CC copy and amplify the probe. The probes and reporters are useful in
CC diagnostic or drug discovery assays for a wide range of biomedical
CC samples, including detection of nucleic acids and gene expression
CC profiles in human diagnostics, forensics and genomic analysis. The
CC methods are useful for amplifying and identifying any unknown DNA
CC fragment and also for improving sensitivity with tissue microarrays or
CC RNA arrays. The methods improve the quantification of gene expression and
CC allow highly improved detection of rare transcripts or very small
CC samples. This sequence represents a poly-T primer used in the
CC construction of probe sets
XX
SQ Sequence 17 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 2 Other;

Query Match 1.0%; Score 15.2; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2e+02; Mismatches 0; Gaps 0;
Matches 15; Conservative 1; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAAA 1495
Db 16 BAAAAAAAAAAAAA 1

RESULT 335
AAQ79185
ID AAQ79185 standard; DNA; 15 BP.
XX
AC AAQ79185;
XX
DT 25-MAR-2003 (revised)
DT 21-JUN-1995 (first entry)
XX
DE Nuclease resistant oligonucleotide.
XX
KW Nuclease resistant oligonucleotide; inhibition of gene expression;
KW 9-methyl-8-acyclo-adenosine; antisense agents; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 13
FT /*tag= a
FT /mod_base= OTHER
FT /note= "9-methyl-acyclo-adenosine"
XX
PN W09422864-A1.
XX
PD 13-OCT-1994.
XX
PF 21-MAR-1994; 94WO-US002995.
XX
PR 30-MAR-1993; 93US-00040326.
XX
PA (STER) STERLING WINTHROP INC.
XX
PI Cook PD, Delecki DJ, Guinosso C;
XX
DR WPI; 1994-333078/41.
XX
PT New acyclic nucleoside analogues - used to prepare nuclease resistant
PT oligo-nucleotide(s) used partic. for inhibiting gene expression.
XX
PS Example 11; Page 20; 37pp; English.
XX
CC AAQ79182-Q79186 contain one or more 9-methyl-acyclo-adenosines, acyclic
CC nucleoside analogues which inhibit nuclease degradation. The nuclease
CC resistant oligonucleotides can themselves be used to inhibit gene
CC expression as antisense agents, in nucleic acid sequencing and diagnostic
CC

CC assays. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 1 AAAAAAAAAAAAAA 15

RESULT 336
AAQ79184
ID AAQ79184 standard; DNA; 15 BP.
XX
AC AAQ79184;
XX
DT 25-MAR-2003 (revised)
DT 21-JUN-1995 (first entry)
XX
DE Nuclease resistant oligonucleotide.
XX
KW Nuclease resistant oligonucleotide; inhibition of gene expression;
KW 9-methyl-8-acyclo-adenosine; antisense agents; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 14
FT /*tag= a
FT /mod_base= OTHER
FT /note= "9-methyl-acyclo-adenosine"
XX
PN W09422864-A1.
XX
PD 13-OCT-1994.
XX
PF 21-MAR-1994; 94WO-US002995.
XX
PR 30-MAR-1993; 93US-00040326.
XX
PA (STER) STERLING WINTHROP INC.
XX
PI Cook PD, Delecki DJ, Guinosso C;
XX
DR WPI; 1994-333078/41.
XX
PT New acyclic nucleoside analogues - used to prepare nuclease resistant
PT oligo-nucleotide(s) used partic. for inhibiting gene expression.
XX
PS Example 10; Page 20; 37pp; English.
XX
CC AAQ79182-Q79186 contain one or more 9-methyl-acyclo-adenosines, acyclic
CC nucleoside analogues which inhibit nuclease degradation. The nuclease
CC resistant oligonucleotides can themselves be used to inhibit gene
CC expression as antisense agents, in nucleic acid sequencing and diagnostic
CC assays. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 1 AAAAAAAAAAAAAA 15

RESULT 337
AAT52136/c


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PR 10-NOV-1994; 94US-00337608.
PR 28-NOV-1994; 94US-00345516.
PR 16-DEC-1994; 94US-00357577.
PR 23-DEC-1994; 94US-00363233.
PR 30-JAN-1995; 95US-00380734.
XX
PR (RIBO-) RIBOZYME PHARM INC.
PA
XX Stinchcomb DT, Chowrira B, Dizenzo A, Draper KG, Dudycz LW;
PI Grimm S, Karpeisky A, Kisch K, Matulic-Adamic J, Mcswiggen JA;
PI Modak A, Favco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
PI Tracz D, Usman N, Wincott PE, Woolf T;
XX
DR WPI; 1995-351090/45.
XX
XX Ribozymes having modified bases and methods for producing them - for use
PT in inhibiting disease related genes.
XX
XX Claim 2; Page 175; 407pp; English.
XX
CC The present sequence represents a preferred target sequence for an
CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA at the
CC nucleotide base position indicated in the DE line. Regions of the mRNA
CC that do not form secondary folding structures and that contain potential
CC hammerhead and hairpin ribozyme cleavage sites were identified by
CC computer analysis. Ribozymes directed against these mRNA sequences were
CC designed and synthesised with modifications that improve their nuclease
CC resistance. The ribozymes cleave the ICAM-1 target sequences and thereby
CC inhibit ICAM-1 expression, making them useful for reducing transplant
CC rejection and alleviating symptoms in patients with rheumatoid arthritis,
CC asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to
CC correct PI field.)
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
DB 15 AAAAAAAAAAAAAA 1

RESULT 339
AAV01604
ID AAV01604 standard; DNA; 15 BP.
XX
AC AAV01604;
XX
DT 25-MAR-2003 (revised)
DT 31-MAR-1998 (first entry)
XX
DE Oligonucleotide containing phosphoramidate linkages.
XX phosphoramidate linkage; solid phase synthesis; ss.
XX Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 1..15
FT /*tag= a
FT /note= "these residues have N3'-->P5' phosphoramidate
FT linkages"
XX
XX WO9731009-A1.
XX
XX 28-AUG-1997.
XX
XX 14-JUN-1996; 96WO-US010418.
XX
XX 21-FEB-1996; 96US-00603566.
XX
XX

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PA (LYNX-) LYNX THERAPEUTICS INC.
XX
XX Hirschbein BL, Fearon KL, Gryaznov SM, Mccurdy SN, Nelson JS;
PI Schultz RG;
XX
XX WPI; 1997-435080/40.
XX
XX Synthesis of N3' to P5' phosphoramidate oligonucleotide - by reacting
XX immobilised 3'-amino nucleotide with new amino:nucleoside 5'-
XX phosphoramidate then oxidation, useful as research, diagnostic and
XX therapeutic agents.
XX
XX Disclosure; Page 28; 60pp; English.
XX
XX A new method is provided for the synthesis of oligonucleotides having N3'
XX -->P5' phosphoramidate linkages. The method comprises (a) attaching a 3'-
XX protected amino nucleoside to a solid support; (b) deprotecting the 3'-
XX amino; (c) reacting with a 3'-protected aminonucleoside-5'-
XX phosphoramidate monomer to form an internucleoside N3'-->P5'
XX phosphoramidate link; (d) oxidising this link to phosphoramidate; and
XX optionally repeating steps (b)-(d) until the required oligonucleotide is
XX completed. This method provides better yields with lower reagent
XX consumption than known processes, and can be operated on a large scale.
XX The obtained oligos, containing phosphoramidate linkages, have favourable
XX binding properties, nuclease resistance and solubility, and are useful as
XX research, diagnostic and therapeutic agents. The present sequence is an
XX example of an oligonucleotide in which N3'-->P5' phosphoramidate linkages
XX have been introduced by the new method. (Updated on 25-MAR-2003 to
XX correct PR field.)
XX
SQ Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
DB 1 AAAAAAAAAAAAAA 15

RESULT 340
AAV01603/c
ID AAV01603 standard; DNA; 15 BP.
XX
AC AAV01603;
XX
DT 25-MAR-2003 (revised)
DT 31-MAR-1998 (first entry)
XX
DE Oligonucleotide containing phosphoramidate linkages.
XX phosphoramidate linkage; solid phase synthesis; ss.
XX Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 1..15
FT /*tag= a
FT /note= "these residues have N3'-->P5' phosphoramidate
FT linkages"
XX
XX WO9731009-A1.
XX
XX 28-AUG-1997.
XX
XX 14-JUN-1996; 96WO-US010418.
XX
XX 21-FEB-1996; 96US-00603566.
XX
XX (LYNX-) LYNX THERAPEUTICS INC.
XX
XX Hirschbein BL, Fearon KL, Gryaznov SM, Mccurdy SN, Nelson JS;
PI

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PI Schultz RG;
 XX WPI; 1997-435080/40.
 XX
 XX Synthesis of N3' to P5' phosphoramidate oligo:nucleotide - by reacting
 PT immobilised 3'-amino nucleotide with new amino:nucleoside 5'-
 PT phosphoramidate then oxidation, useful as research, diagnostic and
 PT therapeutic agents.
 XX
 XX Disclosure; Page 28; 60pp; English.
 XX
 XX A new method is provided for the synthesis of oligonucleotides having N3'
 CC ->P5' phosphoramidate linkages. The method comprises (a) attaching a 3'-
 CC protected amino nucleoside to a solid support; (b) deprotecting the 3'-
 CC amino; (c) reacting with a 3'-protected aminonucleoside-5'-
 CC phosphoramidate monomer to form an internucleoside N3'->P5'
 CC phosphoramidate link; (d) oxidising this link to phosphoramidate; and
 CC optionally repeating steps (b)-(d) until the required oligonucleotide is
 CC completed. This method provides better yields with lower reagent
 CC consumption than known processes, and can be operated on a large scale.
 CC The obtained oligos, containing phosphoramidate linkages, have favourable
 CC binding properties, nuclease resistance and solubility, and are useful as
 CC research, diagnostic and therapeutic agents. The present sequence is an
 CC example of an oligonucleotide in which N3'->P5' phosphoramidate linkages
 CC have been introduced by the new method. (Updated on 25-MAR-2003 to
 CC correct PR field.)
 XX
 XX Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
 SQ
 Query Match 1.0%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1481 AAAAAAAAAAAAAA 1495
 DB 15 AAAAAAAAAAAAAA 1
 RESULT 341
 ID AAV07431/c
 XX AAV07431 standard; DNA; 15 BP.
 XX
 XX AAV07431;
 XX
 XX 27-OCT-1998 (first entry)
 XX
 XX Synthetic peptide-labeled oligonucleotide primer.
 DE
 XX oligonucleotide; peptide; conjugate; release tag compound;
 XX mass spectrometry; detection; identification; diagnosis; primer; ss.
 XX
 XX Synthetic.
 OS
 XX WO9826095-A1.
 PN
 XX
 XX 18-JUN-1998.
 PD
 XX
 XX 10-DEC-1997; 97WO-US022639.
 PF
 XX
 XX 10-DEC-1996; 96US-0033037P.
 PR
 XX 16-MAY-1997; 97US-0046719P.
 PR
 XX
 XX (GENE-) GENETRACE SYSTEMS INC.
 PA
 XX
 XX Montforte JA, Becker CH, Pollart DJ, Shaler TA;
 PI
 XX WPI; 1998-348547/30.
 XX
 XX New release tag compounds for detecting target molecule(s) - comprising a
 PT reactive group, a release group and a releasable non-volatile mass label
 PT detectable by mass spectrometry.
 PT
 XX Example 3; Page 92; 170pp; English.
 XX

XX
 CC The sequence is that of an oligonucleotide primer which was produced as
 CC part of an oligonucleotide peptide conjugate as an example of a release
 CC tag compound (RTC). These comprise a reactive group, a release group and
 CC a non-volatile mass label comprising a synthetic polymer or biopolymer
 CC detectable by mass spectrometry. The RTCs can be used as probes for the
 CC detection of RWS. They can be used for e.g. identification of gene
 CC sequences, identification of non-coding nucleotide sequences,
 CC identification of mutations within a gene or protein sequence, detection
 CC of metals, detection of toxins, detection of receptors on an organism or
 CC a cell, characterisation of antibody-antigen interactions, enzyme-
 CC substrate interactions and characterisation of ligand interactions.
 CC Multiplex applications include multiple pathogen diagnostics, multigene
 CC genetic polymorphism screening, single nucleotide polymorphism (SNP)
 CC genotyping, clone and gene mapping, and gene expression analysis. The
 CC RTCs permit the ready detection of releasable mass labels by mass
 CC spectroscopy. The releasable mass labels permit the multiplexing of tens,
 CC hundreds and perhaps even thousands of different mass labels that can be
 CC used to uniquely identify each desired target
 XX
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
 Query Match 1.0%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1481 AAAAAAAAAAAAAA 1495
 DB 15 AAAAAAAAAAAAAA 1
 RESULT 342
 ID AAT86675/c
 XX AAT86675 standard; DNA; 15 BP.
 XX
 XX AAT86675;
 AC
 XX
 XX 04-JUN-1998 (first entry)
 DT
 XX
 XX Oligonucleotide linked to polyacrylamide.
 DE
 XX
 XX Capillary affinity gel electrophoresis; separation; polymer-gel;
 XX polyacrylamide; ss.
 KW
 XX
 XX Synthetic.
 OS
 XX
 XX Key Location/Qualifiers
 PH modified_base 1
 FT /*tag= a
 FT /note= "Thymine at 5' end attached to a polyacrylamide
 FT gel via a linking group"
 FT
 XX
 XX WO9745721-A1.
 PN
 XX
 XX 04-DEC-1997.
 PD
 XX
 XX 23-MAY-1997; 97WO-EP002647.
 PF
 XX
 XX 24-MAY-1996; 96CH-00001320.
 PR
 XX
 XX (NOVS) NOVARTIS AG.
 PA
 XX
 XX Muscate A, Paulus A, Natt F;
 PI
 XX
 XX WPI; 1998-041763/04.
 XX
 XX Separation of electrically charged target molecules - by capillary
 PT affinity gel electrophoresis using polymer-gel to which receptors for
 PT target molecules are bound.
 PT
 XX Example A1; Page 22; 41pp; English.
 PS
 XX
 XX This sequence represents an oligonucleotide receptor molecule covalently

CC bound to a polyacrylamide gel via a linking group. The invention relates
 CC to selective separation of electrically charged target molecules in an
 CC analytical mixture. It comprises capillary affinity gel electrophoresis
 CC using a capillary tube which is at least partly filled with a polymer
 CC gel. Receptors for target molecules are covalently bound to the polymer.
 CC An electric field of at least 50 volts/cm is applied. The capillary tube
 CC is charged with the analytical mixture. In a first separation stage, the
 CC target molecules in the mixture are bound to the receptors and the
 CC remaining components are eluted, optionally whilst splitting open. In a
 CC second stage, the elution conditions are changed, optionally in stages,
 CC so that the affinity of the target molecules for the receptor is
 CC eliminated and the target molecules are eluted and detected, optionally
 CC whilst splitting open. The process is useful for selective separation
 CC and/or determination of charged organic compounds, such as
 CC oligonucleotides, peptides or carbohydrates. It may be used, e.g. for
 CC isolation of specific proteins and DNA molecules, purification of
 CC antibodies, analysis of antisense compounds or screening for enzyme
 CC inhibitors. The process achieves higher resolution and selectivity than
 CC prior art processes, especially in the case of complex biological
 CC analytical mixtures. It has high sensitivity, even with small amounts of
 CC samples. The derivatised polymers may be synthesised specifically using
 CC standard methods
 XX
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
 |||||
 DB 15 AAAAAAAAAAAAAA 1

RESULT 343
 AAT86605/c
 ID AAT86605 standard; DNA; 15 BP.
 XX
 AC AAT86605;
 XX
 DT 04-JUN-1998 (first entry)
 XX
 DE Oligonucleotide separated by capillary affinity gel electrophoresis.
 XX
 KW Capillary affinity gel electrophoresis; separation; polymer-gel;
 KW polyacrylamide; ss.
 XX
 OS Synthetic.
 XX
 PN W09745721-A1.
 XX
 PD 04-DEC-1997.
 XX
 PF 23-MAY-1997; 97MO-EP002647.
 XX
 PR 24-MAY-1996; 96CH-00001320.
 XX
 PA (NOVS) NOVARTIS AG.
 XX
 PI Muscate A, Paulus A, Natt F;
 XX
 DR WPI; 1998-041763/04.
 XX

PT Separation of electrically charged target molecules - by capillary
 PT affinity gel electrophoresis using polymer-gel to which receptors for
 PT target molecules are bound.
 XX
 PS Example D3; Page 25; 41pp; English.
 XX
 CC A mixture of oligonucleotides (AAT86604-7) were separated by a new
 CC process using capillary affinity gel electrophoresis. The invention
 CC relates to selective separation of electrically charged target molecules
 CC in an analytical mixture. It comprises capillary affinity gel

CC electrophoresis using a capillary tube which is at least partly filled
 CC with a polymer gel. Receptors for target molecules are covalently bound
 CC to the polymer. An electric field of at least 50 volts/cm is applied. The
 CC capillary tube is charged with the analytical mixture. In a first
 CC separation stage, the target molecules in the mixture are bound to the
 CC receptors and the remaining components are eluted, optionally whilst
 CC splitting open. In a second stage, the elution conditions are changed,
 CC optionally in stages, so that the affinity of the target molecules for
 CC the receptor is eliminated and the target molecules are eluted and
 CC detected, optionally whilst splitting open. The process is useful for
 CC selective separation and/or determination of charged organic compounds,
 CC such as oligonucleotides, peptides or carbohydrates. It may be used, e.g.
 CC for isolation of specific proteins and DNA molecules, purification of
 CC antibodies, analysis of antisense compounds or screening for enzyme
 CC inhibitors. The process achieves higher resolution and selectivity than
 CC prior art processes, especially in the case of complex biological
 CC analytical mixtures. It has high sensitivity, even with small amounts of
 CC samples. The derivatised polymers may be synthesised specifically using
 CC standard methods
 XX

SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
 |||||
 DB 15 AAAAAAAAAAAAAA 1

RESULT 344
 AAX31736
 ID AAX31736 standard; DNA; 15 BP.
 XX
 AC AAX31736;
 XX
 DT 21-MAY-1999 (first entry)
 XX
 DE Transcript tag sequence increased in pancreatic and colorectal cancer.
 XX
 KW Tag sequence; colorectal cancer; pancreatic cancer; colon cancer;
 KW diagnosis; prognosis; treatment; ss.
 XX
 OS Homo sapiens.
 XX
 PN W09853319-A2.
 XX
 PD 26-NOV-1998.
 XX
 PF 20-MAY-1998; 98WO-US010277.
 XX
 PR 21-MAY-1997; 97US-0047352P.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI Vogelstein B, Kinzler KW;
 XX
 DR WPI; 1999-070161/06.
 XX

PT Use of isolated gene transcripts - useful for developing products for the
 PT diagnosis, prognosis and treatment of cancers, particularly colon and
 PT pancreatic cancer.
 XX

PS Disclosure; Page 73; 120pp; English.

XX AAX30947-31815 represent tag sequences of transcripts that are
 CC differentially expressed in colorectal cancer, in pancreatic cancer, or
 CC in both. The tag sequences can be used to identify genes by matching the
 CC tag to a gen data base member, or by using the tag sequences as probes to
 CC isolate unidentified genes from cDNA libraries. The tag sequences can
 CC also be used in a method for diagnosing colon or pancreatic cancer in a
 CC sample suspected of being neoplastic. The method comprises comparing the

```

CC level of at least one transcript in a first sample of a tissue to a
CC second sample, where the first sample is a colonic tissue suspected of
CC being neoplastic and the second sample is a normal human colonic tissue.
CC The transcript is identified by a tag selected from AAX30947-31815. The
CC methods of the invention can be used in the diagnosis, prognosis and
CC treatment of cancer
XX
SQ Sequence 15 BP; 10 A; 2 C; 1 G; 2 T; 0 U; 0 Other;

  Query Match          1.0%; Score 15; DB 1; Length 15;
  Best Local Similarity 100.0%; Pred. No. 1.7e+02;
  Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY . 1475 CATGCTAAAAAAA 1489
   |||||
Dd 1 CATGCTAAAAAAA 15

RESULT 345
AAX31131
XX ID AAX31131 standard; DNA; 15 BP.
XX AC AAX31131;
XX
DT 21-MAY-1999 (first entry)
XX
XX Tag sequence of a transcript increased in colorectal cancer.
XX
XX Tag sequence; colorectal cancer; pancreatic cancer; colon cancer;
XX diagnosis; prognosis; treatment; ss.
XX
XX Homo sapiens.
XX OS
XX WO9853319-A2.
XX PN
XX
XX 26-NOV-1998.
XX PD
XX
XX 20-MAY-1998; 98WO-US010277.
XX PF
XX
XX 21-MAY-1997; 97US-0047352P.
XX PR
XX
XX (UJJO ) UNIV JOHNS HOPKINS.
XX PA
XX
XX Vogelstein B, Kinzler KW;
XX PI
XX
XX WPI; 1999-070161/06.
XX DR
XX
XX Use of isolated gene transcripts - useful for developing products for the
XX diagnosis, prognosis and treatment of cancers, particularly colon and
XX pancreatic cancer.
XX
XX Claim 2; Page 32; 120pp; English.
XX
XX AAX30947-31815 represent tag sequences of transcripts that are
XX differentially expressed in colorectal cancer, in pancreatic cancer, or
XX in both. The tag sequences can be used to identify genes by matching the
XX tag to a gen data base member, or by using the tag sequences as probes to
XX isolate unidentified genes from cDNA libraries. The tag sequences can
XX also be used in a method for diagnosing colon or pancreatic cancer in a
XX sample suspected of being neoplastic. The method comprises comparing the
XX level of at least one transcript in a first sample of a tissue to a
XX second sample, where the first sample is a colonic tissue suspected of
XX being neoplastic and the second sample is a normal human colonic tissue.
XX The transcript is identified by a tag selected from AAX30947-31815. The
XX methods of the invention can be used in the diagnosis, prognosis and
XX treatment of cancer
XX
SQ Sequence 15 BP; 10 A; 2 C; 1 G; 2 T; 0 U; 0 Other;

  Query Match          1.0%; Score 15; DB 1; Length 15;
  Best Local Similarity 100.0%; Pred. No. 1.7e+02;
  Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```
DE N3-P5 phosphoramidate oligonucleotide #3.
XX
KW Oligonucleotide; phosphoramidate; phosphoramidite; nucleoside; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_difference 1..15
FT /*tag= a
FT /note= "contains internucleotide N3-P5 phosphoramidate
FT internucleotide linkages"
XX
PN US859233-A.
XX
XX 12-JAN-1999.
XX
XX 20-DEC-1996; 96US-00771789.
XX
XX 21-FEB-1996; 96US-00603566.
XX 14-JUN-1996; 96US-00663918.
XX (LYNX-) LYNX THERAPEUTICS INC.
XX
XX Gryaznov SM, Nelson JS, McCurdy SN, Hirschbein BL, Schultz RG;
XX Fearon KL;
XX WPI; 1999-120007/10.
XX
XX 20-DEC-1996; 96US-00771789.
XX
XX 21-FEB-1996; 96US-00603566.
XX 14-JUN-1996; 96US-00663918.
XX (LYNX-) LYNX THERAPEUTICS INC.
XX
XX Gryaznov SM, Nelson JS, McCurdy SN, Hirschbein BL, Schultz RG;
XX Fearon KL;
XX WPI; 1999-120007/10.
XX
XX New 3'-protected-amino-nucleoside-5'-phosphoramidite monomers - used in
XX the synthesis of oligo-nucleotide(s).
XX
XX Example 10; Col 33; 34pp; English.
XX
XX This sequence represents an example of an oligonucleotide containing
XX novel 3'-amino-5'-phosphoramidite nucleoside of the invention. The
XX sequence is generated synthetically by using an amine-exchange reaction
XX of phosphoramidites in which a deprotected 3'-amino group of an
XX oligonucleotide chain is exchanged for the amino portion of a 5'-
XX phosphoramidite with a protected 3' amino group. The resulting
XX phosphoramidite internucleotide linkage is oxidised to form a stable
XX protected phosphoramidate linkage
XX
XX Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
XX
XX Example 10; Col 33; 34pp; English.
XX
XX This sequence represents an example of an oligonucleotide containing
XX novel 3'-amino-5'-phosphoramidite nucleoside of the invention. The
XX sequence is generated synthetically by using an amine-exchange reaction
XX of phosphoramidites in which a deprotected 3'-amino group of an
XX oligonucleotide chain is exchanged for the amino portion of a 5'-
XX phosphoramidite with a protected 3' amino group. The resulting
XX phosphoramidite internucleotide linkage is oxidised to form a stable
XX protected phosphoramidate linkage
XX
XX Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. NO. 1.7e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1481 AAAAAAAAAAAAAA 1495
XX DB 15 AAAAAAAAAAAAAA 1
XX
XX RESULT 348
XX AAX00788
XX ID AAX00788 standard; DNA; 15 BP.
XX
XX AC AAX00788;
XX
XX DT 13-APR-1999 (first entry)
XX
XX DE N3-P5 phosphoramidate oligonucleotide #4.
XX
XX KW Oligonucleotide; phosphoramidate; phosphoramidite; nucleoside; ss.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX FT misc_difference 1..15
XX FT /*tag= a
XX FT /note= "contains internucleotide N3-P5 phosphoramidate
XX internucleotide linkages"
XX
```

```
PN US859233-A.
XX
XX 12-JAN-1999.
XX
XX 20-DEC-1996; 96US-00771789.
XX
XX 21-FEB-1996; 96US-00603566.
XX 14-JUN-1996; 96US-00663918.
XX (LYNX-) LYNX THERAPEUTICS INC.
XX
XX Gryaznov SM, Nelson JS, McCurdy SN, Hirschbein BL, Schultz RG;
XX Fearon KL;
XX WPI; 1999-120007/10.
XX
XX New 3'-protected-amino-nucleoside-5'-phosphoramidite monomers - used in
XX the synthesis of oligo-nucleotide(s).
XX
XX Example 10; Col 33; 34pp; English.
XX
XX This sequence represents an example of an oligonucleotide containing
XX novel 3'-amino-5'-phosphoramidite nucleoside of the invention. The
XX sequence is generated synthetically by using an amine-exchange reaction
XX of phosphoramidites in which a deprotected 3'-amino group of an
XX oligonucleotide chain is exchanged for the amino portion of a 5'-
XX phosphoramidite with a protected 3' amino group. The resulting
XX phosphoramidite internucleotide linkage is oxidised to form a stable
XX protected phosphoramidate linkage
XX
XX Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. NO. 1.7e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1481 AAAAAAAAAAAAAA 1495
XX DB 1 AAAAAAAAAAAAAA 15
XX
XX RESULT 349
XX AAZ61854/c
XX ID AAZ61854 standard; RNA; 15 BP.
XX
XX AC AAZ61854;
XX
XX DT 28-MAR-2000 (first entry)
XX
XX DE HCV 3' non core region substrate for Hammerhead ribozyme HCV.3-118.
XX
XX KW Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;
XX cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;
XX autoimmune disease; ss.
XX
XX OS Hepatitis C virus.
XX
XX PN WO955847-A2.
XX
XX 04-NOV-1999.
XX
XX 26-APR-1999; 99WO-US009027.
XX
XX 27-APR-1998; 98US-0083217P.
XX 18-SEP-1998; 98US-0100842P.
XX 25-FEB-1999; 99US-00257608.
XX 23-MAR-1999; 99US-00274553.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Blatt L, Mcswiggen JA, Roberts E, Favco PA, Macejak D;
XX WPI; 2000-062023/05.
XX
```

XX Novel ribozymes for the treatment of diseases and conditions related to
PT hepatitis C infection.
XX
XX Claim 1; Page 49; 123pp; English.
XX
XX The present sequence represents the preferred target sequence of an
CC enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves
CC the Hepatitis C virus (HCV) RNA sequence in the 3' non-core region. The
CC HCV sequence was screened for optimal ribozyme target sites using a
CC computer folding algorithm and regions of the mRNA which did not form
CC secondary folding structures and contained potential ribozyme cleavage
CC sites were identified. Ribozymes were synthesised to target these sites
CC and their activities optimised by either varying the length of the
CC binding arms or by modification to prevent degradation by nucleases. The
CC ribozymes of the invention inhibit gene expression and/or viral
CC replication, and are used to treat diseases associated with Hepatitis C
CC virus (HCV) infection, e.g. cirrhosis, liver failure and hepatocellular
CC carcinoma. The ribozymes may be used in combination with interferon to
CC treat HCV infection, other infectious diseases, autoimmune diseases, and
CC cancer
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1495
|||||
Db 15 AAAAAAAAAAAAAA 1

RESULT 350
AAZ64910/C
ID AAZ64910 standard; RNA; 15 BP.
XX
AC AAZ64910;
XX
DT 28-MAR-2000 (first entry)
XX
DE Substrate for HH ribozyme HCV.3-118 which cleaves HCV at nt. 9418.
XX
KW Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;
KW cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;
KW autoimmune disease; ss.
XX
XX Hepatitis C virus.
XX
XX WO9955847-A2.
XX
XX 04-NOV-1999.
XX
XX 26-APR-1999; 99WO-US009027.
XX
XX 27-APR-1998; 98US-0083217P.
XX 18-SEP-1998; 98US-0100842P.
XX 25-FEB-1999; 99US-00257608.
XX 23-MAR-1999; 99US-00274553.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Blatt L, Mcswiggen JA, Roberts E, Pavco PA, Macejak D;
XX
XX WPI; 2000-062023/05.
XX
XX Novel ribozymes for the treatment of diseases and conditions related to
PT hepatitis C infection.
XX
XX Claim 1; Page 102; 123pp; English.
XX
XX The present sequence represents the preferred target sequence of an
CC enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves

CC the Hepatitis C virus (HCV) RNA sequence at the base position given in
CC the descriptor line. The HCV sequence was screened for optimal ribozyme
CC target sites using a computer folding algorithm and regions of the mRNA
CC which did not form secondary folding structures and contained potential
CC ribozyme cleavage sites were identified. Ribozymes were synthesised to
CC target these sites and their activities optimised by either varying the
CC length of the binding arms or by modification to prevent degradation by
CC nucleases. The ribozymes of the invention inhibit gene expression and/or
CC viral replication, and are used to treat diseases associated with
CC Hepatitis C virus (HCV) infection, e.g. cirrhosis, liver failure and
CC hepatocellular carcinoma. The ribozymes may be used in combination with
CC interferon to treat HCV infection, other infectious diseases, autoimmune
CC diseases, and cancer
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1495
|||||
Db 15 AAAAAAAAAAAAAA 1

RESULT 351
AAA46502/C
ID AAA46502 standard; cDNA; 15 BP.
XX
AC AAA46502;
XX
DT 04-SEP-2000 (first entry)
XX
DE PCR primer used to amplify DNA encoding an endo-beta-mannanase.
XX
KW Hydrolysis; polysaccharide; mannan; coffee; endo-beta-mannanase;
KW PCR primer; ss.
XX
XX Coffea arabica.
XX
XX WO200028046-A1.
XX
XX 18-MAY-2000.
XX
XX 28-OCT-1999; 99WO-EP008314.
XX
XX 11-NOV-1998; 98EP-00203742.
XX
XX (NEST) SOC PROD NESTLE SA.
XX
XX Marraccini P, Rogers J;
XX
XX WPI; 2000-399535/34.
XX
XX New DNA encoding endo-beta-mannanase from coffee, used e.g. in
PT pharmaceutical, cosmetic or food compositions to hydrolyze polymannans.
XX
XX Disclosure; Page 32; 41pp; French.
XX
XX PCR primers AAA46501-02 were used to amplify DNA encoding an endo-beta-
CC mannanase enzyme, which is involved in the hydrolysis of polysaccharides
CC that consist of molecules of mannan, either simple or branched, linked
CC together by beta(1-4) bonds. The mannanase polynucleotide sequence is
CC used for in vivo modification of the coffee endo-beta-mannanase gene. It
CC is also used to produce transgenic plant cells (especially coffee cells)
CC which have modified properties of mannan polysaccharide, and thus altered
CC flavour or structure. The enzyme is used for modification, degradation or
CC synthesis of mannan polysaccharides in vitro, particularly to treat
CC coffee beans to increase the percentage of dry matter extraction, and
CC thus reduce the quantity of sediment
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;

```
Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
DB 15 AAAAAAAAAAAAAA 1

RESULT 352
AAA75048/c
ID AAA75048 standard; DNA; 15 BP.
XX
AC AAA75048;
XX
DT 15-JAN-2001 (first entry)
XX
DE Primer used to reverse transcribe human RNA.
XX
KW Human; heparanase; gene therapy; tumour; inflammation; autoimmunity;
KW heparin-binding growth factor; cytokine; neurodegenerative plaque;
KW wound healing; infection; burn; angiogenesis; restenosis;
KW atherosclerosis; inflammation; neurodegenerative disease;
KW Gerstmann-Straussler Syndrome; Creutzfeldt-Jakob disease; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200052178-A1.
XX
PD 08-SEP-2000.
XX
PF 14-FEB-2000; 2000WO-US003542.
XX
PR 01-MAR-1999; 99US-00258892.
XX
PA (INSI-) INSIGHT STRATEGY & MARKETING LTD.
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
PA (FRIE/) FRIEDMAN M M.
XX
PI Pecker I, Vlodavsky I, Feinstein E;
XX
WPI; 2000-579289/54.
XX
PT New polynucleotides encoding a polypeptide having heparanase activity,
PT useful in wound healing and in gene therapy, particularly in treating
PT tumor, inflammation, autoimmunity, neurodegenerative diseases.
XX
PS Disclosure; Page 44; 152pp; English.
XX
CC The present primer was used to reverse transcribe human RNA, from which a
CC cDNA sequence encoding a protein with heparanase catalytic activity was
CC amplified. The heparanase (hpa) polynucleotide is useful in gene therapy,
CC particularly in treating tumour, inflammation or autoimmunity.
CC Particularly, the polynucleotide is useful in modulating the
CC bioavailability of heparin-binding growth factors, cellular responses to
CC heparin-binding growth factors (e.g. bFGF) and cytokines (e.g.
CC interleukin (IL)-8), cell interaction with plasma lipoproteins, cellular
CC susceptibility to certain viral and some bacterial and protozoa
CC infections, or disintegration of neurodegenerative plaques. The
CC polynucleotide is also useful in wound healing (e.g. thermal, chemical or
CC radiation burns), and in the treatment of angiogenesis, restenosis,
CC atherosclerosis, inflammation, neurodegenerative diseases (Gerstmann-
CC Straussler Syndrome or Creutzfeldt-Jakob disease), and some viral,
CC bacterial or protozoa infections
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match      1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
DB 15 AAAAAAAAAAAAAA 1

RESULT 353
AAA07792/c
ID AAA07792 standard; DNA; 15 BP.
XX
AC AAA07792;
XX
DT 23-JUN-2000 (first entry)
XX
DE Nucleic acid sequence of ODN-e.
XX
KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW viral infection; inflammatory response; cellular proliferation;
KW psoriasis; duplex; ss.
XX
OS Synthetic.
XX
PN WO200011013-A1.
XX
PD 02-MAR-2000.
XX
PF 20-AUG-1999; 99WO-US019029.
XX
PR 22-AUG-1998; 98US-0097712P.
XX
PA (UYNE-) UNIV NEBRASKA.
XX
PI Gold B;
XX
WPI; 2000-246530/21.
XX
PT Modified nucleomonomers, used in physiologically stable, non-toxic
PT oligomers used to inhibit expression of nucleic acids and in gene
PT regulation, antisense technology and diagnostics.
XX
PS Disclosure; Page 20; 42pp; English.
XX
CC The invention provides modified nucleomonomers of specified formula and
CC their pharmaceutically acceptable salts. The nucleomonomers are used as
CC monomers in oligomers, which are used in pharmaceutical compositions to
CC inhibit expression of nucleic acid molecules including DNA and RNA in
CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
CC infected cells. They are used in oligomers for gene regulation, antisense
CC technology, diagnostic applications to detect target sequences in
CC biological samples such as those containing pathogenic bacteria, fungi
CC and viruses, oncogenes, growth hormones and enzymes, to target genes or
CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
CC molecules, receptor molecules, cytokines, oncogenes, growth factors and
CC interleukins associated with pathological conditions such as inflammatory
CC conditions, cardiovascular disorders, immune reactions, cancer, viral
CC infections and bacterial infections (see AAA07786 for details of other
CC uses for which the oligomers are suitable for). Oligomers comprising the
CC nucleomonomers exhibit increased duplex DNA stability when hybridizing to
CC target nucleic acid sequences, are physiologically stable, non-toxic and
CC able to penetrate into cells while maintaining stringent base pair
CC fidelity for target DNA sequences. The oligomers demonstrate significant
CC single- or double-stranded target nucleic acid binding activity to form
CC duplexes, triplexes or other forms of stable association. Sequences
CC AAA07788-803 represent oligonucleotides forming a third strand along with
CC the duplex sequences
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other;
```



```

DE XX Nucleic acid sequence of ODN-h.
KW XX Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW XX viral infection; inflammatory response; cellular proliferation;
KW XX psoriasis; duplex; ss.
OS XX Synthetic.
XX XX WO200011013-A1.
XX XX 02-MAR-2000.
XX XX 20-AUG-1999; 99WO-US019029.
XX XX 22-AUG-1998; 98US-0097712P.
XX XX (UYNE-) UNIV NEBRASKA.
XX XX Gold B;
XX XX WPI; 2000-246530/21.
XX XX Modified nucleomonomers, used in physiologically stable, non-toxic
XX XX oligomers used to inhibit expression of nucleic acids and in gene
XX XX regulation, antisense technology and diagnostics.
XX XX Disclosure; Page 20; 42pp; English.
XX XX The invention provides modified nucleomonomers of specified formula and
XX XX their pharmaceutically acceptable salts. The nucleomonomers are used as
XX XX monomers in oligomers, which are used in pharmaceutical compositions to
XX XX inhibit expression of nucleic acid molecules including DNA and RNA in
XX XX cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
XX XX infected cells. They are used in oligomers for gene regulation, antisense
XX XX technology, diagnostic applications to detect target sequences in
XX XX biological samples such as those containing pathogenic bacteria, fungi
XX XX and viruses, oncogenes, growth hormones and enzymes, to target genes or
XX XX encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
XX XX molecules, receptor molecules, cytokines, oncogenes, growth factors and
XX XX interleukins associated with pathological conditions such as inflammatory
XX XX conditions, cardiovascular disorders, immune reactions, cancer, viral
XX XX infections and bacterial infections (see AAA07786 for details of other
XX XX uses for which the oligomers are suitable for). Oligomers comprising the
XX XX nucleomonomers exhibit increased duplex DNA stability when hybridizing to
XX XX target nucleic acid sequences, are physiologically stable, non-toxic and
XX XX able to penetrate into cells while maintaining stringent base pair
XX XX fidelity for target DNA sequences. The oligomers demonstrate significant
XX XX single- or double-stranded target nucleic acid binding activity to form
XX XX duplexes, triplexes or other forms of stable association. Sequences
XX XX AAA07788-803 represent oligonucleotides forming a third strand along with
XX XX the duplex sequences
XX XX Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
DB 15 AAAAAAAAAAAAAA 1

RESULT 359
AAA07797/c
ID AAA07797 standard; DNA; 15 BP.
XX AC AAA07797;
XX XX 23-JUN-2000 (first entry)
XX XX Nucleic acid sequence of ODN-j.
KW XX Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW XX viral infection; inflammatory response; cellular proliferation;

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```

KW XX Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW XX viral infection; inflammatory response; cellular proliferation;
KW XX psoriasis; duplex; ss.
OS XX Synthetic.
XX XX WO200011013-A1.
XX XX 02-MAR-2000.
XX XX 20-AUG-1999; 99WO-US019029.
XX XX 22-AUG-1998; 98US-0097712P.
XX XX (UYNE-) UNIV NEBRASKA.
XX XX Gold B;
XX XX WPI; 2000-246530/21.
XX XX Modified nucleomonomers, used in physiologically stable, non-toxic
XX XX oligomers used to inhibit expression of nucleic acids and in gene
XX XX regulation, antisense technology and diagnostics.
XX XX Disclosure; Page 20; 42pp; English.
XX XX The invention provides modified nucleomonomers of specified formula and
XX XX their pharmaceutically acceptable salts. The nucleomonomers are used as
XX XX monomers in oligomers, which are used in pharmaceutical compositions to
XX XX inhibit expression of nucleic acid molecules including DNA and RNA in
XX XX cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
XX XX infected cells. They are used in oligomers for gene regulation, antisense
XX XX technology, diagnostic applications to detect target sequences in
XX XX biological samples such as those containing pathogenic bacteria, fungi
XX XX and viruses, oncogenes, growth hormones and enzymes, to target genes or
XX XX encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
XX XX molecules, receptor molecules, cytokines, oncogenes, growth factors and
XX XX interleukins associated with pathological conditions such as inflammatory
XX XX conditions, cardiovascular disorders, immune reactions, cancer, viral
XX XX infections and bacterial infections (see AAA07786 for details of other
XX XX uses for which the oligomers are suitable for). Oligomers comprising the
XX XX nucleomonomers exhibit increased duplex DNA stability when hybridizing to
XX XX target nucleic acid sequences, are physiologically stable, non-toxic and
XX XX able to penetrate into cells while maintaining stringent base pair
XX XX fidelity for target DNA sequences. The oligomers demonstrate significant
XX XX single- or double-stranded target nucleic acid binding activity to form
XX XX duplexes, triplexes or other forms of stable association. Sequences
XX XX AAA07788-803 represent oligonucleotides forming a third strand along with
XX XX the duplex sequences
XX XX Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
DB 15 AAAAAAAAAAAAAA 1

RESULT 360
AAA07799/c
ID AAA07799 standard; DNA; 15 BP.
XX AC AAA07799;
XX XX 23-JUN-2000 (first entry)
XX XX Nucleic acid sequence of ODN-l.
KW XX Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW XX viral infection; inflammatory response; cellular proliferation;

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KW psoriasis; duplex; ss.
XX
XX Synthetic.
XX WO200011013-A1.
XX
XX PD 02-MAR-2000.
XX
XX PF 20-AUG-1999; 99WO-US019029.
XX
XX PR 22-AUG-1998; 98US-0097712P.
XX
XX PA (UYNE-) UNIV NEBRASKA.
XX
XX PI Gold B;
XX
XX WPI; 2000-246530/21.
XX
XX Modified nucleomonomers, used in physiologically stable, non-toxic
XX oligomers used to inhibit expression of nucleic acids and in gene
XX regulation, antisense technology and diagnostics.
XX
XX PS Disclosure; Page 20; 42pp; English.
XX
XX CC The invention provides modified nucleomonomers of specified formula and
XX their pharmaceutically acceptable salts. The nucleomonomers are used as
XX monomers in oligomers, which are used in pharmaceutical compositions to
XX inhibit expression of nucleic acid molecules including DNA and RNA in
XX cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
XX infected cells. They are used in oligomers for gene regulation, antisense
XX technology, diagnostic applications to detect target sequences in
XX biological samples such as those containing pathogenic bacteria, fungi
XX and viruses, oncogenes, growth hormones and enzymes, to target genes or
XX encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
XX molecules, receptor molecules, cytokines, oncogenes, growth factors and
XX interleukins associated with pathological conditions such as inflammatory
XX conditions, cardiovascular disorders, immune reactions, cancer, viral
XX infections and bacterial infections (see AAA07786 for details of other
XX uses for which the oligomers are suitable for). Oligomers comprising the
XX nucleomonomers exhibit increased duplex DNA stability when hybridizing to
XX target nucleic acid sequences, are physiologically stable, non-toxic and
XX able to penetrate into cells while maintaining stringent base pair
XX fidelity for target DNA sequences. The oligomers demonstrate significant
XX single- or double-stranded target nucleic acid binding activity to form
XX duplexes, triplexes or other forms of stable association. Sequences
XX AAA07788-803 represent oligonucleotides forming a third strand along with
XX the duplex sequences
XX
XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 1 U; 0 Other;
XX
XX Query Match 1.0%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 1.7e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1481 AAAAAAAAAAAAAA 1495
XX |||||
XX Db 15 AAAAAAAAAAAAAA 1
XX
XX RESULT 361
XX AAA07802/C
XX ID AAA07802 standard; DNA; 15 BP.
XX
XX AC AAA07802;
XX
XX DT 23-JUN-2000 (first entry)
XX
XX DE Nucleic acid sequence of ODN-0.
XX
XX Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
XX viral infection; inflammatory response; cellular proliferation;
XX psoriasis; duplex; ss.
XX
XX OS Synthetic.
XX
XX WO200011013-A1.
XX
XX PD 02-MAR-2000.
XX
XX PF 20-AUG-1999; 99WO-US019029.
XX
XX PR 22-AUG-1998; 98US-0097712P.
XX
XX PA (UYNE-) UNIV NEBRASKA.
XX
XX PI Gold B;
XX
XX WPI; 2000-246530/21.
XX
XX Modified nucleomonomers, used in physiologically stable, non-toxic
XX oligomers used to inhibit expression of nucleic acids and in gene
XX regulation, antisense technology and diagnostics.
XX
XX PS Disclosure; Page 20; 42pp; English.
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XX cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
XX infected cells. They are used in oligomers for gene regulation, antisense
XX technology, diagnostic applications to detect target sequences in
XX biological samples such as those containing pathogenic bacteria, fungi
XX and viruses, oncogenes, growth hormones and enzymes, to target genes or
XX encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
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XX interleukins associated with pathological conditions such as inflammatory
XX conditions, cardiovascular disorders, immune reactions, cancer, viral
XX infections and bacterial infections (see AAA07786 for details of other
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XX nucleomonomers exhibit increased duplex DNA stability when hybridizing to
XX target nucleic acid sequences, are physiologically stable, non-toxic and
XX able to penetrate into cells while maintaining stringent base pair
XX fidelity for target DNA sequences. The oligomers demonstrate significant
XX single- or double-stranded target nucleic acid binding activity to form
XX duplexes, triplexes or other forms of stable association. Sequences
XX AAA07788-803 represent oligonucleotides forming a third strand along with
XX the duplex sequences
XX
XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other;
XX
XX Query Match 1.0%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 1.7e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1481 AAAAAAAAAAAAAA 1495
XX |||||
XX Db 15 AAAAAAAAAAAAAA 1
XX
XX RESULT 362
XX AAA07825/C
XX ID AAA07825 standard; DNA; 15 BP.
XX
XX AC AAA07825;
XX
XX DT 23-JUN-2000 (first entry)
XX
XX DE Nucleic acid sequence of a strand of triplex oligomer 14.
XX
XX Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
XX viral infection; inflammatory response; cellular proliferation;
XX psoriasis; duplex; triplex; ss.
XX
XX OS Synthetic.
XX

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PN WO200011013-A1.
 XX
 PD 02-MAR-2000.
 XX
 XX 20-AUG-1999; 99WO-US019029.
 XX
 XX 22-AUG-1998; 98US-0097712P.
 XX
 XX (UYNE-) UNIV NEBRASKA.
 XX
 XX Gold B;
 XX
 XX WPI; 2000-246530/21.
 XX
 XX Modified nucleomoners, used in physiologically stable, non-toxic
 PT oligomers used to inhibit expression of nucleic acids and in gene
 PT regulation, antisense technology and diagnostics.
 XX
 XX Disclosure; Page 30; 42pp; English.
 XX
 CC The invention provides modified nucleomoners of specified formula and
 CC their pharmaceutically acceptable salts. The nucleomoners are used as
 CC monomers in oligomers, which are used in pharmaceutical compositions to
 CC inhibit expression of nucleic acid molecules including DNA and RNA in
 CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
 CC infected cells. They are used in oligomers for gene regulation, antisense
 CC technology, diagnostic applications to detect target sequences in
 CC biological samples such as those containing pathogenic bacteria, fungi
 CC and viruses, oncogenes, growth hormones and enzymes, to target genes or
 CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
 CC molecules, receptor molecules, cytokines, oncogenes, growth factors and
 CC interleukins associated with pathological conditions such as inflammatory
 CC infections and bacterial infections (see AAA07786 for details of other
 CC uses for which the oligomers are suitable for). Oligomers comprising the
 CC nucleomoners exhibit increased duplex DNA stability when hybridizing to
 CC target nucleic acid sequences, are physiologically stable, non-toxic and
 CC able to penetrate into cells while maintaining stringent base pair
 CC fidelity for target DNA sequences. The oligomers demonstrate significant
 CC single- or double-stranded target nucleic acid binding activity to form
 CC duplexes, triplexes or other forms of stable association. Sequences
 CC AAA07820-834 represent sequences forming triplex oligomers
 XX
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 1 U; 0 Other;
 Query Match 1.0%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1481 AAAAAAAAAAAAAA 1495
 DB 15 AAAAAAAAAAAAAA 1

RESULT 363
 AAA07831/c
 ID AAA07831 standard; DNA; 15 BP.
 XX
 AC AAA07831;
 XX
 XX 23-JUN-2000 (first entry)
 XX
 XX Nucleic acid sequence of a strand of triplex oligomer 16.
 DE
 DE Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
 XX viral infection; inflammatory response; cellular proliferation;
 XX psoriasis; duplex; triplex; ss.
 XX
 XX Synthetic.
 XX
 XX WO200011013-A1.
 PN
 XX 02-MAR-2000.
 XX

XX 20-AUG-1999; 99WO-US019029.
 XX
 XX 22-AUG-1998; 98US-0097712P.
 XX
 XX (UYNE-) UNIV NEBRASKA.
 XX
 XX Gold B;
 XX
 XX WPI; 2000-246530/21.
 XX
 XX Modified nucleomoners, used in physiologically stable, non-toxic
 PT oligomers used to inhibit expression of nucleic acids and in gene
 PT regulation, antisense technology and diagnostics.
 XX
 XX Disclosure; Page 30; 42pp; English.
 XX
 CC The invention provides modified nucleomoners of specified formula and
 CC their pharmaceutically acceptable salts. The nucleomoners are used as
 CC monomers in oligomers, which are used in pharmaceutical compositions to
 CC inhibit expression of nucleic acid molecules including DNA and RNA in
 CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
 CC infected cells. They are used in oligomers for gene regulation, antisense
 CC technology, diagnostic applications to detect target sequences in
 CC biological samples such as those containing pathogenic bacteria, fungi
 CC and viruses, oncogenes, growth hormones and enzymes, to target genes or
 CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
 CC molecules, receptor molecules, cytokines, oncogenes, growth factors and
 CC interleukins associated with pathological conditions such as inflammatory
 CC conditions, cardiovascular disorders, immune reactions, cancer, viral
 CC infections and bacterial infections (see AAA07786 for details of other
 CC uses for which the oligomers are suitable for). Oligomers comprising the
 CC nucleomoners exhibit increased duplex DNA stability when hybridizing to
 CC target nucleic acid sequences, are physiologically stable, non-toxic and
 CC able to penetrate into cells while maintaining stringent base pair
 CC fidelity for target DNA sequences. The oligomers demonstrate significant
 CC single- or double-stranded target nucleic acid binding activity to form
 CC duplexes, triplexes or other forms of stable association. Sequences
 CC AAA07820-834 represent sequences forming triplex oligomers
 XX
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 1 U; 0 Other;
 Query Match 1.0%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1481 AAAAAAAAAAAAAA 1495
 DB 15 AAAAAAAAAAAAAA 1

RESULT 364
 AAA07803/c
 ID AAA07803 standard; DNA; 15 BP.
 XX
 AC AAA07803;
 XX
 XX 23-JUN-2000 (first entry)
 XX
 XX Nucleic acid sequence of ODN-p.
 DE
 DE Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
 XX viral infection; inflammatory response; cellular proliferation;
 XX psoriasis; duplex; ss.
 XX
 XX Synthetic.
 XX
 XX WO200011013-A1.
 PN
 XX 02-MAR-2000.
 XX
 XX 20-AUG-1999; 99WO-US019029.
 XX

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PR 22-AUG-1998; 98US-0097712P.
XX (UYNE-) UNIV NEBRASKA.
PA Gold B;
XX WPI; 2000-246530/21.
XX Modified nucleomoners, used in physiologically stable, non-toxic
XX oligomers used to inhibit expression of nucleic acids and in gene
XX regulation, antisense technology and diagnostics.
XX Disclosure; Page 20; 42pp; English.
XX The invention provides modified nucleomoners of specified formula and
XX their pharmaceutically acceptable salts. The nucleomoners are used as
XX monomers in oligomers, which are used in pharmaceutical compositions to
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XX cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
XX infected cells. They are used in oligomers for gene regulation, antisense
XX technology, diagnostic applications to detect target sequences in
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XX and viruses, oncogenes, growth hormones and enzymes, to target genes or
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XX target nucleic acid sequences, are physiologically stable, non-toxic and
XX able to penetrate into cells while maintaining stringent base pair
XX fidelity for target DNA sequences. The oligomers demonstrate significant
XX single- or double-stranded target nucleic acid binding activity to form
XX duplexes, triplexes or other forms of stable association. Sequences
XX AAA07788-803 represent oligonucleotides forming a third strand along with
XX the duplex sequences
XX Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;
XX Query Match 1.0%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 1.7e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1481 AAAAAAAAAAAAAA 1495
XX |||||
XX 15 AAAAAAAAAAAAAA 1
XX
XX RESULT 365
XX AAA07834/C
XX ID AAA07834 standard; DNA; 15 BP.
XX AC AAA07834;
XX DT 23-JUN-2000 (first entry)
XX DE Nucleic acid sequence of a strand of triplex oligomer 17.
XX Nucleomonmer; cancer; gene regulation; antisense technology; leukemia;
XX viral infection; inflammatory response; cellular proliferation;
XX psoriasis; duplex; triplex; ss.
XX Synthetic.
XX OS WO200011013-A1.
XX PN 02-MAR-2000.
XX PD 20-AUG-1999; 99WO-US019029.
XX PF 22-AUG-1998; 98US-0097712P.
XX PG (UYNE-) UNIV NEBRASKA.
XX PH Gold B;
XX PI

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PA (UYNE-) UNIV NEBRASKA.
XX Gold B;
XX WPI; 2000-246530/21.
XX Modified nucleomoners, used in physiologically stable, non-toxic
XX oligomers used to inhibit expression of nucleic acids and in gene
XX regulation, antisense technology and diagnostics.
XX Disclosure; Page 30; 42pp; English.
XX The invention provides modified nucleomoners of specified formula and
XX their pharmaceutically acceptable salts. The nucleomoners are used as
XX monomers in oligomers, which are used in pharmaceutical compositions to
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XX technology, diagnostic applications to detect target sequences in
XX biological samples such as those containing pathogenic bacteria, fungi
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XX interleukins associated with pathological conditions such as inflammatory
XX conditions, cardiovascular disorders, immune reactions, cancer, viral
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XX able to penetrate into cells while maintaining stringent base pair
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XX single- or double-stranded target nucleic acid binding activity to form
XX duplexes, triplexes or other forms of stable association. Sequences
XX AAA07788-803 represent oligonucleotides forming a third strand along with
XX the duplex sequences
XX Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;
XX Query Match 1.0%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 1.7e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1481 AAAAAAAAAAAAAA 1495
XX |||||
XX 15 AAAAAAAAAAAAAA 1
XX
XX RESULT 366
XX AAA07796/C
XX ID AAA07796 standard; DNA; 15 BP.
XX AC AAA07796;
XX DT 23-JUN-2000 (first entry)
XX DE Nucleic acid sequence of ODN-i.
XX Nucleomonmer; cancer; gene regulation; antisense technology; leukemia;
XX viral infection; inflammatory response; cellular proliferation;
XX psoriasis; duplex; ss.
XX Synthetic.
XX OS WO200011013-A1.
XX PN 02-MAR-2000.
XX PD 20-AUG-1999; 99WO-US019029.
XX PF 22-AUG-1998; 98US-0097712P.
XX PG (UYNE-) UNIV NEBRASKA.
XX PH Gold B;
XX PI

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XX WPI; 2000-246530/21.
XX Modified nucleomonomers, used in physiologically stable, non-toxic
XX oligomers used to inhibit expression of nucleic acids and in gene
XX regulation, antisense technology and diagnostics.
XX
XX Disclosure; Page 20; 42pp; English.
XX
XX The invention provides modified nucleomonomers of specified formula and
XX their pharmaceutically acceptable salts. The nucleomonomers are used as
XX monomers in oligomers, which are used in pharmaceutical compositions to
XX inhibit expression of nucleic acid molecules including DNA and RNA in
XX cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
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XX technology, diagnostic applications to detect target sequences in
XX biological samples such as those containing pathogenic bacteria, fungi
XX and viruses, oncogenes, growth hormones and enzymes, to target genes or
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XX target nucleic acid sequences, are physiologically stable, non-toxic and
XX able to penetrate into cells while maintaining stringent base pair
XX fidelity for target DNA sequences. The oligomers demonstrate significant
XX single- or double-stranded target nucleic acid binding activity to form
XX duplexes, triplexes or other forms of stable association. Sequences
XX AAA07788-803 represent oligonucleotides forming a third strand along with
XX the duplex sequences
XX
XX Sequence 15 BP; 0 A; 0 C; 0 G; 11 T; 4 U; 0 Other;
XX
XX Query Match 1.0%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 1.7e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1481 AAAAAAAAAAAAAA 1495
XX DB 15 AAAAAAAAAAAAAA 1
XX
XX RESULT 367
XX AAA07800/C
XX ID AAA07800 standard; DNA; 15 BP.
XX AC AAA07800;
XX XX
XX DT 23-JUN-2000 (first entry)
XX DE Nucleic acid sequence of ODN-m.
XX XX
XX KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
XX KW viral infection; inflammatory response; cellular proliferation;
XX KW psoriasis; duplex; ss.
XX XX
XX OS Synthetic.
XX XX
XX PN WO200011013-A1.
XX XX
XX PD 02-MAR-2000.
XX XX
XX PF 20-AUG-1999; 99WO-US019029.
XX XX
XX PR 22-AUG-1998; 98US-0097712P.
XX XX
XX PA (UYNE-) UNIV NEBRASKA.
XX XX
XX PI Gold B;
XX XX
XX DR WPI; 2000-246530/21.
XX PT Modified nucleomonomers, used in physiologically stable, non-toxic
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XX WPI; 2000-246530/21.
XX Modified nucleomonomers, used in physiologically stable, non-toxic
XX oligomers used to inhibit expression of nucleic acids and in gene
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XX able to penetrate into cells while maintaining stringent base pair
XX fidelity for target DNA sequences. The oligomers demonstrate significant
XX single- or double-stranded target nucleic acid binding activity to form
XX duplexes, triplexes or other forms of stable association. Sequences
XX AAA07788-803 represent oligonucleotides forming a third strand along with
XX the duplex sequences
XX
XX Sequence 15 BP; 0 A; 0 C; 0 G; 11 T; 4 U; 0 Other;
XX
XX Query Match 1.0%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 1.7e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1481 AAAAAAAAAAAAAA 1495
XX DB 15 AAAAAAAAAAAAAA 1
XX
XX RESULT 367
XX AAA07800/C
XX ID AAA07800 standard; DNA; 15 BP.
XX AC AAA07800;
XX XX
XX DT 23-JUN-2000 (first entry)
XX DE Nucleic acid sequence of ODN-m.
XX XX
XX KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
XX KW viral infection; inflammatory response; cellular proliferation;
XX KW psoriasis; duplex; ss.
XX XX
XX OS Synthetic.
XX XX
XX PN WO200011013-A1.
XX XX
XX PD 02-MAR-2000.
XX XX
XX PF 20-AUG-1999; 99WO-US019029.
XX XX
XX PR 22-AUG-1998; 98US-0097712P.
XX XX
XX PA (UYNE-) UNIV NEBRASKA.
XX XX
XX PI Gold B;
XX XX
XX DR WPI; 2000-246530/21.
XX PT Modified nucleomonomers, used in physiologically stable, non-toxic
```

```
PT oligomers used to inhibit expression of nucleic acids and in gene
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XX
PS Disclosure; Page 20; 42pp; English.
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CC technology, diagnostic applications to detect target sequences in
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CC and viruses, oncogenes, growth hormones and enzymes, to target genes or
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CC interleukins associated with pathological conditions such as inflammatory
CC conditions, cardiovascular disorders, immune reactions, cancer, viral
CC infections and bacterial infections (see AAA07786 for details of other
CC uses for which the oligomers are suitable for). Oligomers comprising the
CC nucleomonomers exhibit increased duplex DNA stability when hybridizing to
CC target nucleic acid sequences, are physiologically stable, non-toxic and
CC able to penetrate into cells while maintaining stringent base pair
CC fidelity for target DNA sequences. The oligomers demonstrate significant
CC single- or double-stranded target nucleic acid binding activity to form
CC duplexes, triplexes or other forms of stable association. Sequences
CC AAA07788-803 represent oligonucleotides forming a third strand along with
CC the duplex sequences
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;
Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1495
DB 15 AAAAAAAAAAAAAA 1
RESULT 369
AAA07798/c
ID AAA07798 standard; DNA; 15 BP.
XX
AC AAA07798;
XX
DT 23-JUN-2000 (first entry)
XX
DE Nucleic acid sequence of ODN-k.
XX
KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW viral infection; inflammatory response; cellular proliferation;
KW psoriasis; duplex; ss.
XX
OS Synthetic.
XX
PN WO200011013-A1.
XX
PD 02-MAR-2000.
XX
PF 20-AUG-1999; 99WO-US019029.
XX
PR 22-AUG-1998; 98US-0097712P.
XX
PA (UYNE-) UNIV NEBRASKA.
XX
PI Gold B;
XX
DR WPI; 2000-246530/21.
XX
PT Modified nucleomonomers, used in physiologically stable, non-toxic
PT oligomers used to inhibit expression of nucleic acids and in gene
PT regulation, antisense technology and diagnostics.
PS Disclosure; Page 20; 42pp; English.
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PS The invention provides modified nucleomonomers of specified formula and
PS their pharmaceutically acceptable salts. The nucleomonomers are used as
PS monomers in oligomers, which are used in pharmaceutical compositions to
PS inhibit expression of nucleic acid molecules including DNA and RNA in
PS cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
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PS technology, diagnostic applications to detect target sequences in
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PS molecules, receptor molecules, cytokines, oncogenes, growth factors and
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PS conditions, cardiovascular disorders, immune reactions, cancer, viral
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PS nucleomonomers exhibit increased duplex DNA stability when hybridizing to
PS target nucleic acid sequences, are physiologically stable, non-toxic and
PS able to penetrate into cells while maintaining stringent base pair
PS fidelity for target DNA sequences. The oligomers demonstrate significant
PS single- or double-stranded target nucleic acid binding activity to form
PS duplexes, triplexes or other forms of stable association. Sequences
PS AAA07788-803 represent oligonucleotides forming a third strand along with
PS the duplex sequences
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;
Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1495
DB 15 AAAAAAAAAAAAAA 1
RESULT 369
AAA07798/c
ID AAA07798 standard; DNA; 15 BP.
XX
AC AAA07798;
XX
DT 23-JUN-2000 (first entry)
XX
DE Nucleic acid sequence of ODN-a.
XX
KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW viral infection; inflammatory response; cellular proliferation;
KW psoriasis; duplex; ss.
XX
OS Synthetic.
XX
PN WO200011013-A1.
XX
PD 02-MAR-2000.
XX
PF 20-AUG-1999; 99WO-US019029.
XX
PR 22-AUG-1998; 98US-0097712P.
XX
PA (UYNE-) UNIV NEBRASKA.
XX
PI Gold B;
XX
DR WPI; 2000-246530/21.
XX
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PT oligomers used to inhibit expression of nucleic acids and in gene
PT regulation, antisense technology and diagnostics.
PS Disclosure; Page 20; 42pp; English.
```


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 CC infected cells. They are used in oligomers for gene regulation, antisense
 CC technology, diagnostic applications to detect target sequences in
 CC biological samples such as those containing pathogenic bacteria, fungi
 CC and viruses, oncogenes, growth hormones and enzymes, to target genes or
 CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
 CC molecules, receptor molecules, cytokines, oncogenes, growth factors and
 CC interleukins associated with pathological conditions such as inflammatory
 CC conditions, cardiovascular disorders, immune reactions, cancer, viral
 CC infections and bacterial infections (see AAA07786 for details of other
 CC uses for which the oligomers are suitable for). Oligomers comprising the
 CC nucleomoners exhibit increased duplex DNA stability when hybridizing to
 CC target nucleic acid sequences, are physiologically stable, non-toxic and
 CC able to penetrate into cells while maintaining stringent base pair
 CC fidelity for target DNA sequences. The oligomers demonstrate significant
 CC single- or double-stranded target nucleic acid binding activity to form
 CC duplexes, triplexes or other forms of stable association. Sequences
 CC AAA07788-803 represent oligonucleotides forming a third strand along with
 CC the duplex sequences

SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAA07791 standard; DNA; 15 BP.
 Db 15 AAAA07791 standard; DNA; 15 BP.

RESULT 371
 AAA07791/C
 ID AAA07791 standard; DNA; 15 BP.

XX AC AAA07791;
 XX DT 23-JUN-2000 (first entry)
 XX DE Nucleic acid sequence of ODN-d.
 XX KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
 XX KW viral infection; inflammatory response; cellular proliferation;
 XX KW psoriasis; duplex; ss.
 XX OS Synthetic.
 XX PN WO200011013-A1.
 XX PD 02-MAR-2000.
 XX PF 20-AUG-1999; 99WO-US019029.
 XX PR 22-AUG-1998; 98US-0097712P.
 XX PA (UYNE-) UNIV NEBRASKA.
 XX PI Gold B;
 XX DR WPI; 2000-246530/21.
 XX PT Modified nucleomoners, used in physiologically stable, non-toxic
 XX PT oligomers used to inhibit expression of nucleic acids and in gene
 XX PT regulation, antisense technology and diagnostics.
 XX PS Disclosure; Page 20; 42pp; English.
 XX CC The invention provides modified nucleomoners of specified formula and

CC their pharmaceutically acceptable salts. The nucleomoners are used as
 CC monomers in oligomers, which are used in pharmaceutical compositions to
 CC inhibit expression of nucleic acid molecules including DNA and RNA in
 CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
 CC infected cells. They are used in oligomers for gene regulation, antisense
 CC technology, diagnostic applications to detect target sequences in
 CC biological samples such as those containing pathogenic bacteria, fungi
 CC and viruses, oncogenes, growth hormones and enzymes, to target genes or
 CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
 CC molecules, receptor molecules, cytokines, oncogenes, growth factors and
 CC interleukins associated with pathological conditions such as inflammatory
 CC conditions, cardiovascular disorders, immune reactions, cancer, viral
 CC infections and bacterial infections (see AAA07786 for details of other
 CC uses for which the oligomers are suitable for). Oligomers comprising the
 CC nucleomoners exhibit increased duplex DNA stability when hybridizing to
 CC target nucleic acid sequences, are physiologically stable, non-toxic and
 CC able to penetrate into cells while maintaining stringent base pair
 CC fidelity for target DNA sequences. The oligomers demonstrate significant
 CC single- or double-stranded target nucleic acid binding activity to form
 CC duplexes, triplexes or other forms of stable association. Sequences
 CC AAA07788-803 represent oligonucleotides forming a third strand along with
 CC the duplex sequences

SQ Sequence 15 BP; 0 A; 0 C; 0 G; 11 T; 4 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAA07801 standard; DNA; 15 BP.
 Db 15 AAAA07801 standard; DNA; 15 BP.

RESULT 372
 AAA07801/C
 ID AAA07801 standard; DNA; 15 BP.

XX AC AAA07801;
 XX DT 23-JUN-2000 (first entry)
 XX DE Nucleic acid sequence of ODN-n.
 XX KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
 XX KW viral infection; inflammatory response; cellular proliferation;
 XX KW psoriasis; duplex; ss.
 XX OS Synthetic.
 XX PN WO200011013-A1.
 XX PD 02-MAR-2000.
 XX PF 20-AUG-1999; 99WO-US019029.
 XX PR 22-AUG-1998; 98US-0097712P.
 XX PA (UYNE-) UNIV NEBRASKA.
 XX PI Gold B;
 XX DR WPI; 2000-246530/21.
 XX PT Modified nucleomoners, used in physiologically stable, non-toxic
 XX PT oligomers used to inhibit expression of nucleic acids and in gene
 XX PT regulation, antisense technology and diagnostics.
 XX PS Disclosure; Page 20; 42pp; English.
 XX CC The invention provides modified nucleomoners of specified formula and
 XX CC their pharmaceutically acceptable salts. The nucleomoners are used as
 XX CC monomers in oligomers, which are used in pharmaceutical compositions to

CC inhibit expression of nucleic acid molecules including DNA and RNA in
 CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
 CC infected cells. They are used in oligomers for gene regulation, antisense
 CC technology, diagnostic applications to detect target sequences in
 CC biological samples such as those containing pathogenic bacteria, fungi
 CC and viruses, oncogenes, growth hormones and enzymes, to target genes or
 CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
 CC molecules, receptor molecules, cytokines, oncogenes, growth factors and
 CC interleukins associated with pathological conditions such as inflammatory
 CC conditions, cardiovascular disorders, immune reactions, cancer, viral
 CC infections and bacterial infections (see AAA07786 for details of other
 CC uses for which the oligomers are suitable for). Oligomers comprising the
 CC nucleomonomers exhibit increased duplex DNA stability when hybridizing to
 CC target nucleic acid sequences, are physiologically stable, non-toxic and
 CC able to penetrate into cells while maintaining stringent base pair
 CC fidelity for target DNA sequences. The oligomers demonstrate significant
 CC single- or double-stranded target nucleic acid binding activity to form
 CC duplexes, triplexes or other forms of stable association. Sequences
 CC AAA07788-803 represent oligonucleotides forming a third strand along with
 CC the duplex sequences

XX
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 11 T; 4 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
 Db 15 AAAAAAAAAAAAAA 1

RESULT 373
 AAA62350/C
 ID AAA62350 standard; DNA; 15 BP.
 AC AAA62350;
 XX
 DT 06-NOV-2000 (first entry)
 DE Oligonucleotide #2 containing 3'-C-amino-5'(S)-C,3'-N-ethanothymidine.
 XX
 KW Conformationally-locked oligonucleotide; antisense inhibitor;
 XX bicyclic sugar nucleoside analogue; gene probe; ds.
 OS Synthetic.

Key	Location/Qualifiers
modified_base	7
	/*tag= a
	/mod_base= OTHER
	/note= "3'-C-amino-5'(S)-C,3'-N-ethanothymidine"
modified_base	9
	/*tag= b
	/mod_base= OTHER
	/note= "3'-C-amino-5'(S)-C,3'-N-ethanothymidine"

US6083482-A.

04-JUL-2000.
 11-MAY-1999; 99US-00309742.
 11-MAY-1999; 99US-00309742.

(ICNC) ICN PHARM INC.

Wang G;

WPI; 2000-451496/39.

New conformationally restricted 3',5'-bridged nucleosides and
 oligonucleotides useful as antisense therapeutics or as gene-specific

PT diagnostics.
 XX
 PS Example 20; Col 16; 10pp; English.
 XX
 CC The present sequence is an oligonucleotide containing 3'-C-amino-5'(S)-
 CC C,3'-N-ethanothymidine, a bicyclic-sugar nucleoside. All nucleotides in
 CC the sequence were incorporated by phosphoramidite chemistry using a DNA
 CC synthesiser. Bicyclic sugar nucleosides are conformationally restricted
 CC 3',5'-bridged nucleosides which can be used as building blocks for
 CC oligonucleotides. Oligonucleotides can be produced that have certain,
 CC desired, geometrical shapes and entropy advantages. They may have
 CC superior hybridisation to DNA and RNA, and excellent biological
 CC stability. The conformationally-modified oligonucleotides may be useful
 CC as antisense inhibitors of gene expression or as gene probes, and may
 CC therefore be used in antisense therapeutics or gene-specific diagnostics

XX
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
 Db 15 AAAAAAAAAAAAAA 1

RESULT 374
 AAA62347/C
 ID AAA62347 standard; DNA; 15 BP.
 AC AAA62347;
 XX
 DT 06-NOV-2000 (first entry)
 DE Oligonucleotide #3 containing 3'-C-amino-5'(R)-C,3'-N-ethanothymidine.
 XX
 KW Conformationally-locked oligonucleotide; antisense inhibitor;
 KW bicyclic sugar nucleoside analogue; gene probe; ds.
 OS Synthetic.

Key	Location/Qualifiers
modified_base	1
	/*tag= a
	/mod_base= OTHER
	/note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"
modified_base	3
	/*tag= b
	/mod_base= OTHER
	/note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"
modified_base	5
	/*tag= c
	/mod_base= OTHER
	/note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"
modified_base	9
	/*tag= d
	/mod_base= OTHER
	/note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"
modified_base	11
	/*tag= e
	/mod_base= OTHER
	/note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"
modified_base	13
	/*tag= f
	/mod_base= OTHER
	/note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"
modified_base	15
	/*tag= g
	/mod_base= OTHER
	/note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"

US6083482-A.

```

XX 04-JUL-2000.
XX
XX 11-MAY-1999; 99US-00309742.
XX PF
XX
XX 11-MAY-1999; 99US-00309742.
XX PR
XX
XX (ICNC ) ICN PHARM INC.
XX PA
XX Wang G;
XX PI
XX WPI; 2000-451496/39.
XX DR
XX New conformationally restricted 3',5'-bridged nucleosides and
XX PT oligonucleotides useful as antisense therapeutics or as gene-specific
XX PT diagnostics.
XX
XX Example 20; Col 15; 10pp; English.
XX PS
XX The present sequence is an oligonucleotide containing 3'-C-amino-5'(R)-
XX CC C,3'-N-ethanothymidine, a bicyclic-sugar nucleoside. All nucleotides in
XX CC the sequence were incorporated by phosphoramidite chemistry using a DNA
XX CC synthesizer. Bicyclic sugar nucleosides are conformationally restricted
XX CC 3',5'-bridged nucleosides which can be used as building blocks for
XX CC oligonucleotides. Oligonucleotides can be produced that have certain,
XX CC desired, geometrical shapes and entropy advantages. They may have
XX CC superior hybridisation to DNA and RNA, and excellent biological
XX CC stability. The conformationally-modified oligonucleotides may be useful
XX CC as antisense inhibitors of gene expression or as gene probes, and may
XX CC therefore be used in antisense therapeutics or gene-specific diagnostics
XX
XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1495
DB 15 AAAAAAAAAAAAAA 1
RESULT 375
AAH62348/c
ID AAA62348 standard; DNA; 15 BP.
XX
XX AAA62348;
AC
XX 06-NOV-2000 (first entry)
DT
XX Oligonucleotide #4 containing 3'-C-amino-5'(R)-C,3'-N-ethanothymidine.
XX Conformationally-locked oligonucleotide; antisense inhibitor;
XX KW bicyclic sugar nucleoside analogue; gene probe; ds.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 7 /*tag= a
XX /mod_base= OTHER
XX /note= "3'-C-amino-5'(R)-C,3'-3'-N-ethanothymidine"
XX modified_base 9
XX /*tag= b
XX /mod_base= OTHER
XX /note= "3'-C-amino-5'(R)-C,3'-3'-N-ethanothymidine"
XX
XX US6083482-A.
XX PN
XX 04-JUL-2000.
XX
XX 11-MAY-1999; 99US-00309742.
XX PF
XX

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PR 11-MAY-1999; 99US-00309742.
XX
XX (ICNC ) ICN PHARM INC.
XX PA
XX Wang G;
XX PI
XX WPI; 2000-451496/39.
XX DR
XX New conformationally restricted 3',5'-bridged nucleosides and
XX PT oligonucleotides useful as antisense therapeutics or as gene-specific
XX PT diagnostics.
XX
XX Example 20; Col 15; 10pp; English.
XX PS
XX The present sequence is an oligonucleotide containing 3'-C-amino-5'(R)-
XX CC C,3'-N-ethanothymidine, a bicyclic-sugar nucleoside. All nucleotides in
XX CC the sequence were incorporated by phosphoramidite chemistry using a DNA
XX CC synthesizer. Bicyclic sugar nucleosides are conformationally restricted
XX CC 3',5'-bridged nucleosides which can be used as building blocks for
XX CC oligonucleotides. Oligonucleotides can be produced that have certain,
XX CC desired, geometrical shapes and entropy advantages. They may have
XX CC superior hybridisation to DNA and RNA, and excellent biological
XX CC stability. The conformationally-modified oligonucleotides may be useful
XX CC as antisense inhibitors of gene expression or as gene probes, and may
XX CC therefore be used in antisense therapeutics or gene-specific diagnostics
XX
XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1495
DB 15 AAAAAAAAAAAAAA 1
RESULT 376
AAH20308/c
ID AAH20308 standard; DNA; 15 BP.
XX
XX AAH20308;
AC
XX 31-JUL-2001 (first entry)
DT
XX Oligo dT15 EDTA labelled probe.
DE
XX
XX Hybridisation probe; DNA cleavage; double-helix; oncogene; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 1 /*tag= a
XX /mod_base= OTHER
XX /note= "Optionally thymidine has EDTA covalently attached
XX at C-5"
XX modified_base 5
XX /*tag= b
XX /mod_base= OTHER
XX /note= "Optionally thymidine has EDTA covalently attached
XX at C-5"
XX modified_base 8
XX /*tag= c
XX /mod_base= OTHER
XX /note= "Optionally thymidine has EDTA covalently attached
XX at C-5"
XX
XX US2001002314-A1.
XX PN
XX 31-MAY-2001.
XX
XX 04-AUG-1998; 98US-00128732.
XX PF
XX

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XX 30-OCT-1987; 87US-00115922.
PR 16-NOV-1990; 90US-00614205.
PR 12-NOV-1993; 93US-00152250.
XX (FLEH-) FLEHR HOHBACH TEST ALBRITTON & HERBERT.
XX Dervan PB, Moser HE;
XX WPI; 2001-342909/36.
XX New hybridization probe for specific triplex formation with large double
PT helices, useful e.g. for site-specific diagnostic cleavage, contains
PT attached functional residue.
XX Example 1; Fig 3B; 20pp; English.
XX This invention relates to hybridisation probes which target a specific
CC sequence within a large double-helical nucleic acid. The probe is
CC complementary to the target sequence and contains at least one nucleotide
CC with an attached molecule that is able to cleave double-helical DNA e.g.
CC EDTA-Fe(II) (ethylenediaminetetraacetic acid-iron complex). The probes
CC where the attached molecule is a label or compound that alters gene
CC expression, are used for specific detection and/or cleavage of double-
CC helical DNA, e.g. for diagnosis, for treatment of disease (particularly
CC caused by viruses, genetic defects or oncogenes), for chromosomal
CC analysis, and for the isolation and mapping of genes. The present
CC sequence represents probe of the invention used in an example
CC illustrating how the probe binds to and cleaves double stranded DNA
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 377
AAF30882/c
ID AAF30882 standard; DNA; 15 BP.
XX AAF30882;
XX 09-JUL-2001 (first entry)
XX Oligonucleotide portion of ODN-MGB-LF conjugate.
XX ODN-MGB-LF; oligonucleotide; minor groove binder; latent fluorophore;
XX hybridisation; detection; fluorescence; probe; ss.
XX Synthetic.
XX WO200131063-A1.
XX 03-MAY-2001.
XX 26-OCT-2000; 2000WO-US029786.
XX 26-OCT-1999; 99US-00428236.
XX (EPOC-) EPOCH BIOSCIENCES INC.
XX Dempcy RO, Afonina IA, Vermeulen NMJ;
XX WPI; 2001-328656/34.
XX Conjugate of oligonucleotide, minor groove binder and latent fluorophore,
XX useful for detecting specific nucleic acids, e.g. for single-nucleotide
XX mismatch discrimination.

XX Disclosure; Page 58; 105pp; English.
XX The present sequence is that of the oligonucleotide (ODN) component of an
CC ODN-MGB (minor groove binder)-LF (latent fluorophore) conjugate of the
CC invention. MGBs bind in a non-intercalating manner to the minor groove of
CC non-single-stranded DNA, RNA or their hybrids, while a LF binds similarly
CC but in an intercalating manner, or lies in the minor groove, or is
CC oriented in some other way to the DNA molecule by MGB, such that it
CC becomes fluorescent (or its fluorescent properties change detectably).
CC The conjugates are used as hybridisation probes and amplification primers
CC for fluorescent detection of specifically hybridising sequences, for
CC analysis or diagnosis, especially (real-time) PCR, for single-nucleotide
CC mismatch discrimination, target or signal amplification, array-based
CC assays and sequencing, including detection of double-stranded DNA by
CC triplex formation. Many different targets can be detected a single
CC reaction vessel. The present ODN-MGB-LF conjugate was used to demonstrate
CC hybridisation-triggered fluorescence. Upon hybridisation to the
CC complementary target sequence there was an increase in fluorescence
CC yield, measured as the ratio of the fluorescence emitted by the hybrid
CC between the ODN-MGB-LF conjugate and its target sequence to the
CC fluorescence emitted by unhybridised (i.e. single-stranded) ODN-MGB-LF,
CC of 8.3
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 378
AAH20511/c
ID AAH20511 standard; DNA; 15 BP.
XX AAH20511;
XX 31-JUL-2001 (first entry)
XX Oligonucleotide b) for solid phase synthesis of oligonucleotides.
XX Cross-linked vinyl acetate copolymer carrier material; AIDS treatment;
XX phosphorothioate; solid phase synthesis; modified oligonucleotide;
XX clinical diagnostic; cancer treatment; ss.
XX Synthetic.
XX Key Location/Qualifiers
FH modified_base 1..14
FT /tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate deoxynucleotides"
XX
PN DE10051726-A1.
XX 10-MAY-2001.
XX 18-OCT-2000; 2000DE-01051726.
XX 30-OCT-1999; 99DE-01052376.
XX (MERE ) MERCK PATENT GMBH.
XX Seliger H, Sobkowski M, Hinz M;
XX WPI; 2001-336414/36.
XX Intermediate for oligonucleotide synthesis comprises partially hydrolysed
PT cross-linked vinyl acetate copolymer loaded with nucleotide derivative.

```

XX Example 2; Page 5; 8pp; German.

XX This invention describes a novel chemical product comprising a partially

CC hydrolysed cross-linked vinyl acetate copolymer carrier material loaded

CC with nucleotide derivative(s). The product is an intermediate for the

CC large (gram) scale solid phase synthesis of modified oligonucleotides

CC useful e.g. as clinical diagnostics and therapeutics, e.g. for the

CC treatment of AIDS and cancers. The presence of the partially hydrolysed

CC copolymer facilitates the synthesis of larger amounts of oligonucleotides

CC compared with the use of Merckogel (RTM; macroporous polyvinyl acetate)

CC described in Nucleic Acid Res. Sympos. Ser. 31, p. 153, 1994.

CC Oligonucleotides are obtained in very good quality and high yields. Also,

CC the nucleosides do not display the reduced activity seen in some prior

CC art procedures, less carrier material, reagents and solvent are required.

CC Further, the carrier material is biodegradable and thus does not present

CC disposal problems. It also swells uniformly in a range of solvents, which

CC obviates expansion or contraction during use or solvent exchange.

CC AAH20510-AAH20513 represent oligonucleotides containing modified

CC deoxynucleotides which are used to illustrate the method of the invention

XX

XX Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

XX

Query Match 1.0%; Score 15; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.7e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495

DB 15 AAAAAAAAAAAAAA 1

RESULT 379

AAF16603

ID AAF16603 standard; DNA; 15 BP.

AC AAF16603;

XX

XX 13-MAR-2001 (first entry)

XX

DE Gastric acid production inhibiting oligonucleotide SEQ ID NO: 90.

XX

XX Gastric acid disturbance; gastric reflux; gastritis; dyspepsia;

KW stomach ulcer; duodenal ulcer; Helicobacter pylori; antisense;

KW DNA-RNA hybrid; ss.

XX

OS Homo sapiens.

XX

XX WO2000071164-A1.

XX

XX 30-NOV-2000.

XX

XX 24-MAY-2000; 2000WO-AU000498.

XX

XX 24-MAY-1999; 99AU-00000510.

XX

XX (TACH/) TACHAS G.

XX

XX Tachas G;

XX

XX WPI; 2001-025093/03.

XX

XX Treating gastric acid disturbance by administering an oligonucleotide

PT which modulates the activity of a polypeptide involved in gastric acid

PT production or secretion.

XX

XX Example 3; Page 148; 164pp; English.

XX

XX The present invention provides oligonucleotides, and methods for their

CC use, which are useful in modulating the action of proteins involved in

CC gastric acid production. The target protein is preferably the histamine

CC H2 receptor or one of the proteins which form part of the gastric proton

CC pump. The sequences and methods of the invention are useful in the

CC treatment of gastric reflux, gastritis, dyspepsia, stomach ulcers,

CC duodenal ulcers and other gastric acid disturbances, most of which are

CC caused by Helicobacter pylori

XX

XX Sequence 15 BP; 14 A; 0 C; 0 G; 1 T; 0 U; 0 Other;

XX

Query Match 1.0%; Score 15; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.7e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAAA 1494

DB 1 TAAAAAAAAAAAAA 15

RESULT 380

AAH49243/c

ID AAH49243 standard; DNA; 15 BP.

XX

AC AAH49243;

XX

XX 26-NOV-2001 (first entry)

XX

XX PNA-forming oligonucleotide #7.

XX

XX Polyamide-oligonucleotide derivative; anticancer; antiproliferative;

KW antiviral; hepatotropic; vasotropic; antisense inhibition; ribozyme;

KW integrin; cell-cell adhesion; cancer; restenosis; stability; PNA;

KW peptide nucleic acid; ss.

XX

XX Synthetic.

OS

XX

XX Key Location/Qualifiers

FT modified_base 9

FT /*tag= a

FT /mod_base= OTHER

FT /note= "t-but"

FT modified_base 15

FT /*tag= b

FT /mod_base= OTHER

FT /note= "t-hex"

XX

XX EPI113021-A2.

XX

XX 04-JUL-2001.

XX

XX 08-MAR-1995; 2001EP-00104012.

XX

XX 14-MAR-1994; 94DE-04408528.

PR 08-MAR-1995; 95EP-00103332.

XX

XX (AVET) AVENTIS PHARMA DEUT GMBH.

XX

XX Uhlmann E, Breipohl G;

XX

XX WPI; 2001-591267/67.

XX

XX New DNA-peptide nucleic acid chimeras, useful e.g. as antisense agents

PT for treating e.g. cancer, also as diagnostic probes and primers.

XX

XX Example 26; Page 40; 54pp; German.

XX

XX This invention describes novel polyamide-oligonucleotide derivatives (I)

CC and their physiologically acceptable salts of formula F(DNA)-Li) Q(PNA-

CC Li) r(DNA-Li) s(PNA) t) xF' where q, r, s, t = 0 or 1, with the sum of

CC two or more adjacent letters at least 2; x = 1-20; DNA = nucleic acid

CC (such as DNA or RNA or their known derivatives); Li = covalent linkage

CC between DNA and PNA, i.e. a bond or a residue containing at least one

CC atom of carbon, nitrogen, oxygen or sulfur; PNA = polyamide structure

CC containing at least one nucleobase different from thymine; and F, F' =

CC end groups and/or are connected through a covalent bond. The products of

CC the invention have anticancer, antiproliferative, antiviral, hepatotropic

CC and vasotropic activity and can be used for the inhibition of gene

expression by antisense, ribozyme, sense, or triple-helix methods, or by binding to proteins (aptamers). (I) are used for treating diseases caused by viruses (human immune deficiency, herpes simplex, influenza, vesicular stomatitis, hepatitis B or papilloma), or mediated by integrins or cell-cell adhesion reactions, for treating cancer, or for inhibiting cell adhesion, particularly as antisense reagents. They are also useful in heterogeneous or homogeneous assays, as primers or probes, particularly where the target is amplified before being detected by hybridization, for diagnosis of genetic, malignant or pathogen-related diseases. (I) retain the increased affinity for complementary strands and better stability in serum, associated with conventional peptide nucleic acids (PNA), but lack the disadvantages, i.e. have improved cellular uptake, do not aggregate in aqueous solution, and have reduced affinity for purification materials, reduced cytotoxicity, better sequence specificity. They are more active than either DNA or PNA oligomers. When used as probes, (I) show different responses to base-pair mismatches in the DNA and PNA segments, allowing better discrimination between pathogenic and non-pathogenic conditions such as the transition from proto-oncogene to oncogene, also, when used as primers, with the PNA segment at the 5'-end, they produce amplicons resistant to 5'-exonuclease, allowing this enzyme to be used to eliminate RNA or DNA primers. The DNA component allows additional reactions not possible with PNA alone, e.g. 3'-tailing and (I) may be incorporated into a gene. AAH49208-AAH49264 represent oligonucleotides used to illustrate the method of the invention

SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 381
ABL40743/C
ID ABL40743 standard; DNA; 15 BP.

XX ABL40743;
AC
XX 03-JUL-2002 (first entry)
XX Chicken heparanase (hpa) cDNA cloning oligo dT(15) primer.

XX Heparanase; catalytic; cytostatic; antiviral; antibacterial; enzyme;
KW anti-protozoan; neuroprotective; heparin; hpa; chicken; PCR primer; ss.
XX Gallus gallus.

OS
XX US2002034810-A1.

PN 21-MAR-2002.

XX 16-AUG-2001; 2001US-00930218.

XX 20-SEP-2000; 2000US-00666390.

XX (INSI-) INSIGHT STRATEGY & MARKETING LTD.

XX Goldshmidt O, Pecker I, Vlodavsky I, Michal I, Zcharia E;

XX WPI; 2002-338926/37.

XX Nucleic acid encoding avian and reptile heparanase polypeptide is useful
PT to treat various heparin-related disorders and the signal peptide is
PT useful in production of membrane-targeted or secreted recombinant
PT proteins.

XX Disclosure; Page 13; 39pp; English.

XX The invention relates to an isolated avian and reptile nucleic acid,

CC encoding a polypeptide with heparanase catalytic activity. The signal
CC peptide of the nucleic acid can be used to express membrane-associated or
CC secreted proteins in heterologous expression systems. The encoded
CC polypeptides can be used to prevent tumour angiogenesis, metastasis and
CC invasion, and to intervene with pathologies associated with impaired
CC heparin-binding growth factors, cellular responses to heparin-binding
CC growth factors and cytokines, cell interaction with plasma lipoproteins,
CC cellular susceptibility to viral, protozoan and bacterial infections or
CC disintegration of neurodegenerative plaques. The present sequence
XX represents a chicken heparanase (hpa) cDNA cloning oligo dT(15) primer
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 382
ABA97403/C
ID ABA97403 standard; DNA; 15 BP.

XX ABA97403;

XX 18-JUN-2002 (first entry)

DE Nucleotide sequence of oligomer # 10 used to compare mismatches.

XX Protein nucleic acid molecule; PNA; ds.

XX Synthetic.

XX WO200168673-A1.

XX 20-SEP-2001.

XX 13-MAR-2001; 2001WO-US008111.

PR 14-MAR-2000; 2000US-0189190P.

PR 30-NOV-2000; 2000US-0250334P.

XX (ACTI-) ACTIVE MOTIF.

XX Efimov V, Fernandez J, Archdeacon D, Archdeacon J;

PI Chakmakchcheau O, Buryakova A, Choob M, Hondorp K;

XX WPI; 2002-041177/05.

XX Oligonucleotides analogs useful in detection, separation and purification

PT of nucleic acid molecules, comprise monomers, dimers and oligomers.

XX Example 20; Page 123; 197pp; English.

XX This invention relates to oligonucleotide analogues comprising a protein
CC nucleic acid molecule (PNA) monomer. They are used in the detection and
CC separation of nucleic acid molecules and as probes, primers, linkers,
CC adapters and antisense agents on solid supports. Modifications enhance
CC their use as capture and detection probes e.g. by the incorporation of
CC biotin, digoxigenin, radioisotopes, fluorescent labels such as
CC fluorescein and reporter molecules such as alkaline phosphatase. They are
CC also used for enhancing or inhibiting the activity of an enzyme or
CC cellular activity. The compounds are stable to nucleases and proteases,
CC have high affinity, binding specificity and solubility. The polyamide
CC backbone of PNAs is resistant to both nucleases and proteases. PNAs bind
CC nucleic acid molecules with greater affinity than DNA or RNA
CC concentration. The compounds are relatively simple to synthesize and are
CC used in a wide variety of applications. This sequence represents a DNA
CC oligomer which is used to represent the effect of single base mismatches
CC on oligonucleotides

```
XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
DB 15 AAAAAAAAAAAAAA 1

RESULT 383
AAL49453
ID AAL49453 standard; DNA; 15 BP.
XX AC AAL49453;
XX DT 14-NOV-2002 (first entry)
XX Mutation detection method tag peptide coding sequence SEQ ID NO: 1.
DE Mutation detection; primer; mutant; tag; tumour suppressor gene;
KW protein production; cancer; ds.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX CDS 1..15
XX FT /*tag= a
XX FT /product= "tag peptide"
XX FT /partial
XX FT /note= "no start or stop"
XX PN WO200266675-A2.
XX PD 29-AUG-2002.
XX PF 15-FEB-2002; 2002WO-EP001651.
XX PR 16-FEB-2001; 2001DE-01007317.
XX PA (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX PI Kahmann S, Mueller O;
XX DR WPI; 2002-674959/72.
XX DR P-PSDB; AAO19054.
XX PT Detecting mutations in nucleic acid, useful for diagnosis and
XX PT characterization of tumors, by amplification, in vitro transcription and
XX PT translation, then protein detection.
XX PS Claim 11; Fig 5; 62pp; German.
XX CC The present invention relates to a method of detecting mutations in a
XX CC nucleic acid by amplifying the nucleic acid to produce a double-stranded
XX CC amplicon, in vitro transcription and translation of this amplicon, and
XX CC detection of the translated protein. The primers used for amplification
XX CC are designed to produce an amplicon that is translatable and allows
XX CC differentiation between translation products of wild-type and mutated
XX CC nucleic acids. The method is used to detect mutations in tumour
XX CC suppressor genes, for (early) diagnosis, monitoring and characterisation
XX CC of tumours (especially of bladder and intestines) and in the germ line
XX CC (using nucleic acids from embryos or blood cells). A new multi-tag vector
XX CC is used to detect or verify the reading frame of a nucleic acid cloned in
XX CC it, and to determine the suitability of detectable peptides for analysis
XX CC and/or purification of a recombinant protein, expressed from a sequence
XX CC cloned in the vector. The present sequence encodes a tag peptide and was
XX CC used in the invention
XX SQ Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
```

```
Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
DB 1 AAAAAAAAAAAAAA 15

RESULT 384
AAL49455
ID AAL49455 standard; DNA; 15 BP.
XX AC AAL49455;
XX DT 14-NOV-2002 (first entry)
XX Mutation detection method tag peptide coding sequence SEQ ID NO: 3.
DE Mutation detection; primer; mutant; tag; tumour suppressor gene;
KW protein production; cancer; ds.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX CDS 1..15
XX FT /*tag= a
XX FT /product= "tag peptide"
XX FT /partial
XX FT /note= "no start or stop"
XX PN WO200266675-A2.
XX PD 29-AUG-2002.
XX PF 15-FEB-2002; 2002WO-EP001651.
XX PR 16-FEB-2001; 2001DE-01007317.
XX PA (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX PI Kahmann S, Mueller O;
XX DR WPI; 2002-674959/72.
XX DR P-PSDB; AAO19056.
XX PT Detecting mutations in nucleic acid, useful for diagnosis and
XX PT characterization of tumors, by amplification, in vitro transcription and
XX PT translation, then protein detection.
XX PS Claim 11; Fig 5; 62pp; German.
XX CC The present invention relates to a method of detecting mutations in a
XX CC nucleic acid by amplifying the nucleic acid to produce a double-stranded
XX CC amplicon, in vitro transcription and translation of this amplicon, and
XX CC detection of the translated protein. The primers used for amplification
XX CC are designed to produce an amplicon that is translatable and allows
XX CC differentiation between translation products of wild-type and mutated
XX CC nucleic acids. The method is used to detect mutations in tumour
XX CC suppressor genes, for (early) diagnosis, monitoring and characterisation
XX CC of tumours (especially of bladder and intestines) and in the germ line
XX CC (using nucleic acids from embryos or blood cells). A new multi-tag vector
XX CC is used to detect or verify the reading frame of a nucleic acid cloned in
XX CC it, and to determine the suitability of detectable peptides for analysis
XX CC and/or purification of a recombinant protein, expressed from a sequence
XX CC cloned in the vector. The present sequence encodes a tag peptide and was
XX CC used in the invention
XX SQ Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
```

```
Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1481 AAAAAAAAAAAAAA 1495
 |||||
 Db 1 AAAAAAAAAAAAAA 15

RESULT 385
 AAD29506/c
 ID AAD29506 standard; DNA; 15 BP.
 XX
 AC AAD29506;
 XX
 DT 17-MAY-2002 (first entry)
 XX
 DE Primer used for the expression of adipocytes in human preadipose cells.
 XX
 KW Pre-adipose cell line; white adipocyte; food ingredient; obesity; lipid;
 KW diabetes; cardiovascular disease; reverse transcription; RT-PCR primer;
 KW ss.
 XX
 OS Unidentified.
 XX
 PN W0200206450-A1.
 XX
 PD 24-JAN-2002.
 XX
 PF 13-JUL-2001; 2001WO-EP008165.
 XX
 PR 18-JUL-2000; 2000EP-00115489.
 XX
 PA (NEST) SOC PROD NESTLE SA.
 XX
 PI Darimont C, Mace K, Pfeifer A;
 XX
 DR WPI; 2002-188539/24.
 XX

New human pre-adipose cell line capable of differentiating to adipose cells, useful in developing drug, food ingredients, and supplements against obesity, diabetes and cardiovascular diseases.

Example 5; Page 10; 30pp; English.

The present invention relates to new human pre-adipose cell lines capable to differentiate to white adipose cells, exhibiting essentially the same cellular properties of normal white adipose cells. The human pre-adipose cell lines are useful for the identification of substances controlling the regulation of lipid uptake and release by human white adipocytes, and substances controlling the differentiation of preadipocytes into mature adipocytes. They are useful for screening compounds capable to regulate the secretion of any metabolites or hormones from human white adipocytes. Sequences of the invention are useful for developing drugs, food ingredients and supplements against obesity, diabetes and cardiovascular diseases. The present DNA sequence is a reverse transcription (RT)-PCR primer which is used for the expression of adipocytes in CC differentiated immortalised human preadipose cells. This primer is used CC in the exemplification of the invention

XX
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
 Query Match 1.0%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
 |||||
 Db 15 AAAAAAAAAAAAAA 1

RESULT 386
 AAD22531
 ID AAD22531 standard; RNA; 15 BP.
 XX
 AC AAD22531;

XX
 DT 29-AUG-2003 (revised)
 DT 07-AUG-2003 (revised)
 DT 12-FEB-2002 (first entry)
 XX
 DE Retroviral reverse transcriptase inhibitor DNP-poly [A] RNA fragment.
 XX
 KW RNase inhibitor; anti-HIV; cytostatic; hepatotropic; antiinflammatory;
 KW virucide; oncogene; cancer; transcription; translation; leukaemia virus;
 KW hepatitis virus; human immunodeficiency virus; retroviral; DNP-poly [A];
 KW poly-2'-O-(2,4-dinitrophenyl)-poly [A]; viral reverse transcriptase; ss.
 XX
 OS unidentified retrovirus.
 OS Unidentified.
 XX
 PN US6291438-B1.
 XX
 PD 18-SEP-2001.
 XX
 PF 06-OCT-1998; 98US-00167375.
 XX
 PR 24-FEB-1993; 93US-00022055.
 PR 23-FEB-1994; 94US-00200650.
 PR 22-FEB-1996; 96US-00604871.
 XX
 PA (WANG/) WANG J H.
 XX
 PI Wang JH;
 XX
 DR WPI; 2002-009339/01.
 XX

Derivatized antisense oligoribonucleotide useful to inhibit e.g. viral reverse transcriptase comprises at the 2'-O position of the oligoribonucleotide, a hydrophobic carrier reagent containing a poly substituted phenyl compound.

Example 3; Col 24; 56pp; English.

The invention relates to derivatised antisense oligoribonucleotides with enhanced membrane permeability and stability. The derivatised antisense oligoribonucleotide complementary to a sequence of nucleotides found in a virus or a cell is useful for inhibiting e.g., viral reverse transcriptase. Derivatized antisense oligoribonucleotide is conjugated at the 2'-O position with a hydrophobic carrier reagent containing a poly substituted phenyl compound. The derivatised oligoribonucleotides are used to decrease the expression of oncogenes and thereby decrease the expression of cancer cells which rely upon oncogene expression for their phenotypic and pathological properties. The oligoribonucleotides are also used for increasing the effectiveness of antisense oligonucleotide targeted to a gene associated with a disease or a condition in an animal. To alter gene transcription and/or translation for any gene or gene segment responsible for expression, to inhibit viral reverse transcriptase, to inhibit the expression of leukaemia virus, hepatitis virus, oncogenes and human immunodeficiency virus. The present sequence is retroviral reverse transcriptase inhibitor DNP-poly [A] RNA fragment which is used in the treatment of moloney murine leukaemia virus (MuLV) in mammals. (Updated on 07-AUG-2003 to correct OS field.) (Updated on 29-AUG-2003 to standardise OS field)

XX
 SQ Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
 Query Match 1.0%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
 |||||
 Db 1 AAAAAAAAAAAAAA 15

RESULT 387
 ABQ82140
 ID ABQ82140 standard; DNA; 15 BP.


```
PA (UYJO ) UNIV JOHNS HOPKINS.
XX
XX Vogelstein B, Kinzler KW, Zhang L, Zhou W;
XX
XX WPI; 2002-153821/20.
XX
XX New human nucleic acid containing specific SAGE tags, useful as
XX diagnostic markers for cancer, also derived probes.
XX
XX Disclosure; Col 68; 161pp; English.
XX
XX The invention relates to an isolated, purified human nucleic acid (I)
XX that has the same sequence as a mRNA found in humans and is a SAGE
XX (serial analysis of gene expression) tag comprising a single stranded
XX probe containing at least 10 consecutive nucleotides. SAGE tags, are
XX diagnostic and prognostic markers of cancer, especially of the colon and
XX pancreas. ABK31900-ABK32770 represent human colon and pancreatic cancer
XX SAGE tags of the invention
XX
XX Sequence 15 BP; 2 A; 6 C; 2 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 1.7e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1390 CATGCACCTGTCCTT 1404
XX |||||
XX 1 CATGCACCTGTCCTT 15
XX
XX RESULT 390
XX ABK32084
XX ID ABK32084 standard; DNA; 15 BP.
XX
XX AC ABK32084;
XX
XX DT 23-APR-2002 (first entry)
XX
XX DE Human colon cancer SAGE tag #185.
XX
XX KW Human; colon cancer; colorectal cancer; pancreatic cancer; SAGE tag;
XX serial analysis of gene expression; diagnostic; prognostic; probe;
XX cancer marker; ss.
XX
XX OS Homo sapiens.
XX
XX PN US6333152-B1.
XX
XX PD 25-DEC-2001.
XX
XX PF 20-MAY-1998; 98US-00081646.
XX
XX PR 20-MAY-1998; 98US-00081646.
XX
XX PA (UYJO ) UNIV JOHNS HOPKINS.
XX
XX PI Vogelstein B, Kinzler KW, Zhang L, Zhou W;
XX
XX WPI; 2002-153821/20.
XX
XX New human nucleic acid containing specific SAGE tags, useful as
XX diagnostic markers for cancer, also derived probes.
XX
XX Disclosure; Col 25; 161pp; English.
XX
XX The invention relates to an isolated, purified human nucleic acid (I)
XX that has the same sequence as a mRNA found in humans and is a SAGE
XX (serial analysis of gene expression) tag comprising a single stranded
XX probe containing at least 10 consecutive nucleotides. SAGE tags, are
XX diagnostic and prognostic markers of cancer, especially of the colon and
XX pancreas. ABK31900-ABK32770 represent human colon and pancreatic cancer
XX SAGE tags of the invention
XX
XX Sequence 15 BP; 2 A; 6 C; 2 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 1.7e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1390 CATGCACCTGTCCTT 1404
XX |||||
XX 1 CATGCACCTGTCCTT 15
XX
XX RESULT 390
XX ABK32084
XX ID ABK32084 standard; DNA; 15 BP.
XX
XX AC ABK32084;
XX
XX DT 23-APR-2002 (first entry)
XX
XX DE Human colon cancer SAGE tag #185.
XX
XX KW Human; colon cancer; colorectal cancer; pancreatic cancer; SAGE tag;
XX serial analysis of gene expression; diagnostic; prognostic; probe;
XX cancer marker; ss.
XX
XX OS Homo sapiens.
XX
XX PN US6333152-B1.
XX
XX PD 25-DEC-2001.
XX
XX PF 20-MAY-1998; 98US-00081646.
XX
XX PR 20-MAY-1998; 98US-00081646.
XX
XX PA (UYJO ) UNIV JOHNS HOPKINS.
XX
XX PI Vogelstein B, Kinzler KW, Zhang L, Zhou W;
XX
XX WPI; 2002-153821/20.
XX
XX New human nucleic acid containing specific SAGE tags, useful as
XX diagnostic markers for cancer, also derived probes.
XX
XX Disclosure; Col 25; 161pp; English.
XX
XX The invention relates to an isolated, purified human nucleic acid (I)
XX that has the same sequence as a mRNA found in humans and is a SAGE
XX (serial analysis of gene expression) tag comprising a single stranded
XX probe containing at least 10 consecutive nucleotides. SAGE tags, are
XX diagnostic and prognostic markers of cancer, especially of the colon and
XX pancreas. ABK31900-ABK32770 represent human colon and pancreatic cancer
XX SAGE tags of the invention
XX
XX Sequence 15 BP; 2 A; 6 C; 2 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 1.7e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1475 CATGCTAAAAA 1489
XX |||||
XX 1 CATGCTAAAAA 15
XX
XX RESULT 391
XX ABX00240/c
XX ID ABX00240 standard; RNA; 15 BP.
XX
XX AC ABX00240;
XX
XX DT 23-DEC-2002 (first entry)
XX
XX DE Hepatitis C virus substrate #22 for HCV hammerhead ribozyme #22.
XX
XX KW Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;
XX HCV ribozyme; HCV expression; HCV replication; cirrhosis; virocid;
XX liver failure; hepatocellular carcinoma; HCV infection; drug therapy;
XX type I interferon; interferon alpha; interferon beta; cytostatic;
XX interferon gamma; consensus interferon; hepatotropic; antiinflammatory;
XX substrate; hammerhead ribozyme; HH ribozyme; ss.
XX
XX OS Hepatitis C virus.
XX
XX PN US2002082225-A1.
XX
XX PD 27-JUN-2002.
XX
XX PF 23-MAR-1999; 99US-00274553.
XX
XX PR 23-MAR-1999; 99US-00274553.
XX
XX PA (BLAT/) BLATT L.
XX (MCSW/) MCSWIGGEN J A.
XX (ROBE/) ROBERTS B.
XX (PAVC/) PAVCO P A.
XX (MACE/) MACEJACK D.
XX
XX PI Blatt L, Mcswiggen JA, Roberts B, Pavco PA, Macejack D;
XX
XX WPI; 2002-617759/66.
XX
XX New ribozymes targeting RNA derived from hepatitis C virus inhibit viral
XX replication and are useful to treat hepatitis C virus infections and
XX cirrhosis, liver failure or hepatocellular carcinoma.
XX
XX Claim 1; Page 21; 80pp; English.
XX
XX The present invention relates to enzymatic nucleic acids which
XX specifically cleave RNA derived from Hepatitis C virus (HCV). The
XX enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin
XX (HP) motif where the binding arms comprise sequences complementary to one
XX of the substrate sequences defined in the specification. The HCV
XX ribozymes are useful for modulating the expression and/or replication of
XX HCV. They can be used to treat cirrhosis, liver failure and/or
XX hepatocellular carcinoma. The HCV ribozymes are also useful for treating
XX a condition associated with HCV infection in conjunction with one or more
XX other drug therapies, particularly type I interferon, especially
XX interferon alpha, beta or gamma or consensus interferon. The present
XX sequence represents a substrate for a HCV hammerhead (HH) ribozyme. Note:
XX Some of the sequence data for this patent did not form part of the
XX printed specification. The complete sequence data for this patent was
XX obtained in electronic format directly from the USPTO web site at
XX seqdata.uspto.gov/pslpsbIDentry.html
XX
XX Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;
```

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
DB 15 AAAAAAAAAAAAAA 1

RESULT 392
ABX03406/c
ID ABX03406 standard; RNA; 15 BP.
XX
AC ABX03406;
XX
DT 24-DEC-2002 (first entry)
XX
DE Hepatitis C virus substrate #1319 for HCV hammerhead ribozyme #1319.
XX
KW Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;
KW HCV ribozyme; HCV expression; HCV replication; cirrhosis; virucide;
KW liver failure; hepatocellular carcinoma; HCV infection; drug therapy;
KW type I interferon; interferon alpha; interferon beta; cytostatic;
KW interferon gamma; consensus interferon; hepatotropic; antiinflammatory;
KW substrate; hammerhead ribozyme; HH ribozyme; ss.
XX
OS Hepatitis C virus.
XX
PN US2002082225-A1.
XX
PD 27-JUN-2002.
XX
PF 23-MAR-1999; 99US-00274553.
XX
PR 23-MAR-1999; 99US-00274553.
XX
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J A.
PA (ROBE/) ROBERTS B.
PA (PAVC/) PAVCO P A.
PA (WACE/) MACEJACK D.
XX
PI Blatt L, Mcswiggen JA, Roberts B, Pavco PA, Macejack D;
XX WPI; 2002-617759/66.
XX
PT New ribozymes targeting RNA derived from hepatitis C virus inhibit viral
PT replication and are useful to treat hepatitis C virus infections and
PT cirrhosis, liver failure or hepatocellular carcinoma.
XX
PS Claim 1; Page 64; 80pp; English.
XX
CC The present invention relates to enzymatic nucleic acids which
CC specifically cleave RNA derived from Hepatitis C virus (HCV). The
CC enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin
CC (HP) motif where the binding arms comprise sequences complementary to one
CC of the substrate sequences defined in the specification. The HCV
CC ribozymes are useful for modulating the expression and/or replication of
CC HCV. They can be used to treat cirrhosis, liver failure and/or
CC hepatocellular carcinoma. The HCV ribozymes are also useful for treating
CC a condition associated with HCV infection in conjunction with one or more
CC other drug therapies, particularly type I interferon, especially
CC interferon alpha, beta or gamma or consensus interferon. The present
CC sequence represents a substrate for a HCV hammerhead (HH) ribozyme. Note:
CC Some of the sequence data for this patent did not form part of the
CC printed specification. The complete sequence data for this patent was
CC obtained in electronic format directly from the USPTO web site at
CC seqdata.uspto.gov/psipsDIDentry.html
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
DB 15 AAAAAAAAAAAAAA 1

RESULT 393
ABL57064/c
ID ABL57064 standard; DNA; 15 BP.
XX
AC ABL57064;
XX
DT 22-JUL-2002 (first entry)
XX
DE Hydrazide precursor phosphoramidite oligonucleotide O35.
XX
KW Macromolecule; hydrazide; immobilisation; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..15
FT /*tag= b
FT /*note= "phosphoramidite linkage"
FT modified_base 1
FT /*tag= a
FT /*mod_base= OTHER
FT /*note= "Diethyl 5-(((2-cyanoethoxy) (diisopropylamino)
FT /*note= "phosphoryloxy) methyl) isophthalate, synthetic branching
FT modified_base 15
FT /*tag= c
FT /*mod_base= OTHER
FT /*note= "3' Cy3 dye"
XX
WO200214558-A2.
XX
PD 21-FEB-2002.
XX
PF 10-AUG-2001; 2001WO-US041663.
XX
PR 11-AUG-2000; 2000WO-US022205.
XX
PA (NANO-) NANOGEN INC.
XX
PI Raddatz S, Mueller-Ibeler J, Schweitzer M, Bruecher C, Windhab N;
PI Havens JR, Onofrey TU, Greef CH, Wang D;
XX
WPI; 2002-404476/43.
XX
PT Compound for binding macromolecule to substrate surface or conjugation
PT targets, contains phosphorus containing reactive group, hydrazide
PT protecting group and benzene ring, and has predefined formula.
XX
PS Example 4; Page 44; 120pp; English.
XX
CC The present sequence is of a hydrazine treated hydrazide precursor
CC phosphoramidite 15-mer, designated oligo O35, which was produced in an
CC example from the invention and which includes a synthetic branching
CC amide compound. The invention describes an improved process for
CC immobilisation of macromolecules including DNA, RNA, peptide nucleic
CC acids, pyranosyl-RNA and peptides, especially macromolecules containing
CC multiple reactive sites, to a substrate surface or other conjugation
CC target. It also describes the preparation of oligos containing one or
CC more hydrazides, which can be used for conjugation to surface binding
CC moieties, or for other conjugation reactions. The process is useful e.g.
CC in nucleic acid hybridisation based assays, DNA chip technology and
CC biosensor applications
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Db	15 AAAAAAAAAAAAAA 1																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																		
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```

Db      15 AAAAAAAAAAAAAA 1
RESULT 396
ABL57066/c
ID      ABL57066 standard; DNA; 15 BP.
XX
XX
AC      ABL57066;
XX
XX      22-JUL-2002 (first entry)
XX
XX      Amino-C6-modified and Cy3 labeled T15 oligonucleotide.
XX
XX      Macromolecule; hydrazide; immobilisation; ss.
XX
XX      Synthetic.
XX
FH      Key      Location/Qualifiers
FT      modified_base 1
FT      /tag= a
FT      /mod_base= OTHER
FT      /note= "Amino-C6 modification"
FT      modified_base 15
FT      /tag= b
FT      /mod_base= OTHER
FT      /note= "3' Cy3 dye"
XX
XX      WO200214558-A2.
XX
XX      21-FEB-2002.
XX
XX      10-AUG-2001; 2001WO-US041663.
XX
XX      11-AUG-2000; 2000WO-US022205.
XX
XX      (NANO-) NANOGEN INC.
XX
XX      Raddatz S, Mueller-Ibeler J, Schweitzer M, Bruecher C, Windhab N;
PI      Havens JR, Onofrey TU, Greef CH, Wang D;
XX
XX      WPI; 2002-404476/43.
XX
XX      Compound for binding macromolecule to substrate surface or conjugation
PT      targets, contains phosphorous containing reactive group, hydrazide
PT      protecting group and benzene ring, and has predefined formula.
XX
XX      Example 12; Page 57; 120pp; English.
XX
XX      The present sequence is of an amino-C6-modified and Cy3 dye labeled T15
CC      oligonucleotide that was used in a comparison of hydrazine and amine
CC      attachment moieties on active ester surfaces in an example from the
CC      invention. The invention describes an improved process for immobilisation
CC      of macromolecules including DNA, RNA, peptide nucleic acids, pyranosyl-
CC      RNA and peptides, especially macromolecules containing multiple reactive
CC      sites, to a substrate surface or other conjugation target. It also
CC      describes the preparation of oligos containing one or more hydrazides,
CC      which can be used for conjugation to surface binding moieties, or for
CC      other conjugation reactions. The process is useful e.g. in nucleic acid
CC      hybridisation based assays, DNA chip technology and biosensor
CC      applications
XX
XX      Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
SQ      Query Match      1.0%; Score 15; DB 1; Length 15;
      Best Local Similarity 100.0%; Pred. No. 1.7e+02;
      Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
      QY      1481 AAAAAAAAAAAAAA 1495
      Db      15 AAAAAAAAAAAAAA 1
RESULT 397

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```

ABL57059/c
ID      ABL57059 standard; DNA; 15 BP.
XX
XX      ABL57059;
XX
XX      22-JUL-2002 (first entry)
XX
XX      Hydrazide precursor phosphoramidite oligonucleotide O33.
XX
XX      Macromolecule; hydrazide; immobilisation; ss.
XX
XX      Synthetic.
XX
FH      Key      Location/Qualifiers
FT      modified_base 1
FT      /tag= b
FT      /note= "phosphoramidite linkage"
FT      modified_base 1
FT      /tag= a
FT      /mod_base= OTHER
FT      /note= "4-((2-cyanoethyl)-(diisopropylamino)
FT      phosphanyloxyethyl)-benzoic acid methyl ester"
FT      modified_base 15
FT      /tag= c
FT      /mod_base= OTHER
FT      /note= "3' Cy3 dye"
XX
XX      WO200214558-A2.
XX
XX      21-FEB-2002.
XX
XX      10-AUG-2001; 2001WO-US041663.
XX
XX      11-AUG-2000; 2000WO-US022205.
XX
XX      (NANO-) NANOGEN INC.
XX
XX      Raddatz S, Mueller-Ibeler J, Schweitzer M, Bruecher C, Windhab N;
PI      Havens JR, Onofrey TU, Greef CH, Wang D;
XX
XX      WPI; 2002-404476/43.
XX
XX      Compound for binding macromolecule to substrate surface or conjugation
PT      targets, contains phosphorous containing reactive group, hydrazide
PT      protecting group and benzene ring, and has predefined formula.
XX
XX      Example 3; Page 43; 120pp; English.
XX
XX      The present sequence is of a hydrazine treated hydrazide precursor
CC      phosphoramidite 15-mer, designated oligo O33, which was produced in an
CC      example from the invention. The invention describes an improved process
CC      for immobilisation of macromolecules including DNA, RNA, peptide nucleic
CC      acids, pyranosyl-RNA and peptides, especially macromolecules containing
CC      multiple reactive sites, to a substrate surface or other conjugation
CC      target. It also describes the preparation of oligos containing one or
CC      more hydrazides, which can be used for conjugation to surface binding
CC      moieties, or for other conjugation reactions. The process is useful e.g.
CC      in nucleic acid hybridisation based assays, DNA chip technology and
CC      biosensor applications
XX
XX      Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
SQ      Query Match      1.0%; Score 15; DB 1; Length 15;
      Best Local Similarity 100.0%; Pred. No. 1.7e+02;
      Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
      QY      1481 AAAAAAAAAAAAAA 1495
      Db      15 AAAAAAAAAAAAAA 1
RESULT 398
ABL57061/c

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```
ID ABL57061 standard; DNA; 15 BP.
XX
AC ABL57061;
XX
DT 22-JUL-2002 (first entry)
XX
DE Hydrazide precursor phosphoramidite oligonucleotide O37.
XX
KW Macromolecule; hydrazide; immobilisation; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..15
FT /tag= b
FT /note= "phosphoramidite linkage"
FT modified_base 1
FT /tag= a
FT /mod_base= OTHER
FT /note= "1,3-Bis-(3',5'-bis(ethyloxycarbonyl)
FT phenylcarbonylamido)-2-((2''-cyanoethyloxy)
FT (diisopropylamino)-phosphanyloxy)-propane"
FT modified_base 15
FT /tag= c
FT /mod_base= OTHER
FT /note= "3' Cy3 dye"
XX
PN WO200214558-A2.
XX
PD 21-FEB-2002.
XX
PF 10-AUG-2001; 2001WO-US041663.
XX
PR 11-AUG-2000; 2000WO-US022205.
XX
PA (NANO-) NANOGEN INC.
XX
PI Raddatz S, Mueller-Ibeler J, Schweitzer M, Bruecher C, Windhab N;
PI Havens JR, Onofrey TJ, Greef CH, Wang D;
XX
DR WPI; 2002-404476/43.
XX
PT Compound for binding macromolecule to substrate surface or conjugation
PT targets, contains phosphorous containing reactive group, hydrazide
PT protecting group and benzene ring, and has predefined formula.
XX
PS Example 3; Page 43; 120pp; English.
XX
CC The present sequence is of a hydrazine treated hydrazide precursor
CC phosphoramidite 15-mer, designated oligo O37, which was produced in an
CC example from the invention. The invention describes an improved process
CC for immobilisation of macromolecules including DNA, RNA, peptide nucleic
CC acids, pyranosyl-RNA and peptides, especially macromolecules containing
CC multiple reactive sites, to a substrate surface or other conjugation
CC target. It also describes the preparation of oligos containing one or
CC more hydrazides, which can be used for conjugation to surface binding
CC moieties, or for other conjugation reactions. The process is useful e.g.
CC in nucleic acid hybridisation based assays, DNA chip technology and
CC biosensor applications
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 399
ABL57056/c

ID ABL57056 standard; DNA; 15 BP.
XX
AC ABL57056;
XX
DT 22-JUL-2002 (first entry)
XX
DE Hydrazide phosphoramidite oligonucleotide O31.
XX
KW Macromolecule; hydrazide; immobilisation; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..15
FT /tag= b
FT /note= "phosphoramidite linkage"
FT modified_base 1
FT /tag= a
FT /mod_base= OTHER
FT /note= "6-((2Cyanoethoxy)(diisopropylamino)
FT phosphanyloxy)-N'-tritylhexanohydrazide"
FT modified_base 15
FT /tag= c
FT /mod_base= OTHER
FT /note= "3' Cy3 dye"
XX
PN WO200214558-A2.
XX
PD 21-FEB-2002.
XX
PF 10-AUG-2001; 2001WO-US041663.
XX
PR 11-AUG-2000; 2000WO-US022205.
XX
PA (NANO-) NANOGEN INC.
XX
PI Raddatz S, Mueller-Ibeler J, Schweitzer M, Bruecher C, Windhab N;
PI Havens JR, Onofrey TJ, Greef CH, Wang D;
XX
DR WPI; 2002-404476/43.
XX
PT Compound for binding macromolecule to substrate surface or conjugation
PT targets, contains phosphorous containing reactive group, hydrazide
PT protecting group and benzene ring, and has predefined formula.
XX
PS Example 2; Page 40; 120pp; English.
XX
CC The present sequence is of a trityl deprotected hydrazide phosphoramidite
CC 15-mer, designated oligo O31, which was produced in an example from the
CC invention. The invention describes an improved process for immobilisation
CC of macromolecules including DNA, RNA, peptide nucleic acids, pyranosyl-
CC RNA and peptides, especially macromolecules containing multiple reactive
CC sites, to a substrate surface or other conjugation target. It also
CC describes the preparation of oligos containing one or more hydrazides,
CC which can be used for conjugation to surface binding moieties, or for
CC other conjugation reactions. The process is useful e.g. in nucleic acid
CC hybridisation based assays, DNA chip technology and biosensor
CC applications
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 400
ABL57060/c

ID ABL57060 standard; DNA; 15 BP.
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XX AC ABL57060;
XX DT 22-JUL-2002 (first entry)
XX DE Hydrizide precursor phosphoramidite oligonucleotide O34.
XX KW Macromolecule; hydrazide; immobilisation; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT modified_base 1..15
XX FT /*tag= b
XX FT /note= "phosphoramidite linkage"
XX FT modified_base 1
XX FT /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "Diethyl 5-((2-cyanoethoxy)(diisopropylamino)
XX FT phosphanyloxy)methyl isophthalate"
XX FT modified_base 15
XX FT /*tag= c
XX FT /mod_base= OTHER
XX FT /note= "3' Cy3 dye"
XX PN WO200214558-A2.
XX DT 21-FEB-2002.
XX PF 10-AUG-2001; 2001WO-US041663.
XX PR 11-AUG-2000; 2000WO-US022205.
XX PA (NANO-) NANOGEN INC.
XX PI Raddatz S, Mueller-Ibeler J, Schweitzer M, Bruecher C, Windhab N;
XX PI Havens JR, Onofrey IV, Greef CH, Wang D;
XX DR WPI; 2002-40476/43.
XX PT Compound for binding macromolecule to substrate surface or conjugation
XX PT targets, contains phosphorous containing reactive group, hydrazide
XX PT protecting group and benzene ring, and has predefined formula.
XX PS Example 3; Page 43; 120pp; English.
XX CC The present sequence is of a hydrazine treated hydrazide precursor
XX CC phosphoramidite 15-mer, designated oligo O34, which was produced in an
XX CC example from the invention. The invention describes an improved process
XX CC for immobilisation of macromolecules including DNA, RNA, peptide nucleic
XX CC acids, pyranosyl-RNA and peptides, especially macromolecules containing
XX CC multiple reactive sites, to a substrate surface or other conjugation
XX CC target. It also describes the preparation of oligos containing one or
XX CC more hydrazides, which can be used for conjugation to surface binding
XX CC moieties, or for other conjugation reactions. The process is useful e.g.
XX CC in nucleic acid hybridisation based assays, DNA chip technology and
XX CC biosensor applications
XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1495
DB 15 AAAAAAAAAAAAAA 1
RESULT 401
ABK98141/c
ID ABK98141 standard; DNA; 15 BP.
XX

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```

AC ABK98141;
XX DT 07-OCT-2002 (first entry)
XX DE Triple helix forming associated oligonucleotide #26.
XX KW Triple-helix formation; purine-rich target sequence; double-helix DNA;
XX KW gene expression; regulatory sequence; pathogenic double-stranded DNA;
XX KW pathogenic bacteria; virus; replication; virulence; cancer;
XX KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.
XX OS Synthetic.
XX PN US6403302-B1.
XX PD 11-JUN-2002.
XX PF 16-DEC-1993; 93US-00168920.
XX PR 17-SEP-1992; 92US-00946976.
XX PA (CALY ) CALIFORNIA INST OF TECHNOLOGY.
XX PI Dervan PB, Beal PA;
XX DR WPI; 2002-536030/57.
XX PT A triple-helix comprising a double helical nucleic acid (DHNA) and an
XX PT oligonucleotide which binds in parallel and antiparallel orientation,
XX PT respectively, for targetting sequences on alternate strands of DHNA to
XX PT control gene expression.
XX PS Example 1; Fig 3B; 108pp; English.
XX CC The present invention relates to methods and oligonucleotides for forming
XX CC a triple-helix comprising a double helical nucleic acid comprising first
XX CC and second substantially complementary strands, and an oligonucleotide
XX CC bound to a purine-rich target sequence within the double helical nucleic
XX CC acid, where the oligonucleotide binds in a parallel and antiparallel
XX CC orientation, respectively, to target sequences on alternate strands of
XX CC the double helical nucleic acid. The method has therapeutic applications,
XX CC where gene expression is controlled by selective triple-helix formation
XX CC within expression regulatory sequences of a target gene. The
XX CC oligonucleotides can be used to form triple-helices, and are useful to
XX CC detect the presence or absence of specific sequences within genomic DNA
XX CC for diagnostic and therapeutic purposes. The oligonucleotides can be
XX CC selected to specifically bind to pathogenic double-stranded DNA including
XX CC specific sequences required by pathogenic bacteria or viruses for
XX CC replication or virulence, reducing their pathogenicity. Alternatively,
XX CC the oligonucleotide can be chosen to target a unique sequence of the
XX CC pathogen which is not found in the genome of pathogen's host. The
XX CC oligonucleotides can be used in cancer treatment by way of triple-helix
XX CC suppression of specific oncogenes including those of endogenous or viral
XX CC origin. Such therapeutic oligonucleotides are capable of forming triple-
XX CC helices with such sequences in cancerous cells containing the activated
XX CC oncogene, so preferentially killing or repressing the cancer causing
XX CC cell. The present sequence represents an oligonucleotide used in the
XX CC methods of the present invention
XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1495
DB 15 AAAAAAAAAAAAAA 1
RESULT 402
ABK98184/c
ID ABK98184 standard; DNA; 15 BP.
XX

```

XX ABK98184;
AC
XX
DT 07-OCT-2002 (first entry)
XX
DE Triple helix forming associated oligonucleotide #48.
XX
XX Triple-helix formation; purine-rich target sequence; double-helix DNA;
KW gene expression; regulatory sequence; pathogenic double-stranded DNA;
KW pathogenic bacteria; virus; replication; virulence; cancer; ss.
KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.
XX
OS Synthetic.
XX
PN US6403302-B1.
XX
PD 11-JUN-2002.
XX
PF 16-DEC-1993; 93US-00168920.
XX
PR 17-SEP-1992; 92US-00946976.
XX
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
XX
PI Dervan PB, Beal PA;
XX
XX WPI; 2002-536030/57.
XX
PT A triple-helix comprising a double helical nucleic acid (DHNA) and an
PT oligonucleotide which binds in parallel and antiparallel orientation,
PT respectively, for targeting sequences on alternate strands of DHNA to
PT control gene expression.
XX
PS Example 7; Fig 24A; 108pp; English.
XX
XX The present invention relates to methods and oligonucleotides for forming
CC a triple-helix comprising a double helical nucleic acid comprising first
CC and second substantially complementary strands, and an oligonucleotide
CC bound to a purine-rich target sequence within the double helical nucleic
CC acid, where the oligonucleotide binds in a parallel and antiparallel
CC orientation, respectively, to target sequences on alternate strands of
CC the double helical nucleic acid. The method has therapeutic applications,
CC where gene expression is controlled by selective triple-helix formation
CC within expression regulatory sequences of a target gene. The
CC oligonucleotides can be used to form triple-helices, and are useful to
CC detect the presence or absence of specific sequences within genomic DNA
CC for diagnostic and therapeutic purposes. The oligonucleotides can be
CC selected to specifically bind to pathogenic double-stranded DNA including
CC specific sequences required by pathogenic bacteria or viruses for
CC replication or virulence, reducing their pathogenicity. Alternatively,
CC the oligonucleotide can be chosen to target a unique sequence of the
CC pathogen which is not found in the genome of pathogen's host. The
CC oligonucleotides can be used in cancer treatment by way of triple-helix
CC suppression of specific oncogenes including those of endogenous or viral
CC origin. Such therapeutic oligonucleotides are capable of forming triple-
CC helices with such sequences in cancerous cells containing the activated
CC oncogene, so preferentially killing or repressing the cancer causing
CC cell. The present sequence represents an oligonucleotide used in the
CC methods of the present invention
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred.No.1.7e-02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
|||||
Db 15 AAAAAAAAAAAAAA 1

RESULT 403
ABZ37501/C

ID ABZ37501 standard; DNA; 15 BP.
XX
AC ABZ37501;
XX
DT 18-FEB-2003 (first entry)
XX
DE Oligonucleotide SEQ ID NO:622.
XX
KW Library; cleavage; display; diverse family; ss.
XX
OS Synthetic.
XX
PN WO200283872-A2.
XX
PD 24-OCT-2002.
XX
PF 17-APR-2002; 2002WO-US012405.
XX
PR 17-APR-2001; 2001US-00837306.
PR 24-OCT-2001; 2001US-00000516.
PR 25-OCT-2001; 2001US-00045674.
XX
XX (LADN/) LADNER R C.
PA (COHE/) COHEN E H.
PA (NAST/) NASTRI H G.
PA (ROOK/) ROOKEY K L.
PA (HOET/) HOET R.
PA (HOOG/) HOOGENBOOM H R J M.
XX
XX Ladhner RC, Cohen EH, Nastri HG, Rookey KL, Hoet R;
PI Hoogenboom HRJM;
XX
DR WPI; 2003-093015/08.
XX
PT Cleaving single-stranded nucleic acid sequences at a desired location by
PT contacting the nucleic acid with an single strand oligonucleotide
PT complementary to a nucleic acid region where cleavage is desired.
XX
PS Disclosure; Page 481; 485pp; English.
XX
XX The present invention describes a method for cleaving single-stranded
CC nucleic acid sequences at a desired location. Also described: (1) methods
CC for displaying or expressing a member of a diverse family of peptides,
CC polypeptides or proteins on the surface of a genetic package and
CC collectively displaying at least a part of the diversity of the family,
CC where the displayed or expressed peptide, polypeptide or protein is
CC encoded at least in part by a nucleic acid that has been cleaved at a
CC desired location; (2) a method for preparing single-stranded nucleic
CC acids; (3) a method for preparing a library comprising a collection of
CC genetic packages that display a member of a diverse family of peptides,
CC polypeptides or proteins and that collectively display at least a portion
CC of the family; (4) a vector comprising a DNA sequence encoding an
CC antibody variable region linked to a version of P111 anchor which does
CC not mediate infection of phage particles, and wild-type gene III; (5) a
CC method for producing a population or a library of immunoglobulin genes;
CC and (6) a library of immunoglobulins that comprise members having at
CC least one variable domain in which at least one of CDR1 and CDR2 contain
CC synthetic diversity and CDR3 diversity is captured from B cells. The
CC method is useful for cleaving single-stranded nucleic acid sequences at a
CC desired location, which can be subsequently used to produce libraries or
CC genetic packages that display and/or express a diverse family of
CC peptides, polypeptides or proteins. ABZ36912 to ABZ37510 and ABP55464 to
CC ABP55499 represent sequences used in the exemplification of the present
CC invention
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred.No.1.7e-02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
|||||

Db 15 AAAAAAAAAAAAAA 1

RESULT 404
ABV74142
ID ABV74142 standard; DNA; 15 BP.
AC ABV74142;
XX
XX
XX 23-JAN-2003 (first entry)
XX 5' End of cDNA library clone.
XX
KW G-protein coupled receptor; odourant; receptor; olfaction; array;
KW microarray; anosmia; attractant; aromatic; pesticide; ss.
XX
XX Synthetic.
XX
PN WO200277200-A2.
XX
PD 03-OCT-2002.
XX
XX 26-MAR-2002; 2002WO-US009559.
XX
XX 27-MAR-2001; 2001US-0279168P.
PR 31-JAN-2002; 2002US-0353392P.
XX
PA (INSC-) INSCENT INC.
XX
XX Woods D, Dimitratos S;
PI
XX WPI; 2003-0299930/02.
XX
XX Identifying nucleic acid encoding novel sex-linked-tissue-linked
PT receptors, useful for isolating odorant binding proteins or pesticide
PT alternatives, by analyzing sequences from a male- and female-specific
PT nucleic acid library.
XX
XX Disclosure; Fig 5; 83pp; English.
XX
XX The present sequence is that of the 5' end of a cDNA clone isolated from
CC a cDNA library e.g. a mosquito antenna library. A clone was isolated
CC using a method designed to rapidly array and normalize a complex cDNA
CC library obtained from a target species. Clones are arrayed into multi-
CC well plates. Each well contains 16 oligonucleotides (see ABV74137) with a
CC 5' polylinker, a poly-T run capable of binding cDNAs by their poly-A tail
CC and a unique 3' sequence, which allows an anchored oligonucleotide in
CC each well to selectively hybridise only to those cDNA clones with a
CC complementary 5' end. The unique 3' key sequences are designed to give a
CC comprehensive level of degeneracy since they are diverse and numerous
CC enough to ensure that every possible cDNA sequence can be bound by an
CC individual, specific oligonucleotide in a single well. The cDNA library
CC is heated to denature the clones into single stranded DNA, and an aliquot
CC is added to every well. The anchored oligonucleotide serves as the 3'
CC primer in PCR, and the common 5' region present in every cDNA clone
CC serves as the 5' priming site. Denaturing and washing leave anchored cDNA
CC in each well. The library is now arrayed and normalised. The method was
CC used to identify and isolate clones encoding G-protein coupled receptors,
CC especially odourant receptors, and active effectors involved in the
CC olfactory pathway of invertebrates and vertebrates, e.g. odourant binding
CC proteins, or other olfactory or neuronal proteins. The identified
CC receptors and proteins are useful for identifying compounds that reduce a
CC target animal's sensitivity to odours, for manufacturing compounds or
CC devices that mask odours, or trapping invertebrates with odourants.
CC Semiochemicals (e.g. aromatics or pheromone mimetics) can be developed
CC with desirable effects on specific species, for the development of pest
CC monitoring systems or non-toxic, species-specific pesticide alternatives,
CC for controlling insect feeding and breeding behaviour, detecting the
CC presence of small air-borne molecules, etc
XX
SQ Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 1.0%; Score 15; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.7e-02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
DB 1 AAAAAAAAAAAAAA 15

RESULT 405
ABV74141/c
ID ABV74141 standard; DNA; 15 BP.
XX
AC ABV74141;
XX
XX 23-JAN-2003 (first entry)
XX
DE Oligonucleotide used in cDNA library array.
XX
KW G-protein coupled receptor; odourant; receptor; olfaction; array;
KW microarray; anosmia; attractant; aromatic; pesticide; PCR; primer; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH modified_base 1
FT /*tag= a
FT /mod_base= OTHER
FT /note= "5' polylinker"
XX
XX WO200277200-A2.
XX
XX 03-OCT-2002.
XX
XX 26-MAR-2002; 2002WO-US009559.
XX
XX 27-MAR-2001; 2001US-0279168P.
PR 31-JAN-2002; 2002US-0353392P.
XX
XX (INSC-) INSCENT INC.
XX
XX Woods D, Dimitratos S;
PI
XX WPI; 2003-0299930/02.
XX
XX Identifying nucleic acid encoding novel sex-linked-tissue-linked
PT receptors, useful for isolating odorant binding proteins or pesticide
PT alternatives, by analyzing sequences from a male- and female-specific
PT nucleic acid library.
XX
XX Disclosure; Fig 5; 83pp; English.
XX
XX The present sequence is that of a poly-T oligonucleotide used in a method
CC designed to rapidly array and normalize a complex cDNA library obtained
CC from a target species. Clones are arrayed into multi-well plates. Each
CC well contains 16 oligonucleotides with a 5' polylinker, a poly-T run
CC capable of binding cDNAs by their poly-A tail and a unique 3' sequence,
CC which allows an anchored oligonucleotide in each well to selectively
CC hybridise only to those cDNA clones with a complementary 5' end. The
CC unique 3' key sequences are designed to give a comprehensive level of
CC degeneracy since they are diverse and numerous enough to ensure that
CC every possible cDNA sequence can be bound by an individual, specific
CC oligonucleotide in a single well. The cDNA library is heated to denature
CC the clones into single stranded DNA, and an aliquot is added to every
CC well. The anchored oligonucleotide serves as the 3' primer in PCR, and
CC the common 5' region present in every cDNA clone serves as the 5' priming
CC site. Denaturing and washing leave anchored cDNA in each well. The
CC library is now arrayed and normalised. The method was used to identify
CC and isolate clones encoding G-protein coupled receptors, especially
CC odourant receptors, and active effectors involved in the olfactory
CC pathway of invertebrates and vertebrates, e.g. odourant binding proteins,
CC or other olfactory or neuronal proteins. The identified receptors and
CC proteins are useful for identifying compounds that reduce a target
CC animal's sensitivity to odours, for manufacturing compounds or devices

CC that mask odours, or trapping invertebrates with odourants.
 CC Semiochemicals (e.g. aromatics or pheromone mimetics) can be developed
 CC with desirable effects on specific species, for the development of pest
 CC monitoring systems or non-toxic, species-specific pesticide alternatives,
 CC for controlling insect feeding and breeding behaviour, detecting the
 CC presence of small air-borne molecules, etc
 XX
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
 |||||
 Db 15 AAAAAAAAAAAAAA 1

RESULT 406
 ABV75865/C
 ID ABV75865 standard; DNA; 15 BP.

XX
 AC ABV75865;
 DT 05-FEB-2003 (first entry)
 XX
 DE Oligonucleotide T15-Q-CDPI3.
 XX
 KW Deprotection; phosphoramidite; ss.
 XX
 OS Synthetic.

FH Key Location/Qualifiers
 FT modified_base 1. .15
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "phosphoramidite linkage"
 FT modified_base 15
 FT /tag= b
 FT /mod_base= OTHER
 FT /note= "3' Q-CDPI3"

XX WO200272864-A2.

XX 19-SEP-2002.

XX 04-MAR-2002; 2002WO-US0067739.

XX 08-MAR-2001; 2001US-0274309P.

XX (PEKE) PE CORP NY.

XX Nelson J;

XX WPI; 2003-046740/04.

XX New oligonucleotide deprotection reagent useful for deprotecting
 FT oligonucleotide comprises an active methylene compound and an amine
 PT reagent.

XX Example 2; Page 25; 46pp; English.

XX The present invention provides a method for deprotection of an
 CC oligonucleotide. This involves reacting a protected oligonucleotide,
 CC which is preferably covalently attached to a solid support through a
 CC linkage, with a deprotection reagent comprising an active methylene
 CC compound and an amine reagent. The process and reagent minimise side-
 CC reactions leading to certain impurities that contaminate synthetic
 CC oligonucleotides. The present sequence is a T15 phosphoramidite
 CC oligonucleotide having a quencher moiety (Q) and minor groove binder
 CC (CDPI3) at the 3' end, which was synthesised in an example of the
 CC invention. This protected oligonucleotide was treated either with 15%
 CC ethanolic ammonia or with 3% diethylmalonate (DEM) dissolved in 15%

CC ethanolic ammonia for 2 hours at 55 degrees C. HPLC analysis showed that
 CC deprotection without DEM yielded a complex mixture of products containing
 CC only 26.5% of the desired product. When DEM was used, 76.8% of the
 CC desired product was obtained

XX Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
 |||||
 Db 15 AAAAAAAAAAAAAA 1

RESULT 407
 ADA14836
 ID ADA14836 standard; DNA; 15 BP.

XX ADA14836;

XX 06-NOV-2003 (first entry)

XX Hairpin target sequence, #1, used in an example of the invention.

XX Hairpin sensor; hairpin loop; complementary probe; inverse repeat arm;
 KW quenchable fluorescing agent; microarray; semiconductor; nanocrystal;
 KW rhodamine B-labelled dye; detection; gold support; ss.
 XX
 OS Synthetic.

FH Key Location/Qualifiers
 FT misc_binding 1. .15
 FT /tag= a
 FT /bound_moiety= "Hairpin oligonucleotide #1"
 FT /note= "Forms a double-stranded region with the hairpin
 FT oligonucleotide shown in example 2"

XX US2003013109-A1.

XX 16-JAN-2003.

XX 21-JUN-2002; 2002US-00176055.

XX 21-JUN-2001; 2001US-0299460P.

XX (BALL/) BALLINGER C T.

XX (LOCA/) LOCASCIO M.

XX (LAND/) LANDRY D P.

XX Ballinger CT, Locascio M, Landry DP;

XX WPI; 2003-596312/56.

XX Hairpin sensor useful for detecting a target nucleotide sequence in a
 FT sample, comprises a hairpin loop assembly including a complementary probe
 FT and a quenchable fluorescing agent.

XX Example 2; Page 11; 16pp; English.

XX The invention discloses a hairpin sensor comprising a hairpin loop
 CC assembly including a complementary probe positioned between a first
 CC inverse repeat arm and a second inverse repeat arm, and a quenchable
 CC fluorescing agent joined, directly or indirectly, to the end of the
 CC second inverse repeat arm of the hairpin loop assembly opposite the
 CC complementary probe. Also claimed is a microarray comprising the hairpin
 CC sensor, where the end of the first inverse repeat arm opposite the
 CC complementary probe is bound, directly or indirectly, to a support, a kit
 CC for detecting a target nucleotide sequence in a sample comprising the
 CC hairpin sensor, and a support, and a hairpin sensor system, in which the
 CC particle is conductive or semi-conductive, including at least one of the
 CC above hairpin sensor assemblies. The hairpin sensor further comprises a

CC functional group joined to the end of the first inverse repeat arm
 CC opposite the complementary probe, or first spacer opposite the first
 CC inverse repeat arm, the functional group selected from amino, carboxyl,
 CC thiol and hydroxyl. Further, the sensor comprises a ligand positioned
 CC between the second inverse repeat arm and the quenchable fluorescing
 CC agent, where the ligand is selected from mercapto, hydroxyl, amino,
 CC nitrile and carboxyl, carboxylic acid, organic acid and amino acid. The
 CC second spacer is positioned between the second inverse repeat arm and the
 CC quenchable fluorescing agent which comprises a semiconductor nanocrystal
 CC or rhodamine B-labelled dye. Within the microarray the support is capable
 CC of accepting a charge. At least one hairpin sensor comprises two or more
 CC hairpin sensors. The two or more hairpin sensors include complementary
 CC probes that are the same or different and respective quenchable
 CC fluorescing agents that are the same or different. The two or more
 CC hairpin sensors are arranged in a spatially-defined pattern. The sensor
 CC and system are useful for detecting a target nucleotide sequence in a
 CC sample. Further, the method involves identifying the target nucleotide
 CC sequence by the location of the complementary probe to which the target
 CC nucleotide sequence binds. The two or more hairpin sensors include
 CC complementary probes or quenchable fluorescing agents, that are
 CC different. The sequence presented is the hairpin oligonucleotide target
 CC sequence, #1, used in an example of the invention.

XX
 SQ Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
 DB 1 AAAAAAAAAAAAAA 15

RESULT 408
 ADB68520/C
 ID ADB68520 standard; DNA; 15 BP.
 AC ADB68520;
 DT 04-DEC-2003 (first entry)
 DE Single-base mismatch oligonucleotide SEQ ID 10 DNA.
 XX hydroxyproline nucleic acid; HypNA; PNA; peptide nucleic acid;
 KW gene expression; respiration; secretion; signalling;
 KW ion-channel activity; cell motility; developmental phenotype;
 KW tumour regression; single-base mismatch; ss;
 KW phosphono-peptide nucleic acid; ppNA.
 OS Synthetic.
 XX WO2003068798-A2.
 PN 21-AUG-2003.
 XX 07-FEB-2003; 2003WO-US003904.
 PF 09-FEB-2002; 2002US-00072975.
 PR (ACTI-) ACTIVE MOTIF.
 PA Efimov V, Fernandez J, Archdeacon D, Archdeacon J, Choob M;
 PI WPI; 2003-689653/65.
 DR Method of inhibiting expression of genes or RNA transcripts, useful for
 PT therapy and determining effects of genes, by administering oligomers
 PT containing hydroxyproline nucleic acid.
 XX Example 20; Page 234; 240pp; English.
 PS The invention relates to a novel method of inhibiting the expression of

CC one or more genes or RNA transcripts by administering at least one
 CC oligonucleotide analogue that includes at least one hydroxyproline
 CC nucleic acid (HypNA) monomer to a cell or organism or their extracts. The
 CC oligonucleotides of the invention may be used to monitor properties
 CC including gene expression, respiration, secretion, signalling, ion-
 CC channel activity, cell motility, developmental phenotype and tumour
 CC regression. Furthermore, they may be utilised to determine the effects of
 CC particular genes, as antisense or homologous recombination constructs
 CC e.g. for creating animal models of disease and finally, for increasing
 CC the activity of some enzymes, such as polymerases. The current sequence
 CC is that of the single-base mismatch oligonucleotide SEQ ID 10 DNA of the
 CC invention. This sequence may also comprise a peptide nucleic acid (PNA),
 CC a phosphono-PNA (ppNA) or a HypNA.

XX
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
 DB 15 AAAAAAAAAAAAAA 1

RESULT 409
 ADC18592/C
 ID ADC18592 standard; DNA; 15 BP.
 AC ADC18592;
 XX 18-DEC-2003 (first entry)
 DT Annealing control primer Oligo-dT15 SEQ ID NO:54.
 DE annealing control primer; ACP; annealing specificity;
 KW nucleic acid amplification; hybridisation; DNA fingerprinting;
 KW genomic DNA; RNA fingerprint; primer; ss.
 XX Synthetic.
 OS WO2003050305-A1.
 PN 19-JUN-2003.
 XX 19-SEP-2002; 2002WO-KR001781.
 PF 08-DEC-2001; 2001WO-KR002133.
 PR 01-MAY-2002; 2002WO-KR000816.
 XX (SEEG-) SERGENE INC.
 PA Chun J;
 PI WPI; 2003-627256/59.
 DR Annealing control primer to improve annealing specificity in nucleic acid
 PT amplification, has region complementary to target, arbitrary nucleotide
 PT sequence, regulator with universal base/non-discriminatory base analog.

Example 2; SEQ ID NO 54; 190pp; English.

XX The present invention describes an annealing control primer (ACP) (I) for
 XX improving the annealing specificity in nucleic acid amplification. (I)
 CC has a 3'-end portion with a nucleotide sequence complementary to a site
 CC on a template nucleic acid for hybridisation, a 5'-end portion having a
 CC pre-selected arbitrary nucleotide sequence, and a regulator portion
 CC between the 3' and 5'-end portions, comprising a universal or non-
 CC discriminatory base analogue, where the regulator portion is capable of
 CC regulating an annealing portion of the primer in association with
 CC annealing temperature. (I) is useful for improving annealing specificity
 CC in nucleic acid amplification. (I) is useful for amplifying a nucleic
 CC acid sequence from a DNA or a mixture of nucleic acids, for selectively

CC amplifying a target nucleic acid sequence from a DNA, and for selectively
 CC amplifying a target nucleic acid sequence from a mRNA, by reverse
 CC transcribing the mRNA and performing an amplification reaction using (I).
 CC (I) is also useful for detecting DNA complementary to differentially
 CC expressed mRNA in two or more nucleic acid samples, by reverse
 CC transcribing the mRNA and performing an amplification reaction using (I).
 CC (I) is also useful for rapidly amplifying a target cDNA fragment
 CC comprising a cDNA region corresponding to the 3'-end or 5'-end region of
 CC an mRNA, for amplifying a population of full-length double-stranded cDNAs
 CC complementary to mRNAs, and amplifying 5'-enriched double-stranded cDNAs
 CC complementary to mRNA. (I) is also useful for amplifying more than one
 CC target nucleotide sequence simultaneously using more than one pair of
 CC primers in the same reaction, where the primers are derived from (I), for
 CC producing a DNA fingerprint of genomic DNA (gDNA), for producing a RNA
 CC fingerprint of an mRNA sample, identifying conserved homology segments in
 CC a multigene family from a mRNA sample, and for identifying conserved
 CC homology segments in a multigene family from gDNA. (I) is also useful for
 CC identifying a nucleotide variation in a target nucleic acid, and for
 CC mutagenesis in a target nucleic acid. The present sequence represents a
 CC primer which is used in the exemplification of the present invention.

XX Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
 SQ Query Match 1.0%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
 Db 15 AAAAAAAAAAAAAA 1

RESULT 410
 AAX18369/C
 ID AAX18369 standard; DNA; 16 BP.
 XX AAX18369;
 AC AAX18369;
 DT 11-MAY-1999 (first entry)
 XX RT-PCR primer of the invention SEQ ID 10.
 DE RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
 KW RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
 XX Synthetic.
 OS JP11032765-A.
 PN 09-FEB-1999.
 PD 18-JUL-1997; 97JP-00208312.
 XX 18-JUL-1997; 97JP-00208312.
 PR (TAKI) TAKARA SHUZO CO LTD.
 PA WPI; 1999-183822/16.
 DR Peptides having at least two new nucleotides - useful as primers in RT-PCR.
 XX Disclosure; Page 10; 19pp; Japanese.

XX This sequence represents a primer of the invention. The invention relates
 CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
 CC -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
 CC a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
 CC natural number indicating the repetition of alpha; beta, delta = V or N;
 CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
 CC thymine; gamma = thymine; k = natural number of 3 or over indicating the
 CC repetition of gamma, in which thymine expressed by gamma is composed of
 CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
 CC useful as primers for RT-PCR and determination of base sequences. The new

CC sequences allow for reproductive and highly efficient analysis of gene
 CC sequences
 XX Sequence 16 BP; 1 A; 1 C; 0 G; 14 T; 0 U; 0 Other;
 SQ Query Match 1.0%; Score 15; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAAA 1494
 Db 15 TAAAAAAAAAAAAA 1

RESULT 411
 ABL57075
 ID ABL57075 standard; DNA; 16 BP.
 XX ABL57075;
 AC ABL57075;
 DT 22-JUL-2002 (first entry)
 XX Molecular beacon target sequence.
 DE Molecular beacon; fluorophore; nanoparticle; nucleic acid detection; ss.
 KW Synthetic.
 OS WO200218951-A2.
 PN 07-MAR-2002.
 PD 29-AUG-2001; 2001WO-US041941.
 XX 29-AUG-2000; 2000US-0228728P.
 PR 30-MAR-2001; 2001US-0280350P.
 XX (UYRQ) UNIV ROCKEFELLER.
 PA Dubertret B, Calame M, Libhaber A;
 PI WPI; 2002-404569/43.
 DR Sensitive detecting proximity changes in a system that utilizes an
 PT interacting fluorophore and quencher, for high sensitivity applications,
 PT involves utilizing a metal surface as quencher.

Example 3; Page 30; 62pp; English.

XX The present sequence is that of a perfectly matched target sequence for a
 CC molecular beacon comprising an oligonucleotide probe (see ABL57069)
 CC covalently attached at the 3' end to fluorescent dye and at the 5' end to
 CC a nanoparticle. In the native state, the probe forms a hairpin
 CC conformation with hybridised termini. The proximity of the fluorophore
 CC and quencher (gold nanoparticle) in the molecular beacon results in
 CC little or no detectable fluorescence. Upon hybridisation of the central
 CC complementary stretch of the probe to a target sequence, such as the
 CC present sequence, the hairpin undergoes a conformational change resulting
 CC in an increase in fluorescence, the extent of which is proportional to
 CC the amount of target sequence present. Single mismatches can be detected.
 CC The invention relates generally to the use of metal surface quenchers
 CC such as particles or films for high sensitivity applications in, for
 CC example, detection and diagnostic systems

XX Sequence 16 BP; 15 A; 0 C; 1 G; 0 T; 0 U; 0 Other;
 SQ

```

Query Match      1.0%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
DB 2 AAAAAAAAAAAAAA 16

RESULT 412
ABQ94572
ID ABQ94572 standard; DNA; 16 BP.
XX
AC ABQ94572;
XX
DT 28-OCT-2002 (first entry)
XX
DE Tumour suppression-related oligonucleotide #223.
XX
KW Tumour; cytostatic; antiviral; neuroprotective; nootropic; neuroleptic;
KW tumour suppression; tumour reversion; apoptosis; viral resistance; human;
KW viral infection; cell degeneration disease; neurodegeneration; ds;
KW Alzheimer's disease; schizophrenia; immune disease; inflammatory disease.
XX
OS Homo sapiens.
XX
PN FR2819824-A1.
XX
PD 26-JUL-2002.
XX
PF 23-JAN-2001; 2001FR-00000899.
XX
PR 23-JAN-2001; 2001FR-00000899.
XX
PA (MOL-) MOLECULAR ENGINES LAB SA.
XX
PI Teleman A, Anson R, Tuijnder M, Susini L;
XX
DR WPI; 2002-610803/66.
XX
PT New nucleic acid implicated e.g. in tumor suppression, useful for
PT diagnosis of tumors, viral infection and cellular degeneration and for
PT drug screening.
XX
PS Claim 1; Page 90; 623pp; French.
XX
CC The present invention relates to novel human nucleic acid sequences (I).
CC The present sequence is one such nucleic acid sequence. Expression of (I)
CC are implicated in tumour suppression or reversion and apoptosis and viral
CC resistance. (I) are useful as probes or primers for detecting,
CC identifying, measuring and/or amplifying nucleic acid sequences, as
CC antisense reagents and for recombinant production of polypeptides. (I),
CC polypeptides (II) encoded by (I), vector containing (I), cells containing
CC these vectors and antibodies (AB) against (II) are all useful for
CC treatment/prevention of viral, tumour and cell degeneration diseases
CC (especially neurodegeneration, such as Alzheimer's disease and
CC schizophrenia). Analysing the expression of (I) is also useful for
CC diagnosis and/or prognosis of such diseases. Transgenic animals carrying
CC (I) are used for studying the aetiology of these diseases (also immune
CC and inflammatory diseases). Note: In the present specification, SEQ ID 1
CC to 2280 are claimed in Claim 1, however only SEQ ID 1 to 2270 are shown
CC in the specification
XX
SQ Sequence 16 BP; 11 A; 1 C; 1 G; 3 T; 0 U; 0 Other;

Query Match      1.0%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1477 TGCTAAAAAAAAAAAA 1491
DB 2 TGCTAAAAAAAAAAAA 16

RESULT 413
AAD57845
ID AAD57845 standard; DNA; 16 BP.
XX
AC AAD57845;
XX
DT 20-NOV-2003 (first entry)
XX
DE Target oligonucleotide #2 used in nonlinear optical technique.
XX
KW Nonlinear optical technique; screening; ss.
XX
OS Unidentified.
XX
PN WO2003064991-A2.
XX
PD 07-AUG-2003.
XX
PF 17-JUL-2002; 2002WO-US022681.
XX
PR 17-JUL-2001; 2001US-0306040P.
PR 23-OCT-2001; 2001US-0347821P.
PR 06-FEB-2002; 2002US-0354668P.
XX
PA (SALA/) SALAFSKY J S.
XX
PI Salafsky JS;
XX
DR WPI; 2003-646172/61.
XX
PT Screening candidate binding partner(s) for binding to test molecule by
PT applying external force field to sample in homogeneous phase,
PT illuminating sample with light beam(s) at fundamental frequencies, and
PT measuring physical properties.
XX
PS Disclosure; Fig 20-B; 146pp; English.
XX
CC The present invention relates to a method for detecting interactions
CC between biological components using a nonlinear optical technique. The
CC invention is used for screening candidate binding partner(s) for binding
CC to test molecule. It can also be used to detect changes in orientation or
CC conformation of the probe and/or target. The present sequence is a target
CC oligonucleotide used in nonlinear optical technique
XX
SQ Sequence 16 BP; 15 A; 0 C; 1 G; 0 T; 0 U; 0 Other;

Query Match      1.0%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
DB 2 AAAAAAAAAAAAAA 16

RESULT 414
ADB68508/c
ID ADB68508 standard; DNA; 16 BP.
XX
AC ADB68508;
XX
DT 04-DEC-2003 (first entry)
XX
DE PNA-HypNA hybridisation oligomer.
XX
KW hydroxyproline nucleic acid; HypNA; PNA; peptide nucleic acid;
KW gene expression; respiration; secretion; signalling;
KW ion-channel activity; cell motility; developmental phenotype;
KW tumour regression; hybridisation; ss; serine nucleic acid; SerNA;
KW phosphono-peptide nucleic acid; pPNA.
XX
OS Synthetic.

```



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PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX WPI; 1997-259017/23.
XX
XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
XX stability - useful for treating e.g. tumour angiogenesis, psoriasis,
XX rheumatoid arthritis, etc., in a human patient.
XX
XX Claim 4; Page 79; 218pp; English.
XX
XX The present invention describes nucleic acid molecules which modulate the
XX synthesis, expression and/or stability of a mRNA encoding 1 or more
XX receptors of vascular endothelial growth factor (VEGF). A patient
XX (preferably human) having a condition associated with the level of the
XX fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
XX receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
XX angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
XX treated by administering the nucleic acid molecule or the expression
XX vector to the patient. AAX67275 to AAX75752 represent specific examples
XX of nucleic acid molecules from the present invention
XX
XX Sequence 17 BP; 0 A; 2 C; 0 G; 0 T; 15 U; 0 Other;
XX
XX Query Match 1.0%; Score 15; DB 1; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 2.1e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1481 AAAAAAAAAAAAAA 1495
XX Db 15 AAAAAAAAAAAAAA 1
XX
XX RESULT 417
XX AAV37934/C
XX ID AAV37934 standard; cDNA; 17 BP.
XX AC AAV37934;
XX DT 05-OCT-1998 (first entry)
XX DE Primer of the specification.
XX
XX KW Leukocyte; IgA nephropathy; diagnosis; treatment; PCR primer; ss.
XX OS Synthetic.
XX PN WO9824815-A1.
XX
XX PD 11-JUN-1998.
XX PF 05-DEC-1997; 97WO-JP004469.
XX PR 05-DEC-1996; 96JP-00325752.
XX PS (KYOW ) KYOWA HAKKO KOGYO KK.
XX PA (KAZU-) KAZUSA DNA RES INST FOUND.
XX
XX PI Ishiwata T, Sakurada M, Nishimura A, Nakagawa S, Kuga T, Nishi T;
XX Nomura N, Nagase T, Sawada S, Takei M;
XX WPI; 1998-333259/29.
XX
XX Protein from leukocytes and DNA encoding it - useful as reagents for
XX diagnosing and treating IgA nephropathy.
XX
XX Example 2; Page 33; 41pp; Japanese.
XX
XX PCR primers AAV37933-39 are used in the course of the invention. The
XX specification describes a novel protein isolated from leukocytes of
XX patients with IgA nephropathy. Oligonucleotides based on the DNA sequence
XX encoding this protein are useful as reagents for diagnosing and treating
XX IgA nephropathy
XX
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 15; DB 1; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 2.1e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1481 AAAAAAAAAAAAAA 1495
XX Db 16 AAAAAAAAAAAAAA 2
XX
XX RESULT 418
XX AAA30181/C
XX ID AAA30181 standard; DNA; 17 BP.
XX AC AAA30181;
XX DT 16-AUG-2000 (first entry)
XX DE PCR primer GT15G used in pollenosis associated gene identification.
XX
XX KW Pollenosis-associated protein; high pollen-specific immunoglobulin E;
XX IgE; diagnose; cedar pollenosis; treatment; human; PCR primer; ss.
XX OS Synthetic.
XX PN WO200020575-A1.
XX
XX PD 13-APR-2000.
XX PF 06-OCT-1999; 99WO-JP005506.
XX PR 06-OCT-1998; 98JP-00284610.
XX PA (GENO-) GENOX RES INC.
XX
XX PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
XX Obayashi I, Imai Y, Lu N, Ogawa K;
XX WPI; 2000-317712/27.
XX
XX Gene highly expressed in patients with high cedar pollen-specific IgE
XX levels, useful for diagnosing pollenosis, and screening candidate
XX compounds for pollenosis treatment.
XX
XX Example 6; Page 38; 44pp; Japanese.
XX
XX This sequence represents a PCR primer used in the identification of a
XX human pollenosis associated gene. The gene is highly expressed in
XX individuals with high pollen-specific immunoglobulin E (IgE) levels. The
XX invention relates to the nucleotide sequence encoding the pollenosis
XX associated protein, diagnosing pollenosis and screening candidate
XX compounds for treating pollenosis. The gene can be used in diagnosing
XX pollenosis, particularly cedar pollenosis, and screening candidate
XX compounds for pollenosis treatment
XX
XX Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 15; DB 1; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 2.1e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1481 AAAAAAAAAAAAAA 1495
XX Db 16 AAAAAAAAAAAAAA 2
XX
XX RESULT 419
XX AAA30180/C
XX ID AAA30180 standard; DNA; 17 BP.
XX AC AAA30180;
XX

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DT 16-AUG-2000 (first entry)
XX PCR primer GT15C used in pollenosis associated gene identification.
DE
XX
XX Pollenosis-associated protein; high pollen-specific immunoglobulin E;
KW IGE; diagnose; cedar pollenosis; treatment; human; PCR primer; ss.
XX
XX Synthetic.
OS
XX WO200020575-A1.
PN
XX 13-APR-2000.
PD
XX
XX 06-OCT-1999; 99WO-JP005506.
XX
XX 06-OCT-1998; 98JP-00284610.
PR
XX (GENO-) GENOX RES INC.
PA
XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Lu N, Ogawa K;
PI
XX WPI; 2000-317712/27.
DR
XX Gene highly expressed in patients with high cedar pollen-specific IGE
XX levels, useful for diagnosing pollenosis, and screening candidate
XX compounds for pollenosis treatment.
XX
XX Example 6; Page 38; 44pp; Japanese.
PS
XX This sequence represents a PCR primer used in the identification of a
XX human pollenosis associated gene. The gene is highly expressed in
XX individuals with high pollen-specific immunoglobulin E (IGE) levels. The
XX invention relates to the nucleotide sequence encoding the pollenosis
XX associated protein, diagnosing pollenosis and screening candidate
XX compounds for treating pollenosis. The gene can be used in diagnosing
XX pollenosis, particularly cedar pollenosis, and screening candidate
XX compounds for pollenosis treatment
XX
XX Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
SQ
Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1495
DB 16 AAAAAAAAAAAAAA 2
RESULT 420
AAZ35714/C
ID AAZ35714 standard; DNA; 17 BP.
XX
XX AAZ35714;
AC
XX 31-JAN-2000 (first entry)
DT
XX Murine gene anchor PCR primer SEQ ID NO:3.
DE
XX Rare expressed gene; analysis; expression; nucleic acid sample;
KW PCR primer; ss.
XX
XX Synthetic.
OS Mus sp.
XX
XX EP959141-A2.
PN
XX 24-NOV-1999.
PD
XX
XX 18-MAY-1999; 99EP-00109795.
PF
XX 20-MAY-1998; 98JP-00153651.
PR
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XX (HITA ) HITACHI LTD.
PA
XX Muramatsu T, Fujita T, Kiyama M, Irie T, Okano K;
PI
XX WPI; 2000-001284/01.
DR
XX Preparation of nucleic acid sample, useful for analysis of rare expressed
XX genes.
PT
XX Disclosure; Page 11; 22pp; English.
PS
XX
XX The present invention describes a process for the preparation of a
XX nucleic acid sample comprising: (a) providing a nucleic acid sample
XX having a plurality of species of sequences, and providing one or a
XX plurality of kinds of probes having a known sequence substantially
XX complementary to a portion of sequence of the nucleic acid sample; (b)
XX mixing and hybridizing the nucleic acid sample with probes; (c)
XX subsequently recovering nucleic acid molecules; or (i) providing a
XX nucleic acid sample having a plurality of species of sequences, and
XX providing one or a plurality of kinds of probes having a known sequence
XX substantially complementary to a portion of sequence of the nucleic acid
XX sample; (ii) mixing and hybridizing the nucleic acid sample with the
XX probes; (iii) treating the product of (ii) with nuclease activity of an
XX enzyme or the probe itself; and (iv) subsequently recovering the nucleic
XX acid molecules not digested by the nuclease activity in (iii); or (I)
XX providing a nucleic acid sample having a plurality of species of
XX sequences and oligonucleotides primer having predetermined sequences for
XX synthesizing DNA strands; (iii) providing one or a plurality of kinds of
XX probes having a known sequence substantially complementary to a portion
XX of a sequence of the nucleic acid sample having such a structure to
XX prevent a polymerase reaction from its 3' end and a nuclease reaction
XX from its 5' end; (III) mixing and hybridizing the nucleic acid sample
XX with the primers and probes; (IV) executing polymerase chain reaction for
XX the samples prepared in (III); and (V) subsequently recovering nucleic
XX acid molecules synthesized in (IV). The method is useful for the
XX preparation of a nucleic acid sample for the analysis of rare expressed
XX genes. The present sequence represents a PCR primer used in the
XX exemplification of the present invention
XX
XX Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;
SQ
Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1495
DB 16 AAAAAAAAAAAAAA 2
RESULT 421
AAZ82722/C
ID AAZ82722 standard; DNA; 17 BP.
XX
XX AAZ82722;
AC
XX 10-NOV-2000 (first entry)
DT
XX
XX Human Iga nephropathy-associated cDNA primer #63.
DE
XX Iga nephropathy-associated protein; diagnosis; treatment; antisense;
KW human; primer; ss.
XX
XX Homo sapiens.
OS
XX WO963085-A1.
PN
XX 09-DEC-1999.
PD
XX
XX 28-MAY-1999; 99WO-JP002855.
PF
XX 02-JUN-1998; 98JP-00152603.
PR
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XX PA (KYOW) KYOWA HAKKO KOGYO KK.
 XX PI Ishiwata T, Sakurada M, Kawabata A, Nakagawa S, Nishi T, Kuga T;
 XX PI Sawada S, Takei M, Shibata K, Furuya A;
 XX DR WPI; 2000-097328/08.
 XX CC DNA sequences preferentially expressed in IgA nephropathy patients,
 XX PT proteins encoded by them, and antibodies to those proteins.
 XX PS Claim 3; Page 170; 180pp; Japanese.
 XX CC This invention describes novel DNA sequences preferentially expressed in
 XX CC IgA nephropathy patients, and DNA sequences stringently hybridizing to
 XX CC them. Independent claims cover diagnostic reagents for IgA nephropathy
 XX CC incorporating the antisense sequences; the treatment of IgA nephropathy
 XX CC using the antisense sequences for mRNA inhibition; proteins associated
 XX CC with IgA nephropathy, containing sequences encoded by the DNA sequences;
 XX CC antibodies recognizing these proteins; the production of the proteins by
 XX CC culture of host cells transformed with DNA encoding them; diagnostic
 XX CC reagents for IgA nephropathy containing the antibodies; and compositions
 XX CC for the treatment of IgA nephropathy which contain the antibodies. The
 XX CC products of the invention can be used for the diagnosis and treatment of
 XX CC IgA nephropathy. This sequence represents a primer used in the isolation
 XX CC and identification of the human IgA nephropathy-associated proteins
 XX CC described in the method of the invention
 XX SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
 Query Match 1.0%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1481 AAAAAAAAAAAAAA 1495
 Db |||||
 16 AAAAAAAAAAAAAA 2
 RESULT 422
 AAX82721/C
 ID AAX82721 standard; DNA; 17 BP.
 AC AAX82721;
 XX 10-NOV-2000 (first entry)
 XX Human IgA nephropathy-associated cDNA primer #62.
 XX IgA nephropathy-associated protein; diagnosis; treatment; antisense;
 XX KW human; primer; ss.
 XX OS Homo sapiens.
 XX XX WO963085-A1.
 XX PD 09-DEC-1999.
 XX PF 28-MAY-1999; 99WO-JP002855.
 XX PR 02-JUN-1998; 98JP-00152603.
 XX PA (KYOW) KYOWA HAKKO KOGYO KK.
 XX PI Ishiwata T, Sakurada M, Kawabata A, Nakagawa S, Nishi T, Kuga T;
 XX PI Sawada S, Takei M, Shibata K, Furuya A;
 XX DR WPI; 2000-097328/08.
 XX CC DNA sequences preferentially expressed in IgA nephropathy patients,
 XX PT proteins encoded by them, and antibodies to those proteins.
 XX PS Claim 3; Page 170; 180pp; Japanese.

XX CC This invention describes novel DNA sequences preferentially expressed in
 XX CC IgA nephropathy patients, and DNA sequences stringently hybridizing to
 XX CC them. Independent claims cover diagnostic reagents for IgA nephropathy
 XX CC incorporating the antisense sequences; the treatment of IgA nephropathy
 XX CC using the antisense sequences for mRNA inhibition; proteins associated
 XX CC with IgA nephropathy, containing sequences encoded by the DNA sequences;
 XX CC antibodies recognizing these proteins; the production of the proteins by
 XX CC culture of host cells transformed with DNA encoding them; diagnostic
 XX CC reagents for IgA nephropathy containing the antibodies; and compositions
 XX CC for the treatment of IgA nephropathy which contain the antibodies. The
 XX CC products of the invention can be used for the diagnosis and treatment of
 XX CC IgA nephropathy. This sequence represents a primer used in the isolation
 XX CC and identification of the human IgA nephropathy-associated proteins
 XX CC described in the method of the invention
 XX SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;
 Query Match 1.0%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1481 AAAAAAAAAAAAAA 1495
 Db |||||
 16 AAAAAAAAAAAAAA 2
 RESULT 423
 AAZ36740/C
 ID AAZ36740 standard; DNA; 17 BP.
 AC AAZ36740;
 XX 13-MAR-2000 (first entry)
 XX Anchored oligo(dT) primer G715G used for modified differential display.
 XX Stimulus-regulated nucleic acid; sequence profile; nucleic acid level;
 XX KW differentially expressed nucleic acid; disease state; cancer;
 XX KW autoimmune disease; infectious disease; aging; developmental disorder;
 XX KW proliferative disorder; neurological disorder; toxicity; primer;
 XX KW treatment resistance; differential expression; drug discovery;
 XX KW growth factor; epidermal growth factor; radiation; stress; pathogen; ss.
 XX OS Synthetic.
 XX XX WO955913-A2.
 XX PD 04-NOV-1999.
 XX PF 27-APR-1999; 99WO-US009119.
 XX PR 27-APR-1998; 98US-0083331P.
 XX PR 27-AUG-1998; 98US-0098070P.
 XX PR 04-FEB-1999; 99US-0118624P.
 XX PA (KIMM-) KIMMEL CANCER CENT SIDNEY.
 XX PI McClelland M, Welsh J, Trenkle T;
 XX DR WPI; 2000-086388/07.
 XX PT Measuring expression of low abundance reduced complexity target nucleic
 XX PT acid molecules.
 XX PS Example 3; Page 91; 187pp; English.
 XX CC AAZ36739-41 represent oligo(dT) primers used for modified differential
 XX CC display, in the method of the invention. The specification describes a
 XX CC method for measuring the level of two or more nucleic acid molecules in a
 XX CC target. The method comprises contacting a probe with an arbitrarily or
 XX CC statistically sampled target and detecting the amount of specific binding
 XX CC of the target to the probe. The methods can be used to identify

CC differentially expressed nucleic acid molecules associated with disease
 CC states, such as cancer, autoimmune disease, infectious disease, aging,
 CC developmental disorder, proliferative disorder or neurological disorder.
 CC Alternatively the methods can be used to assess the efficacy or toxicity
 CC of or a resistance to a treatment. Also the methods can be used to
 CC determine differential expression of nucleic acid molecules in response
 CC to a stimulus, e.g. a chemical, drug or growth factor (especially
 CC epidermal growth factor), radiation, stress or a pathogen. The methods
 CC can also be used to determine co-regulated genes that can be potential
 CC targets for drug discovery

XX
 SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
 |||||
 Db 16 AAAAAAAAAAAAAA 2

RESULT 424
 AAA25448/c
 ID AAA25448 standard; DNA; 17 BP.

XX
 AC AAA25448;

XX
 DT 19-JUL-2000 (first entry)

XX
 DE Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1946.

XX
 KW Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
 KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
 KW Gene expression modification; cancer; phosphorothioate; endonuclease;
 KW anticancer; breast cancer; endometrium cancer; ss.

XX
 OS Homo sapiens.

XX
 PN WO9954459-A2.

XX
 PD 28-OCT-1999.

XX
 PF 19-APR-1999; 99WO-US008547.

XX
 PR 20-APR-1998; 98US-0082404P.

XX
 PR 23-JUN-1998; 98US-00103636.

XX
 PA (RIBO-) RIBOZYME PHARM INC.

XX
 PI Thompson JD, Beigelman L, Mcswiggen JA, Karpeisky A, Bellon L;
 PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haeberli P;
 PI Matulic-Adamic J;

XX
 DR WPI; 2000-013248/01.

XX
 PT New nucleic acids that interact, and optionally cleave, target sequences,
 PT used to treat cancer.

XX
 PS Claim 77; Page 79; 148pp; English.

XX
 CC The present invention describes nucleic acids (A) that interact stably
 CC with a target sequence and contain at least one phosphorodithioate
 CC link, having endonuclease activity. (A), and more generally any catalytic
 CC nucleic acid (A') that modulates expression of the oestrogen receptor
 CC gene, are used to treat cancer (particularly of breast or endometrium),
 CC in vivo or by transforming cells ex vivo and implanting treated cells, or
 CC because of the high selectivity for targeted RNA, (A) can also be used to
 CC correlate inhibition of gene expression with alterations in phenotype,
 CC particularly for identification of therapeutic targets, and as research
 CC reagents (for RNA, in the same way that restriction endonucleases are
 CC used with DNA). The combination of modifications in (A) improves

CC resistance to nucleases, binding affinity and/or activity. AAA23503 to
 CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
 CC AAA24748 to AAA25992 represent their corresponding target sequences.
 CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
 CC sequences, and AAA26107 to AAA26218 represent their corresponding target
 CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
 CC antisense oligonucleotides used in the exemplification of the present
 CC invention

XX
 SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
 |||||
 Db 17 AAAAAAAAAAAAAA 3

RESULT 425
 AAA25452/c
 ID AAA25452 standard; DNA; 17 BP.

XX
 AC AAA25452;

XX
 DT 19-JUL-2000 (first entry)

XX
 DE Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1950.

XX
 KW Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
 KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
 KW Gene expression modification; cancer; phosphorothioate; endonuclease;
 KW anticancer; breast cancer; endometrium cancer; ss.

XX
 OS Homo sapiens.

XX
 PN WO9954459-A2.

XX
 PD 28-OCT-1999.

XX
 PF 19-APR-1999; 99WO-US008547.

XX
 PR 20-APR-1998; 98US-0082404P.

XX
 PR 23-JUN-1998; 98US-00103636.

XX
 PA (RIBO-) RIBOZYME PHARM INC.

XX
 PI Thompson JD, Beigelman L, Mcswiggen JA, Karpeisky A, Bellon L;
 PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haeberli P;
 PI Matulic-Adamic J;

XX
 DR WPI; 2000-013248/01.

XX
 PT New nucleic acids that interact, and optionally cleave, target sequences,
 PT used to treat cancer.

XX
 PS Claim 77; Page 79; 148pp; English.

XX
 CC The present invention describes nucleic acids (A) that interact stably
 CC with a target sequence and contain at least one phosphorodithioate
 CC link, having endonuclease activity. (A), and more generally any catalytic
 CC nucleic acid (A') that modulates expression of the oestrogen receptor
 CC gene, are used to treat cancer (particularly of breast or endometrium),
 CC in vivo or by transforming cells ex vivo and implanting treated cells, or
 CC because of the high selectivity for targeted RNA, (A) can also be used to
 CC correlate inhibition of gene expression with alterations in phenotype,
 CC particularly for identification of therapeutic targets, and as research
 CC reagents (for RNA, in the same way that restriction endonucleases are
 CC used with DNA). The combination of modifications in (A) improves
 CC resistance to nucleases, binding affinity and/or activity. AAA23503 to
 CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and

CC AAA24748 to AAA25992 represent their corresponding target sequences.
 CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
 CC sequences, and AAA26107 to AAA26218 represent their corresponding target
 CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
 CC antisense oligonucleotides used in the exemplification of the present
 CC invention

XX SQ Sequence 17 BP; 0 A; 0 C; 1 G; 16 T; 0 U; 0 Other;
 Query Match 1.0%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
 DB 15 AAAAAAAAAAAAAA 1

RESULT 426
 AAC64203/C
 ID AAC64203 standard; DNA; 17 BP.
 XX AC AAC64203;
 XX DT 21-FEB-2001 (first entry)
 XX DE PCR anchor primer, SEQ ID NO:4, used in human gene 373 isolation.
 XX KW Human; pollinosis-associated gene 373; IGE; immunoglobulin E;
 KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
 KW drug screening; allergic disease; PCR primer; ss.
 XX OS Synthetic.
 XX PN WO200065046-A1.
 XX PD 02-NOV-2000.
 XX PF 26-APR-2000; 2000WO-JP002730.
 XX PR 27-APR-1999; 99JP-00120489.
 XX PA (GENO-) GENOX RES INC.
 XX PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
 PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
 XX WPI; 2000-687339/67.

XX Pollinosis-associated gene 373 undergoing significantly low expression in
 PT subjects with high cedar pollen-specific immunoglobulin-E levels, useful
 PT in diagnosis of allergic diseases and screening drug candidates.
 XX Example 6; Page 70; 80pp; Japanese.

XX The invention relates to the human pollinosis-associated gene 373 which
 CC exhibits significantly reduced expression in the T-cells of individuals
 CC with high cedar pollen-specific IGE (immunoglobulin E) levels. The gene
 CC was isolated from T-cells from individuals allergic to cedar pollen using
 CC the differential display method. The invention also relates also relates
 CC to the protein encoded by pollinosis gene 373; expression constructs and
 CC host cells comprising pollinosis-associated gene 373 nucleic acids;
 CC pollinosis-associated gene 373 primers and probes; antibodies against the
 CC protein encoded by the gene; methods of detection of pollinosis-
 CC associated gene 373 nucleic acids; and a method of diagnosis of allergic
 CC diseases via the detection of pollinosis-associated gene 373 nucleic
 CC acids. The invention additionally encompasses methods of screening drug
 CC candidates for the treatment of allergic disease by measuring the
 CC expression of pollinosis-associated gene 373 in pollen antigen-stimulated
 CC T-cells in the presence of a test compound relative to a control.
 CC Pollinosis-associated gene 373 is useful in the diagnosis of allergic
 CC diseases and in the screening of drug candidates for the treatment of
 CC such diseases. The present sequence represents a PCR primer used in the

CC isolation of human pollinosis-associated gene 373 cDNA .
 XX SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
 Query Match 1.0%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
 DB 16 AAAAAAAAAAAAAA 2

RESULT 427
 AAC64204/C
 ID AAC64204 standard; DNA; 17 BP.
 XX AC AAC64204;
 XX DT 21-FEB-2001 (first entry)
 XX DE PCR anchor primer, SEQ ID NO:5, used in human gene 373 isolation.
 XX KW Human; pollinosis-associated gene 373; IGE; immunoglobulin E;
 KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
 KW drug screening; allergic disease; PCR primer; ss.
 XX OS Synthetic.
 XX PN WO200065046-A1.
 XX PD 02-NOV-2000.
 XX PF 26-APR-2000; 2000WO-JP002730.
 XX PR 27-APR-1999; 99JP-00120489.
 XX PA (GENO-) GENOX RES INC.
 XX PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
 PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
 XX WPI; 2000-687339/67.

XX Pollinosis-associated gene 373 undergoing significantly low expression in
 PT subjects with high cedar pollen-specific immunoglobulin-E levels, useful
 PT in diagnosis of allergic diseases and screening drug candidates.
 XX Example 6; Page 70; 80pp; Japanese.

XX The invention relates to the human pollinosis-associated gene 373 which
 CC exhibits significantly reduced expression in the T-cells of individuals
 CC with high cedar pollen-specific IGE (immunoglobulin E) levels. The gene
 CC was isolated from T-cells from individuals allergic to cedar pollen using
 CC the differential display method. The invention also relates also relates
 CC to the protein encoded by pollinosis gene 373; expression constructs and
 CC host cells comprising pollinosis-associated gene 373 nucleic acids;
 CC pollinosis-associated gene 373 primers and probes; antibodies against the
 CC protein encoded by the gene; methods of detection of pollinosis-
 CC associated gene 373 nucleic acids; and a method of diagnosis of allergic
 CC diseases via the detection of pollinosis-associated gene 373 nucleic
 CC acids. The invention additionally encompasses methods of screening drug
 CC candidates for the treatment of allergic disease by measuring the
 CC expression of pollinosis-associated gene 373 in pollen antigen-stimulated
 CC T-cells in the presence of a test compound relative to a control.
 CC Pollinosis-associated gene 373 is useful in the diagnosis of allergic
 CC diseases and in the screening of drug candidates for the treatment of
 CC such diseases. The present sequence represents a PCR primer used in the
 CC isolation of human pollinosis-associated gene 373 cDNA

XX SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;
 Query Match 1.0%; Score 15; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 2.1e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0

QY 1481 AAAAAAAAAAAAAA 1495
Db 16 AAAAAAAAAAAAAA 2

RESULT 428
AAC64183/c
ID AAC64183 standard; DNA; 17 BP.
XX
AC AAC64183;
XX
DT 21-FEB-2001 (first entry)
XX
DE PCR anchor primer, SEQ ID NO:4, used in human gene 419 isolation.
XX
KW Human; pollinosis-associated gene 419; FAF-1 homologue;
KW Fas-associated factor-1; IGE; immunoglobulin E; cedar pollen allergy;
KW T-cell; reduced expression; detection; diagnosis; drug screening;
KW allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200065045-A1.
XX
PD 02-NOV-2000.
XX
PF 26-APR-2000; 2000WO-JP002729.
XX
PP 27-APR-1999; 99JP-00120490.
XX
PR 27-APR-2000; 2000WO-JP002729.
XX
PA (GENO-) GENOX RES INC.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsu K;
XX
XX WPI; 2000-687338/67.
XX
XX Pollinosis-associated gene 419 undergoing significantly low expression in
PT subjects with high cedar pollen-specific IGE levels, useful in diagnosis
PT of allergic diseases and screening drug candidates.
XX
XX Example 6; Page 50; 77pp; Japanese.
XX
XX The invention relates to the human pollinosis-associated gene 419 which
CC exhibits reduced expression in the T-cells of individuals with high cedar
CC pollen-specific IGE (immunoglobulin E) levels. The gene was isolated from
CC T-cells from individuals allergic to cedar pollen using the differential
CC display method. Pollinosis-associated gene 419 has homology with the gene
CC encoding human Fas-associated factor-1 (FAF-1). The invention also
CC relates to the protein encoded by pollinosis gene 419; expression
CC constructs and host cells comprising pollinosis-associated gene 419
CC nucleic acids; pollinosis-associated gene 419 primers and probes;
CC antibodies against the protein encoded by the gene; methods of detection
CC of pollinosis-associated gene 419 nucleic acids; and a method of
CC diagnosis of allergic diseases via the detection of pollinosis-
CC associated gene 419 nucleic acids. The invention additionally encompasses
CC methods of screening drug candidates for the treatment of allergic
CC disease by measuring the expression of pollinosis-associated gene 419 in
CC pollen antigen-stimulated T-cells in the presence of a test compound
CC relative to a control. Pollinosis-associated gene 419 is useful in the
CC diagnosis of allergic diseases and in the screening of drug candidates
CC for the treatment of such diseases. The present sequence represents a PCR
CC primer used in the isolation of human pollinosis-associated gene 419 cDNA
XX
SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;
Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 16 AAAAAAAAAAAAAA 2

RESULT 429
AAC64182/c
ID AAC64182 standard; DNA; 17 BP.
XX
AC AAC64182;
XX
DT 21-FEB-2001 (first entry)
XX
DE PCR anchor primer, SEQ ID NO:3, used in human gene 419 isolation.
XX
KW Human; pollinosis-associated gene 419; FAF-1 homologue;
KW Fas-associated factor-1; IGE; immunoglobulin E; cedar pollen allergy;
KW T-cell; reduced expression; detection; diagnosis; drug screening;
KW allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200065045-A1.
XX
PD 02-NOV-2000.
XX
PF 26-APR-2000; 2000WO-JP002729.
XX
PP 27-APR-1999; 99JP-00120490.
XX
PR (GENO-) GENOX RES INC.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsu K;
XX
XX WPI; 2000-687338/67.
XX
XX Pollinosis-associated gene 419 undergoing significantly low expression in
PT subjects with high cedar pollen-specific IGE levels, useful in diagnosis
PT of allergic diseases and screening drug candidates.
XX
XX Example 6; Page 49; 77pp; Japanese.
XX
XX The invention relates to the human pollinosis-associated gene 419 which
CC exhibits reduced expression in the T-cells of individuals with high cedar
CC pollen-specific IGE (immunoglobulin E) levels. The gene was isolated from
CC T-cells from individuals allergic to cedar pollen using the differential
CC display method. Pollinosis-associated gene 419 has homology with the gene
CC encoding human Fas-associated factor-1 (FAF-1). The invention also
CC relates to the protein encoded by pollinosis gene 419; expression
CC constructs and host cells comprising pollinosis-associated gene 419
CC nucleic acids; pollinosis-associated gene 419 primers and probes;
CC antibodies against the protein encoded by the gene; methods of detection
CC of pollinosis-associated gene 419 nucleic acids; and a method of
CC diagnosis of allergic diseases via the detection of pollinosis-
CC associated gene 419 nucleic acids. The invention additionally encompasses
CC methods of screening drug candidates for the treatment of allergic
CC disease by measuring the expression of pollinosis-associated gene 419 in
CC pollen antigen-stimulated T-cells in the presence of a test compound
CC relative to a control. Pollinosis-associated gene 419 is useful in the
CC diagnosis of allergic diseases and in the screening of drug candidates
CC for the treatment of such diseases. The present sequence represents a PCR
CC primer used in the isolation of human pollinosis-associated gene 419 cDNA
XX
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 16 AAAAAAAAAAAAAA 2

```

XX DE
XX DE
XX KW Human; pollinosis-associated gene 513; IGE; immunoglobulin E;
XX KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
XX KW drug screening; allergic disease; PCR primer; ss.
XX OS Synthetic.
XX PN WO200065049-A1.
XX PD 02-NOV-2000.
XX PF 26-APR-2000; 2000WO-JP002733.
XX PR 27-APR-1999; 99JP-00120491.
XX PA (GENO-) GENOX RES INC.
XX PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
XX PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX DR WPI; 2000-687342/67.
XX PT Pollinosis-associated gene 513 undergoing significantly low expression in
XX PT subjects with high cedar pollen-specific IGE levels, useful in diagnosis
XX PT of allergic diseases and screening drug candidates.
XX PS Example 6; Page 38; 46pp; Japanese.
XX CC The invention relates to the human pollinosis-associated gene 513 which
XX CC exhibits significantly reduced expression in the T-cells of individuals
XX CC with high cedar pollen-specific IGE (immunoglobulin E) levels. The gene
XX CC was isolated from T-cells from individuals allergic to cedar pollen using
XX CC the differential display method. The invention also relates to methods of
XX CC detection of pollinosis-associated gene 513 nucleic acids; a method of
XX CC diagnosis of allergic diseases via the detection of pollinosis-associated
XX CC gene 513 nucleic acids; and methods of screening drug candidates for the
XX CC treatment of allergic disease by measuring the expression of pollinosis-
XX CC associated gene 513 in pollen antigen-stimulated T-cells in the presence
XX CC of a test compound relative to a control. Pollinosis-associated gene 513
XX CC is useful in the diagnosis of allergic diseases and in the screening of
XX CC drug candidates for the treatment of such diseases. The present sequence
XX CC represents a PCR primer used in the isolation of human pollinosis-
XX CC associated gene 513 cDNA
XX SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 16 AAAAAAAAAAAAAA 2

RESULT 432
AAC64163/c
ID AAC64163 standard; DNA; 17 BP.
XX AC AAC64163;
XX DT 21-FEB-2001 (first entry)
XX DE
XX DE PCR anchor primer, SEQ ID NO:4, used in human gene 581 isolation.
XX KW Human; pollinosis-associated gene 581; IGE; immunoglobulin E;
XX KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
XX KW drug screening; allergic disease; PCR primer; ss.
XX OS Synthetic.
XX PN WO200065049-A1.
XX PD 02-NOV-2000.
XX PF 26-APR-2000; 2000WO-JP002733.
XX PR 27-APR-1999; 99JP-00120491.
XX PA (GENO-) GENOX RES INC.
XX PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
XX PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX DR WPI; 2000-687342/67.
XX PT Pollinosis-associated gene 513 undergoing significantly low expression in
XX PT subjects with high cedar pollen-specific IGE levels, useful in diagnosis
XX PT of allergic diseases and screening drug candidates.
XX PS Example 6; Page 39; 46pp; Japanese.
XX CC The invention relates to the human pollinosis-associated gene 513 which
XX CC exhibits significantly reduced expression in the T-cells of individuals
XX CC with high cedar pollen-specific IGE (immunoglobulin E) levels. The gene
XX CC was isolated from T-cells from individuals allergic to cedar pollen using
XX CC the differential display method. The invention also relates to methods of
XX CC detection of pollinosis-associated gene 513 nucleic acids; a method of
XX CC diagnosis of allergic diseases via the detection of pollinosis-associated
XX CC gene 513 nucleic acids; and methods of screening drug candidates for the
XX CC treatment of allergic disease by measuring the expression of pollinosis-
XX CC associated gene 513 in pollen antigen-stimulated T-cells in the presence
XX CC of a test compound relative to a control. Pollinosis-associated gene 513
XX CC is useful in the diagnosis of allergic diseases and in the screening of
XX CC drug candidates for the treatment of such diseases. The present sequence
XX CC represents a PCR primer used in the isolation of human pollinosis-
XX CC associated gene 513 cDNA
XX SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 16 AAAAAAAAAAAAAA 2

RESULT 431
AAC64172/c
ID AAC64172 standard; DNA; 17 BP.
XX AC AAC64172;
XX DT 21-FEB-2001 (first entry)

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PN WO200065048-A1.
XX
XX
PD 02-NOV-2000.
XX
XX
PF 26-APR-2000; 2000WO-JP002732.
XX
XX
PR 27-APR-1999; 99JP-00120492.
XX
XX
PA (GENO-) GENOX RES INC.
XX
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX
XX
DR WPI; 2000-687341/67.
XX
XX
PT Pollenosis-associated gene 581 undergoing significantly low expression in
PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis
PT of allergic diseases and screening drug candidates.
XX
XX
PS Example 6; Page 40; 69pp; Japanese.
XX
XX
CC The invention relates to the human pollinosis-associated gene 581 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC was isolated from T-cells from individuals allergic to cedar pollen using
CC the differential display method. The invention also relates also relates
CC to the protein encoded by pollinosis-associated gene 581; to expression
CC constructs and host cells comprising pollinosis-associated gene 581
CC nucleic acids; pollinosis-associated gene 581 primers and probes;
CC antibodies against the protein encoded by the gene; methods of detection
CC of pollinosis-associated gene 581 nucleic acids; and a method of
CC diagnosis of allergic diseases via the detection of pollinosis-associated
CC gene 581 nucleic acids. The invention additionally encompasses methods of
CC screening drug candidates for the treatment of allergic disease by
CC measuring the expression of pollinosis-associated gene 581 in pollen
CC antigen-stimulated T-cells in the presence of a test compound relative to
CC a control. Pollinosis-associated gene 581 is useful in the diagnosis of
CC allergic diseases and in the screening of drug candidates for the
CC treatment of such diseases. The present sequence represents a PCR primer
CC used in the isolation of human pollinosis-associated gene 581 cDNA
XX
XX
SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;
Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1495
Db 16 AAAAAAAAAAAAAA 2
RESULT 433
AAC64162/c
ID AAC64162 standard; DNA; 17 BP.
AC AAC64162;
XX
XX
DT 21-FEB-2001 (first entry)
DE PCR anchor primer, SEQ ID NO:3, used in human gene 581 isolation.
XX
XX
KW Human; pollinosis-associated gene 581; IgE; immunoglobulin E;
KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
KW drug screening; allergic disease; PCR primer; ss.
XX
XX
OS Synthetic.
XX
XX
PN WO200065048-A1.
XX
XX
PD 02-NOV-2000.
XX
XX
PF 26-APR-2000; 2000WO-JP002732.
XX
XX
PR 27-APR-1999; 99JP-00120492.
XX
XX
PA (GENO-) GENOX RES INC.
XX
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX
XX
DR WPI; 2000-687341/67.
XX
XX
PT Pollenosis-associated gene 581 undergoing significantly low expression in
PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis
PT of allergic diseases and screening drug candidates.
XX
XX
PS Example 6; Page 40; 69pp; Japanese.
XX
XX
CC The invention relates to the human pollinosis-associated gene 581 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC was isolated from T-cells from individuals allergic to cedar pollen using
CC the differential display method. The invention also relates also relates
CC to the protein encoded by pollinosis-associated gene 581; to expression
CC constructs and host cells comprising pollinosis-associated gene 581
CC nucleic acids; pollinosis-associated gene 581 primers and probes;
CC antibodies against the protein encoded by the gene; methods of detection
CC of pollinosis-associated gene 581 nucleic acids; and a method of
CC diagnosis of allergic diseases via the detection of pollinosis-associated
CC gene 581 nucleic acids. The invention additionally encompasses methods of
CC screening drug candidates for the treatment of allergic disease by
CC measuring the expression of pollinosis-associated gene 581 in pollen
CC antigen-stimulated T-cells in the presence of a test compound relative to
CC a control. Pollinosis-associated gene 581 is useful in the diagnosis of
CC allergic diseases and in the screening of drug candidates for the
CC treatment of such diseases. The present sequence represents a PCR primer
CC used in the isolation of human pollinosis-associated gene 581 cDNA
XX
XX
SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;
Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1495
Db 16 AAAAAAAAAAAAAA 2
RESULT 433
AAC64162/c
ID AAC64162 standard; DNA; 17 BP.
AC AAC64162;
XX
XX
DT 21-FEB-2001 (first entry)
DE PCR anchor primer, SEQ ID NO:4, used in human gene 627 isolation.
XX
XX
KW Human; pollinosis-associated gene 627; IgE; immunoglobulin E;
KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
KW drug screening; allergic disease; PCR primer; ss.
XX
XX
OS Synthetic.
XX
XX
PN WO200065051-A1.
XX
XX
PD 02-NOV-2000.
XX
XX
PF 26-APR-2000; 2000WO-JP002735.
XX
XX
PR 27-APR-1999; 99JP-00120493.
XX
XX
PA (GENO-) GENOX RES INC.
XX
XX

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CC homology with the human vimentin gene. The invention also relates also
 CC relates to the protein encoded by pollinosis gene 795; to expression
 CC constructs and host cells comprising pollinosis-associated gene 795
 CC nucleic acids; pollinosis-associated gene 795 primers and probes;
 CC antibodies against the protein encoded by the gene; methods of detection
 CC of pollinosis-associated gene 795 nucleic acids; and a method of
 CC diagnosis of allergic diseases via the detection of pollinosis-associated
 CC gene 795 nucleic acids. The invention additionally encompasses methods of
 CC screening drug candidates for the treatment of allergic disease by
 CC measuring the expression of pollinosis-associated gene 795 in pollen
 CC antigen-stimulated T-cells in the presence of a test compound relative to
 CC a control. Pollinosis-associated gene 795 is useful in the diagnosis of
 CC allergic diseases and in the screening of drug candidates for the
 CC treatment of such diseases. The present sequence represents a PCR primer
 CC used in the isolation of human pollinosis-associated gene 795 cDNA
 XX
 SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
 |||||
 Db 16 AAAAAAAAAAAAAA 2

RESULT 437
 AAC64232/C
 ID AAC64232 standard; DNA; 17 BP.
 XX
 AC AAC64232;
 XX
 DT 21-FEB-2001 (first entry)
 DE PCR anchor primer, SEQ ID NO:4, used in human gene 795 isolation.
 XX
 KW Human; pollinosis-associated gene 795; vimentin homologue; IGB;
 KW immunoglobulin E; cedar pollen allergy; T-cell; reduced expression;
 KW detection; diagnosis; drug screening; allergic disease; PCR primer; ss.
 XX
 OS Synthetic.
 XX
 PN WO200065050-A1.
 XX
 PD 02-NOV-2000.
 XX
 PF 26-APR-2000; 2000WO-JP002734.
 XX
 PR 27-APR-1999; 99JP-00120494.
 XX
 PA (GENO-) GENOX RES INC.
 PA (EISA) EISAI CO LTD.
 XX
 PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
 PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;
 PI Yokoi A;
 XX
 DR WPI; 2000-687343/67.
 XX
 PT Pollinosis-associated gene 795 undergoing significantly low expression in
 PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis
 PT of allergic diseases and screening drug candidates.
 XX
 PS Page 46; Example 6; 73pp; Japanese.
 XX

CC The invention relates to the human pollinosis-associated gene 795 which
 CC exhibits significantly reduced expression in the T-cells of individuals
 CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
 CC was isolated from T-cells from individuals allergic to cedar pollen using
 CC the differential display method. Pollinosis-associated gene 795 has
 CC homology with the human vimentin gene. The invention also relates also
 CC relates to the protein encoded by pollinosis gene 795; to expression

CC constructs and host cells comprising pollinosis-associated gene 795
 CC nucleic acids; pollinosis-associated gene 795 primers and probes;
 CC antibodies against the protein encoded by the gene; methods of detection
 CC of pollinosis-associated gene 795 nucleic acids; and a method of
 CC diagnosis of allergic diseases via the detection of pollinosis-associated
 CC gene 795 nucleic acids. The invention additionally encompasses methods of
 CC screening drug candidates for the treatment of allergic disease by
 CC measuring the expression of pollinosis-associated gene 795 in pollen
 CC antigen-stimulated T-cells in the presence of a test compound relative to
 CC a control. Pollinosis-associated gene 795 is useful in the diagnosis of
 CC allergic diseases and in the screening of drug candidates for the
 CC treatment of such diseases. The present sequence represents a PCR primer
 CC used in the isolation of human pollinosis-associated gene 795 cDNA
 XX
 SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
 |||||
 Db 16 AAAAAAAAAAAAAA 2

RESULT 438
 AAC92294/C
 ID AAC92294 standard; DNA; 17 BP.
 XX
 AC AAC92294;
 XX
 DT 22-MAR-2001 (first entry)
 DE Human pollinosis-associated gene 465 related PCR primer SEQ ID NO:4.
 XX
 KW Human; pollinosis-associated gene 465; pollen scattering; allergy;
 KW allergic disease; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200073439-A1.
 XX
 PD 07-DEC-2000.
 XX
 PF 18-MAY-2000; 2000WO-JP003191.
 XX
 PR 27-MAY-1999; 99JP-00148784.
 XX
 PA (GENO-) GENOX RES INC.
 PA (EISA) EISAI CO LTD.
 XX
 PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
 PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;
 PI Yokoi A;
 XX
 DR WPI; 2001-061528/07.
 XX

PT Pollinosis-associated gene 465 undergoing significantly low expression in
 PT subjects after pollen scattering, useful in diagnosis of allergic
 PT diseases and screening candidate compounds to regulate response of T
 PT cells to antigen stimulus.
 XX
 PS Example 6; Page 44; 61pp; Japanese.
 XX

CC The present invention describes the human pollinosis-associated gene 465
 CC which has a nucleic acid sequence of 3442 base pairs (bp), given in
 CC (AAC92291), that undergoes significantly low expression in subjects after
 CC pollen scattering, and is useful in the diagnosis of allergic diseases
 CC and screening candidate compounds for remedies capable of regulating the
 CC response of T cells to the stimulus by an antigen. The gene is useful in
 CC the diagnosis of allergic diseases and screening candidate compounds for
 CC remedies capable of regulating the response of T cells to the stimulus by
 CC an antigen. The present sequence represents a PCR primer which is used in


```
CC an example from the present invention
XX
SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;
    Query Match 1.0%; Score 15; DB 1; Length 17;
    Best Local Similarity 100.0%; Pred. No. 2.1e+02;
    Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 16 AAAAAAAAAAAAAA 2

RESULT 439
AAC92293/c
ID AAC92293 standard; DNA; 17 BP.
XX
AC AAC92293;
XX
DT 22-MAR-2001 (first entry)
XX
DE Human pollinosis-associated gene 465 related PCR primer SEQ ID NO:3.
XX
DE Human pollinosis-associated gene 465; pollen scattering; allergy;
XX
KW allergic disease; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200073439-A1.
XX
PD 07-DEC-2000.
XX
PF 18-MAY-2000; 2000WO-JP003191.
XX
PR 27-MAY-1999; 99JP-00148784.
XX
PA (GENO-) GENOX RES INC.
PA (EISA) EISAI CO LTD.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;
PI Yokoi A;
XX
XX WPI; 2001-061528/07.
XX
DR Pollinosis-associated gene 465 undergoing significantly low expression in
PT subjects after pollen scattering, useful in diagnosis of allergic
PT diseases and screening candidate compounds to regulate response of T
PT cells to antigen stimulus.
XX
PS Example 6; Page 44; 61pp; Japanese.
XX
CC The present invention describes the human pollinosis-associated gene 465
CC which has a nucleic acid sequence of 3442 base pairs (bp), given in
CC (AAC92291), that undergoes significantly low expression in subjects after
CC pollen scattering, and is useful in the diagnosis of allergic diseases
CC and screening candidate compounds for remedies capable of regulating the
CC response of T cells to the stimulus by an antigen. The gene is useful in
CC the diagnosis of allergic diseases and screening candidate compounds for
CC remedies capable of regulating the response of T cells to the stimulus by
CC an antigen. The present sequence represents a PCR primer which is used in
CC an example from the present invention
XX
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
    Query Match 1.0%; Score 15; DB 1; Length 17;
    Best Local Similarity 100.0%; Pred. No. 2.1e+02;
    Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 16 AAAAAAAAAAAAAA 2

RESULT 440
AAC91720/c
ID AAC91720 standard; DNA; 17 BP.
XX
AC AAC91720;
XX
DT 27-MAR-2001 (first entry)
XX
DE PCR anchor primer, SEQ ID NO:3, used in human gene 787 isolation.
XX
DE Human; pollinosis-associated gene 787; pollen allergy; T-cell;
XX
KW reduced expression; detection; diagnosis; drug screening;
XX
KW allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200073440-A1.
XX
PD 07-DEC-2000.
XX
PF 18-MAY-2000; 2000WO-JP003192.
XX
PR 27-MAY-1999; 99JP-00148785.
XX
PA (GENO-) GENOX RES INC.
PA (EISA) EISAI CO LTD.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;
PI Yokoi A;
XX
XX WPI; 2001-032159/04.
XX
DR Pollinosis-associated gene 787 undergoing significantly low expression in
PT subjects after pollen scattering, useful in diagnosis of allergic
PT diseases and screening candidate compounds to regulate response of T
PT cells to antigen stimulus.
XX
PS Example 6; Page 40; 54pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 787 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC after the pollen-scattering season, relative to expression levels in T-
CC cells before the pollen-scattering season. The gene was isolated from T-
CC cells from individuals allergic to pollen using the differential display
CC method. The invention also relates to pollinosis-associated gene 787
CC primers and probes; methods of detection of pollinosis-associated gene
CC 787 nucleic acids; and a method of diagnosis of allergic diseases via the
CC detection of pollinosis-associated gene 787 nucleic acids. The invention
CC additionally encompasses a method of screening drug candidates for the
CC treatment of allergic disease by measuring the expression of pollinosis-
CC associated gene 787 in pollen antigen-stimulated T-cells in the presence
CC of a test compound relative to a control. Pollinosis-associated gene 787
CC is useful in the diagnosis of allergic diseases and in the screening of
CC drug candidates for the treatment of such diseases. The present sequence
CC represents a PCR primer used in the isolation of human pollinosis-
CC associated gene 787 cDNA
XX
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
    Query Match 1.0%; Score 15; DB 1; Length 17;
    Best Local Similarity 100.0%; Pred. No. 2.1e+02;
    Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
Db 16 AAAAAAAAAAAAAA 2

RESULT 441
AAC91721/c
ID AAC91721 standard; DNA; 17 BP.
```

```

XX AAC91721;
AC
XX
DT 27-MAR-2001 (first entry)
DE PCR anchor primer, SEQ ID NO:4, used in human gene 787 isolation.
XX
XX Human; pollinosis-associated gene 787; pollen allergy; T-cell;
KW reduced expression; detection; diagnosis; drug screening;
XX allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
XX WO200073440-A1.
PN
XX
PD 07-DEC-2000.
XX
XX 18-MAY-2000; 2000WO-JP003192.
PF
XX
XX 27-MAY-1999; 99JP-00148785.
PR
XX
XX (GENO-) GENOX RES INC.
PA (EISA) EISAI CO LTD.
XX
XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;
PI Yokoi A;
XX
XX WPI; 2001-032159/04.
DR
XX
XX Pollinosis-associated gene 787 undergoing significantly low expression in
PT subjects after pollen scattering, useful in diagnosis of allergic
PT diseases and screening candidate compounds to regulate response of T
PT cells to antigen stimulus.
XX
XX Example 6; Page 41; 54pp; Japanese.
PS
XX
CC The invention relates to the human pollinosis-associated gene 787 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC after the pollen-scattering season, relative to expression levels in T-
CC cells before the pollen-scattering season. The gene was isolated from T-
CC cells from individuals allergic to pollen using the differential display
CC method. The invention also relates to pollinosis-associated gene 787
CC primers and probes; methods of detection of pollinosis-associated gene
CC 787 nucleic acids; and a method of diagnosis of allergic diseases via the
CC detection of pollinosis-associated gene 787 nucleic acids. The invention
CC additionally encompasses a method of screening drug candidates for the
CC treatment of allergic disease by measuring the expression of pollinosis-
CC associated gene 787 in pollen antigen-stimulated T-cells in the presence
CC of a test compound relative to a control. Pollinosis-associated gene 787
CC is useful in the diagnosis of allergic diseases and in the screening of
CC drug candidates for the treatment of such diseases. The present sequence
CC represents a PCR primer used in the isolation of human pollinosis-
CC associated gene 787 cDNA
XX
XX Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;
SQ
Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
DB 16 AAAAAAAAAAAAAA 2

RESULT 442
AAC82876/c
ID AAC82876 standard; DNA; 17 BP.
XX
AC AAC82876;
XX
DT 20-MAR-2001 (first entry)
DE Human pollinosis-associated gene 441 primer #2.
XX
XX Pollinosis; pollinosis-associated gene 441; allergy; T cell;
KW pollen scattering; antigen; primer; ss.
XX
OS Homo sapiens.
XX
XX WO200073435-A1.
PN
XX
PD 07-DEC-2000.
XX
XX 18-MAY-2000; 2000WO-JP003190.
PF
XX
XX 27-MAY-1999; 99JP-00148783.
PR
XX
XX (GENO-) GENOX RES INC.
PA
XX
XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI

```

```

XX Human pollinosis-associated gene 441 primer #3.
DE
XX
KW Pollinosis; pollinosis-associated gene 441; allergy; T cell;
KW pollen scattering; antigen; primer; ss.
XX
OS Homo sapiens.
XX
XX WO200073435-A1.
PN
XX
PD 07-DEC-2000.
XX
XX 18-MAY-2000; 2000WO-JP003190.
PF
XX
XX 27-MAY-1999; 99JP-00148783.
PR
XX
XX (GENO-) GENOX RES INC.
PA
XX
XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX
XX WPI; 2001-061526/07.
DR
XX
XX Pollinosis-associated gene 441 which undergoes lower expression in
PT subjects after pollen scattering, useful in diagnosis of allergic
PT diseases and screening candidate compounds to regulate response of T
PT cells to antigen stimulus.
XX
XX Example 6; Page 36; 42pp; Japanese.
PS
XX
CC This invention describes a novel nucleic acid molecule comprising a
CC sequence (I) which undergoes significantly low expression in subjects
CC after pollen scattering, and is useful in diagnosis of allergic diseases
CC and screening candidate compounds for remedies capable of regulating the
CC response of T cells to the stimulus by an antigen
XX
XX Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;
SQ
Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
DB 16 AAAAAAAAAAAAAA 2

RESULT 443
AAC82875/c
ID AAC82875 standard; DNA; 17 BP.
XX
AC AAC82875;
XX
DT 20-MAR-2001 (first entry)
DE Human pollinosis-associated gene 441 primer #2.
XX
XX Pollinosis; pollinosis-associated gene 441; allergy; T cell;
KW pollen scattering; antigen; primer; ss.
XX
OS Homo sapiens.
XX
XX WO200073435-A1.
PN
XX
PD 07-DEC-2000.
XX
XX 18-MAY-2000; 2000WO-JP003190.
PF
XX
XX 27-MAY-1999; 99JP-00148783.
PR
XX
XX (GENO-) GENOX RES INC.
PA
XX
XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI

```

```

PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX WPI; 2001-061526/07.
XX
XX Pollinosis-associated gene 441 which undergoes lower expression in
PT subjects after pollen scattering, useful in diagnosis of allergic
PT diseases and screening candidate compounds to regulate response of T
PT cells to antigen stimulus.
XX
XX Example 6; Page 35; 42pp; Japanese.
XX
XX This invention describes a novel nucleic acid molecule comprising a
CC sequence (I) which undergoes significantly low expression in subjects
CC after pollen scattering, and is useful in diagnosis of allergic diseases
CC and screening candidate compounds for remedies capable of regulating the
CC response of T cells to the stimulus by an antigen
XX
XX Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
SQ
Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1495
DB 16 AAAAAAAAAAAAAA 2
RESULT 444
AAH47128/C
XX AAH47128;
XX AC
XX 30-NOV-2001 (first entry)
XX DT
XX DE Nucleotide sequence of primer GT15C.
XX KW B1001; B1466; B1072; B1151; T-cell; allergy; atopic dermatitis; human;
XX KW PCR primer; ss.
XX OS Homo sapiens.
XX PN WO200165259-A1.
XX PD 07-SEP-2001.
XX PF 23-FEB-2001; 2001WO-JP001372.
XX PR 02-MAR-2000; 2000JP-00061832.
XX PA (GENO-) GENOX RES INC.
XX PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX PI Nagasu T, Oshida T, Obayashi I, Matsui K, Saito H;
XX WPI; 2001-557789/62.
XX DR
XX PT Diagnosis of allergies including atopic dermatitis.
XX PS Example 6; Page 66; 83pp; Japanese.
XX CC The invention provides a method of diagnosis of allergies that involves:
CC assaying the levels of expression of genes B1001, B1466, B1072 or B1151
CC in T-cells; and comparing them with the level of expression in healthy T-
CC cells. The method is useful for diagnosing allergies, particularly atopic
CC dermatitis. The present sequence represents a PCR primer used for
CC analysis of the expression of the above genes
XX
XX Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
SQ
Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1495
DB 16 AAAAAAAAAAAAAA 2
RESULT 446
ABK49636/C
XX ABK49636;
XX AC
XX 15-JUL-2002 (first entry)
XX DT
XX DE Human Acetyltransferase-like protein 20-90-05 PCR primer GT15G.
XX KW Human; ss; PCR; acetyltransferase; 20-90-05; allergic disease; primer;
XX KW differential display; eosinophil; antiallergic; atopic dermatitis; GT15G.
XX OS Homo sapiens.

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```
PF 25-SEP-2000; 2000JP-00291316.
XX
PR 25-SEP-2000; 2000JP-00291316.
XX
PA (GENO-) GENOX SOYAKU KENKYUSHO KK.
PA (KOKU-) KOKURITSU SHONI BYOIN INCHO.
XX
XX WPI; 2002-439993/47.
XX
XX Examining allergosis, involves measuring the expression levels of a
PT specific gene, and comparing it to the levels in the eosinophils of a
PT healthy control.
XX
XX Example 1; Page 17; 20pp; Japanese.
XX
CC The specification describes a method for examining allergosis. The method
CC comprises measuring the expression level of the gene given in ABL59037,
CC and comparing it with the expression level of the gene in the eosinophils
CC of a healthy person. The method is used for the examination of
CC allergosis. The present sequence represents a PCR primer, which is used
CC in the course of the invention
XX
SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;
Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1495
Db 16 AAAAAAAAAAAAAA 2
RESULT 449
ABL59039/c
ID ABL59039 standard; DNA; 17 BP.
XX
AC ABL59039;
XX
XX 20-AUG-2002 (first entry)
XX
DE Nucleotide sequence of PCR primer GT15C.
XX
XX Human; allergosis; eosinophil; PCR; primer; ss.
XX
XX Homo sapiens.
XX
PN JP2002095500-A.
XX
PD 02-APR-2002.
XX
XX 25-SEP-2000; 2000JP-00291316.
XX
XX 25-SEP-2000; 2000JP-00291316.
XX
XX (GENO-) GENOX SOYAKU KENKYUSHO KK.
XX (KOKU-) KOKURITSU SHONI BYOIN INCHO.
XX
XX WPI; 2002-439993/47.
XX
XX Examining allergosis, involves measuring the expression levels of a
PT specific gene, and comparing it to the levels in the eosinophils of a
PT healthy control.
XX
XX Example 1; Page 17; 20pp; Japanese.
XX
CC The specification describes a method for examining allergosis. The method
CC comprises measuring the expression level of the gene given in ABL59037,
CC and comparing it with the expression level of the gene in the eosinophils
CC of a healthy person. The method is used for the examination of
CC allergosis. The present sequence represents a PCR primer, which is used
CC in the course of the invention
XX
SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;
Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1495
Db 16 AAAAAAAAAAAAAA 2
RESULT 450
ABN99831/c
ID ABN99831 standard; DNA; 17 BP.
XX
XX AC ABN99831;
XX
XX 15-AUG-2002 (first entry)
XX
DE Human allergic disease related PCR primer SEQ ID NO: 20.
XX
XX Human; allergy; atopic dermatitis; eosinophil; anti-allergic; PCR;
XX primer; ss.
XX
XX Homo sapiens.
XX
XX WO200233069-A1.
XX
XX 25-APR-2002.
XX
XX 28-SEP-2001; 2001WO-JP008574.
XX
XX 13-OCT-2000; 2000JP-00314093.
XX
XX (GENO-) GENOX RES INC.
XX (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX
XX Sugita Y, Hashida R, Ogawa K, Obayashi M, Nagasu T, Saito H;
XX WPI; 2002-372311/40.
XX
XX Method for examining allergic diseases by differential display of
PT seventeen genes showing different expression particularly significant
PT increase in eosinophils in patients with mild atopic dermatitis, also
PT applicable in screening compounds.
XX
XX Example 1; Page 110; 165pp; Japanese.
XX
CC The present invention relates to a method for examining allergic diseases
CC which involves determining the expression level of a gene, having one of
CC the 17 nucleotide sequences shown in ABN99812-ABN99828, in the
CC eosinophils in a patient and comparing the expression level with that in
CC the eosinophils of a healthy individual. The method can be used to
CC examine allergic diseases, particularly atopic dermatitis, and its early
CC diagnosis, which is also applicable in screening candidate compounds for
CC remedies. The present sequence is a PCR primer described in the
CC exemplification of the invention
XX
SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;
Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1495
Db 16 AAAAAAAAAAAAAA 2
RESULT 451
ABN99830/c
ID ABN99830 standard; DNA; 17 BP.
XX
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```
AC ABN99830;
XX
XX 15-AUG-2002 (first entry)
XX
XX Human allergic disease related PCR primer SEQ ID NO: 19.
DE
XX Human; allergy; atopic dermatitis; eosinophil; anti-allergic; PCR;
KW primer; ss.
XX
XX Homo sapiens.
XX
XX WO200233069-A1.
XX
XX 25-APR-2002.
XX
XX 28-SEP-2001; 2001WO-JP008574.
XX
XX 13-OCT-2000; 2000JP-00314093.
XX
XX (GENO-) GENOX RES INC.
XX (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX
XX Sugita Y, Hashida R, Ogawa K, Obayashi M, Nagasu T, Saito H;
XX WPI; 2002-372311/40.
XX
XX Method for examining allergic diseases by differential display of
XX seventeen genes showing different expression particularly significant
XX increase in eosinophils in patients with mild atopic dermatitis, also
XX applicable in screening compounds.
XX
XX Example 1; Page 109; 165pp; Japanese.
XX
XX The present invention relates to a method for examining allergic diseases
XX which involves determining the expression level of a gene, having one of
XX the 17 nucleotide sequences shown in ABN99812-ABN99828, in the
XX eosinophils in a patient and comparing the expression level with that in
XX the eosinophils of a healthy individual. The method can be used to
XX examine allergic diseases, particularly atopic dermatitis, and its early
XX diagnosis, which is also applicable in screening candidate compounds for
XX remedies. The present sequence is a PCR primer described in the
XX exemplification of the invention
XX
XX Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
DB |||||||||||||
16 AAAAAAAAAAAAAA 2

RESULT 452
AAL49950/C
ID AAL49950 standard; DNA; 17 BP.
XX
XX AAL49950;
XX
XX 10-DEC-2002 (first entry)
XX
XX Human B1153 expression in allergic disease related PCR primer GT15G.
XX
XX Human; allergy; B1153; differential expression; antiallergic; asthma;
XX antiasthmatic; antiinflammatory; atopic skin inflammation; PCR; primer;
XX ss.
XX
XX Unidentified.
XX
XX WO200250269-A1.
XX
XX 27-JUN-2002.
XX
XX 21-DEC-2001; 2001WO-JP011286.
XX
XX 21-DEC-2000; 2000JP-00389476.
XX
XX (GENO-) GENOX RES INC.
XX (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX
XX Matsumoto Y, Imai Y, Oshida T, Sugita Y, Nagasu T, Tsujimoto G;
XX WPI; 2002-713252/77.
XX
XX Examination of allergic diseases comprises detecting gene B1153 over-
XX expressed in T cells of allergy patients for diagnosis treatment and
XX investigation of atopic skin inflammation and asthma.
XX
XX Example 6; Page 82; 102pp; Japanese.
```

```
XX
XX 21-DEC-2001; 2001WO-JP011286.
XX
XX 21-DEC-2000; 2000JP-00389476.
XX
XX (GENO-) GENOX RES INC.
XX (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX
XX Matsumoto Y, Imai Y, Oshida T, Sugita Y, Nagasu T, Tsujimoto G;
XX WPI; 2002-713252/77.
XX
XX Examination of allergic diseases comprises detecting gene B1153 over-
XX expressed in T cells of allergy patients for diagnosis treatment and
XX investigation of atopic skin inflammation and asthma.
XX
XX Example 6; Page 82; 102pp; Japanese.
XX
XX The present invention relates to a method of examining allergic diseases
XX which comprises comparing the expression level of gene B1153 in allergy
XX patients with the expression level in healthy subjects. The method is
XX useful for the treatment, prevention, diagnosis and study of allergic
XX diseases including atopic skin inflammation and asthma. The present
XX sequence is a PCR primer described in the exemplification of the
XX invention
XX
XX Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
DB |||||||||||||
16 AAAAAAAAAAAAAA 2

RESULT 453
AAL49949/C
ID AAL49949 standard; DNA; 17 BP.
XX
XX AAL49949;
XX
XX 10-DEC-2002 (first entry)
XX
XX Human B1153 expression in allergic disease related PCR primer GT15C.
XX
XX Human; allergy; B1153; differential expression; antiallergic; asthma;
XX antiasthmatic; antiinflammatory; atopic skin inflammation; PCR; primer;
XX ss.
XX
XX Unidentified.
XX
XX WO200250269-A1.
XX
XX 27-JUN-2002.
XX
XX 21-DEC-2001; 2001WO-JP011286.
XX
XX 21-DEC-2000; 2000JP-00389476.
XX
XX (GENO-) GENOX RES INC.
XX (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX
XX Matsumoto Y, Imai Y, Oshida T, Sugita Y, Nagasu T, Tsujimoto G;
XX WPI; 2002-713252/77.
XX
XX Examination of allergic diseases comprises detecting gene B1153 over-
XX expressed in T cells of allergy patients for diagnosis treatment and
XX investigation of atopic skin inflammation and asthma.
XX
XX Example 6; Page 82; 102pp; Japanese.
```

XX The present invention relates to a method of examining allergic diseases
 CC which comprises comparing the expression level of gene B1153 in allergy
 CC patients with the expression level in healthy subjects. The method is
 CC useful for the treatment, prevention, diagnosis and study of allergic
 CC diseases including atopic skin inflammation and asthma. The present
 CC sequence is a PCR primer described in the exemplification of the
 CC invention
 XX
 SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
 Query Match 1.0%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1481 AAAAAAAAAAAAAA 1495
 Db 16 AAAAAAAAAAAAAA 2
 |||||
 RESULT 454
 AAL47236/c
 ID AAL47236 standard; DNA; 17 BP.
 XX
 AC AAL47236;
 XX
 DT 22-AUG-2002 (first entry)
 DE Allergic disease examination method related anchor primer SEQ ID NO: 4.
 XX Allergic disease; allergy; antiallergic; intersectin 2; eosinophil;
 KW atopic dermatitis; human; PCR; primer; ss.
 XX Unidentified.
 OS
 XX WO200233122-A1.
 PN
 XX 25-APR-2002.
 PD
 XX 11-OCT-2001; 2001WO-JP008937.
 PF
 XX 13-OCT-2000; 2000JP-00314093.
 PR
 XX (GENO-) GENOX RES INC.
 PA (NIGS-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
 PA (EISA) EISAI CO LTD.
 XX
 XX Sugita Y, Hashida R, Ogawa K, Obayashi M, Nagasu T, Saito H;
 PI Takahashi E;
 PI WPI; 2002-372313/40.
 DR
 XX 25-APR-2002.
 PD
 XX 11-OCT-2001; 2001WO-JP008937.
 PF
 XX 13-OCT-2000; 2000JP-00314093.
 PR
 XX (GENO-) GENOX RES INC.
 PA (NIGS-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
 PA (EISA) EISAI CO LTD.
 XX
 XX Sugita Y, Hashida R, Ogawa K, Obayashi M, Nagasu T, Saito H;
 PI Takahashi E;
 PI WPI; 2002-372313/40.
 DR
 XX Method for examining allergic diseases by differential display of
 FT intersectin 2 gene showing different expression particularly significant
 PT increase in eosinophils in patients.
 XX
 PS Example 1; Page 53; 90pp; Japanese.
 XX The present invention relates to a method for examining allergic diseases
 CC with intersectin 2 gene or a gene with equivalent function of intersectin
 CC 2 as an indicator gene, which comprises determining the expression level
 CC of the gene in the eosinophils in a patient, and comparing the expression
 CC level with that in the eosinophils of a healthy individual. The method is
 CC for examining allergic diseases, particularly atopic dermatitis, which is
 CC also applicable in screening candidate compounds for remedies. The
 CC present sequence is an anchor primer described in the exemplification of
 CC the invention
 XX
 SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;
 Query Match 1.0%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
 Db 16 AAAAAAAAAAAAAA 2
 |||||
 RESULT 455
 AAL47235/c
 ID AAL47235 standard; DNA; 17 BP.
 XX
 AC AAL47235;
 XX
 DT 22-AUG-2002 (first entry)
 DE Allergic disease examination method related anchor primer SEQ ID NO: 3.
 XX Allergic disease; allergy; antiallergic; intersectin 2; eosinophil;
 KW atopic dermatitis; human; PCR; primer; ss.
 XX Unidentified.
 OS
 XX WO200233122-A1.
 PN
 XX 25-APR-2002.
 PD
 XX 11-OCT-2001; 2001WO-JP008937.
 PF
 XX 13-OCT-2000; 2000JP-00314093.
 PR
 XX (GENO-) GENOX RES INC.
 PA (NIGS-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
 PA (EISA) EISAI CO LTD.
 XX
 XX Sugita Y, Hashida R, Ogawa K, Obayashi M, Nagasu T, Saito H;
 PI Takahashi E;
 PI WPI; 2002-372313/40.
 DR
 XX Method for examining allergic diseases by differential display of
 FT intersectin 2 gene showing different expression particularly significant
 PT increase in eosinophils in patients.
 XX
 PS Example 1; Page 53; 90pp; Japanese.
 XX The present invention relates to a method for examining allergic diseases
 CC with intersectin 2 gene or a gene with equivalent function of intersectin
 CC 2 as an indicator gene, which comprises determining the expression level
 CC of the gene in the eosinophils in a patient, and comparing the expression
 CC level with that in the eosinophils of a healthy individual. The method is
 CC for examining allergic diseases, particularly atopic dermatitis, which is
 CC also applicable in screening candidate compounds for remedies. The
 CC present sequence is an anchor primer described in the exemplification of
 CC the invention
 XX
 SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
 Query Match 1.0%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1481 AAAAAAAAAAAAAA 1495
 Db 16 AAAAAAAAAAAAAA 2
 |||||
 RESULT 456
 ABK49757/c
 ID ABK49757 standard; DNA; 17 BP.
 XX
 AC ABK49757;
 XX
 DT 15-JUL-2002 (first entry)
 XX

DE Human atopic dermatitis cDNA related PCR primer GT15c.
XX Atopic dermatitis; ss; differential display; primer; PCR; eosinophil;
KW allergic disease; antiallergic; dermatological; GT15c.
XX Synthetic.
OS
XX WO200226962-A1.
PN
XX
XX 04-APR-2002.
PD
XX
XX 21-SEP-2001; 2001WO-JP008247.
PF
XX
XX 26-SEP-2000; 2000JP-00293021.
PR
XX
XX (GENO-) GENOX RES INC.
PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX
XX Sugita Y, Hashida R, Ogawa K, Fujishima T, Nagasu T, Saito H;
PI
XX WPI; 2002-330097/36.
DR
XX
XX Examining allergic diseases by differential display of genes showing
PT different expression particularly increase in remission stage in
PT eosinophils in patients.
XX
XX Example 1; Page 55; 74pp; Japanese.
PS
XX This invention relates to gene sequences that are differentially
CC expressed in eosinophils from patients with atopic dermatitis in the
CC increment stage as compared with those in the remission stage. These
CC sequences are used in a novel method for examining allergic diseases
CC comprising determining the expression levels of these genes and comparing
CC the expression level with that in the eosinophils of a healthy
CC individual. The method of the invention may have antiallergic or
CC dermatological activities. The method can be used to diagnose allergic
CC diseases particularly atopic dermatitis, and may also be used to screen
CC candidate compounds for remedies. The method of the invention can be
CC performed in high throughput, at low cost. The present sequence
CC represents the GT15c PCR primer used to amplify the differentially
CC amplified atopic dermatitis related cDNA sequences of the invention
XX
XX Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
SQ
Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1495
DB 16 AAAAAAAAAAAAAA 2
RESULT 457
ID ABK49758/c
XX ABK49758 standard; DNA; 17 BP.
AC
XX ABK49758;
XX
XX 15-JUL-2002 (first entry)
DT
XX
XX Human atopic dermatitis cDNA related PCR primer GT15g.
DE
XX
KW Atopic dermatitis; ss; differential display; primer; PCR; eosinophil;
KW allergic disease; antiallergic; dermatological; GT15g.
XX
XX Synthetic.
OS
XX WO200226962-A1.
PN
XX
XX 04-APR-2002.
PD
XX
XX 21-SEP-2001; 2001WO-JP008247.
PF

XX 26-SEP-2000; 2000JP-00293021.
PR
XX (GENO-) GENOX RES INC.
PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX
XX Sugita Y, Hashida R, Ogawa K, Fujishima T, Nagasu T, Saito H;
PI
XX WPI; 2002-330097/36.
DR
XX
XX Examining allergic diseases by differential display of genes showing
PT different expression particularly increase in remission stage in
PT eosinophils in patients.
XX
XX Example 1; Page 55; 74pp; Japanese.
PS
XX This invention relates to gene sequences that are differentially
CC expressed in eosinophils from patients with atopic dermatitis in the
CC increment stage as compared with those in the remission stage. These
CC sequences are used in a novel method for examining allergic diseases
CC comprising determining the expression levels of these genes and comparing
CC the expression level with that in the eosinophils of a healthy
CC individual. The method of the invention may have antiallergic or
CC dermatological activities. The method can be used to diagnose allergic
CC diseases particularly atopic dermatitis, and may also be used to screen
CC candidate compounds for remedies. The method of the invention can be
CC performed in high throughput, at low cost. The present sequence
CC represents the GT15g PCR primer used to amplify the differentially
CC amplified atopic dermatitis related cDNA sequences of the invention
XX
XX Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;
SQ
Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1495
DB 16 AAAAAAAAAAAAAA 2
RESULT 458
ID AAD44151/c
XX AAD44151 standard; DNA; 17 BP.
AC
XX AAD44151;
XX
XX 13-DEC-2002 (first entry)
DT
XX
XX Oligo-AT PCR primer #2 used to illustrate the method of the invention.
DE
XX
KW Sequential consensus region-directed amplification; gene expression;
KW disease diagnosis; gene analysis; human; matrix metalloproteinase; PCR;
KW primer; ss.
XX
XX Unidentified.
OS
XX
XX US6277571-B1.
PN
XX
XX 21-AUG-2001.
PD
XX
XX 30-SEP-1998; 98US-00163485.
PF
XX
XX 03-OCT-1997; 97US-00943162.
PR
XX 03-OCT-1997; 97US-0108152P.
XX
XX (UYVI-) UNIV VIRGINIA COMMONWEALTH INTELLECTUAL.
PA
XX
XX Fillmore H, Broadus W, Gillies G;
PI
XX WPI; 2002-412824/44.
DR
XX
XX Sequential consensus region-directed amplification for sorting mixture of

PT DNAs into 2 or more subsets or distinguishing gene expression patterns in 2 samples, useful for disease diagnosis and gene analysis.

XX Example; Fig 1D; 19pp; English.

PS The invention relates to a method of sequential consensus region-directed amplification for sorting a mixture of DNAs into 2 or more subsets or distinguishing gene expression patterns in 2 samples. The methods, kits and oligonucleotides are useful for sorting a mixture of DNAs into 2 or more subsets or distinguishing gene expression patterns in 2 samples e.g. for disease diagnosis and gene analysis. The present sequence is oligo AT PCR primer used to illustrate the method of the invention

XX Sequence 17 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 1 Other;

Query Match 1.0%; Score 15; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1481 AAAAAAAAAAAAAA 1495

Db 17 AAAAAAAAAAAAAA 3

RESULT 459

ID ABX79793/c

XX ABX79793 standard; cDNA; 17 BP.

XX AC ABX79793;

XX DT 17-APR-2003 (first entry)

XX EST polymorphic DNA repeat polynucleotide #118.

DE EST; expressed sequence tag; ss; polymorphic repeat: tandem repeat;

XX Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;

XX Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;

XX Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;

XX Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;

XX Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;

XX Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;

XX Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;

XX Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;

XX Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;

XX Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;

XX Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;

XX Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;

XX Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;

XX Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;

XX Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;

XX Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;

XX Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;

XX Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;

XX Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;

XX Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;

XX Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;

XX Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;

XX Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;

XX Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;

XX Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;

XX Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;

XX Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;

XX Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;

XX Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;

XX Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;

XX Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;

XX Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;

XX Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;

XX Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;

XX Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;

XX Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;

XX Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;

XX Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;

XX Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;

CC diseases, predispositions or adverse drug-treatment reactions. Examples of diseases linked to nucleotide repeats are Machado-Joseph, Haw River syndrome, Huntington's disease, fragile-X syndrome, Friedreich's ataxia, myotonic dystrophy, hyperandrogenemia, spinal and bulbar atrophy and spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are the polymorphic repeats identified for a search of human ESTs

XX Sequence 17 BP; 0 A; 2 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1481 AAAAAAAAAAAAAA 1495

Db 15 AAAAAAAAAAAAAA 1

RESULT 460

ADB04270/c

XX ID ADB04270 standard; DNA; 17 BP.

XX AC ADB04270;

XX DT 20-NOV-2003 (first entry)

XX Human MD27 scanning oligonucleotide SEQ ID 5256.

XX Cytostatic; immunostimulant; gene therapy; vaccine; human;

XX zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;

XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;

XX developmental disorder; ss.

XX Homo sapiens.

XX EP1281758-A2.

XX 05-FEB-2003.

XX 30-JUL-2002; 2002EP-00016874.

XX 02-AUG-2001; 2001US-00922181.

XX (AEOM-) AEOMICA INC.

XX Shannon M, Gu Y, Nguyen C;

XX WPI; 2003-423107/40.

XX New zinc finger-containing proteins and nucleic acids, useful in manufacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MD23, MD24, MD27 or MD212, e.g. cancer.

XX Example 8; SEQ ID NO 5256; 103pp; English.

XX The present invention relates to novel human zinc finger-containing proteins and their coding sequences; MD23, MD24, MD27, MD212. MD23 is encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2, MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy, or in manufacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MD23, MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic acids and proteins are also useful for diagnosing or monitoring a disease caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic acids can also be used as probes to detect and characterize gross alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are useful in constructing microarrays for measuring gene expression. The proteins are useful as therapeutic agents for gene therapy or as vaccines. The present sequence was used to illustrate the invention.

XX Sequence 17 BP; 0 A; 1 C; 0 G; 16 T; 0 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
| | | | | | | | | | | | | | | | | |
Db 17 AAAAAAAAAAAAAA 3

RESULT 461
ID ABZ61566/c
AC ABZ61566;
XX
XX 21-MAR-2003 (first entry)
DE Human H-Ras DNazyme target #357.
XX
KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosstatic; anti-HIV;
KW anti-rheumatic; cancer; AIDS; ss.
XX
OS Homo sapiens.
XX
PN WO200297114-A2.
XX
PD 05-DEC-2002.
XX
PF 29-MAY-2002; 2002WO-US016840.
XX
PR 29-MAY-2001; 2001US-0294140P.
PR 06-JUN-2001; 2001US-0296249P.
PR 10-SEP-2001; 2001US-0318471P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA
PI Mcswiggen J;
XX
XX WPI; 2003-140484/13.
XX
XX Novel short interfering RNA and enzymatic nucleic acid useful for
XX treating cancer, modulates the expression of a nucleic acid encoding
XX HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.

XX Claim 58; Page 117; 185pp; English.
XX The invention relates to a novel short interfering RNA (siRNA) nucleic
XX acid molecule or an enzymatic nucleic acid molecule, that modulates
XX expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
XX human immunodeficiency virus (HIV) or a component of HIV. The nucleic
XX acid molecule of the invention has cytosstatic, anti-HIV, and anti-
XX rheumatic activity. The nucleic acid molecules are useful for reducing
XX HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
XX also useful for treating breast, ovarian, colorectal, lung, prostate,
XX bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
XX shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,
XX ABZ66530 - ABZ66585 represent substrate/target sequences for the human
XX ribozymes of the invention
XX Sequence 17 BP; 2 A; 4 C; 8 G; 0 T; 3 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1228 CTGCTCAGCCAGGCC 1242
| | | | | | | | | | | | | | | | | |
Db 17 CTGCTCAGCCAGGCC 3

RESULT 462

ABZ64568
ID ABZ64568 standard; RNA; 17 BP.
XX
AC ABZ64568;
XX
XX 21-MAR-2003 (first entry)
DE Human HER2 DNazyme substrate #25.
XX
XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosstatic; anti-HIV;
KW anti-rheumatic; cancer; AIDS; ss.
XX
OS Homo sapiens.
XX
PN WO200297114-A2.
XX
PD 05-DEC-2002.
XX
PF 29-MAY-2002; 2002WO-US016840.
XX
PR 29-MAY-2001; 2001US-0294140P.
PR 06-JUN-2001; 2001US-0296249P.
PR 10-SEP-2001; 2001US-0318471P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA
PI Mcswiggen J;
XX
XX WPI; 2003-140484/13.
XX
XX Novel short interfering RNA and enzymatic nucleic acid useful for
XX treating cancer, modulates the expression of a nucleic acid encoding
XX HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.

XX Claim 4; Page 133; 185pp; English.
XX The invention relates to a novel short interfering RNA (siRNA) nucleic
XX acid molecule or an enzymatic nucleic acid molecule, that modulates
XX expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
XX human immunodeficiency virus (HIV) or a component of HIV. The nucleic
XX acid molecule of the invention has cytosstatic, anti-HIV, and anti-
XX rheumatic activity. The nucleic acid molecules are useful for reducing
XX HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
XX also useful for treating breast, ovarian, colorectal, lung, prostate,
XX bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
XX shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,
XX ABZ66530 - ABZ66585 represent substrate/target sequences for the human
XX ribozymes of the invention
XX Sequence 17 BP; 1 A; 12 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 90 CCCCCGCCCCCGCC 104
| | | | | | | | | | | | | | | | | |
Db 3 CCCCCGCCCCCGCC 17

RESULT 463
ADC84469/c
ID ADC84469 standard; DNA; 17 BP.
XX
AC ADC84469;
XX
XX 01-JAN-2004 (first entry)

XX PCR primer for amplifying plant blastogenesis specific gene #SEQ ID 2.
XX Plant blastogenesis; transformation; gene expression; tissue specific;
KW PCR; primer; ss.

```

XX OS Synthetic.
XX PN JP2003159071-A.
XX PD 03-JUN-2003.
XX PF 22-NOV-2001; 2001JP-00358366.
XX PR 22-NOV-2001; 2001JP-00358366.
XX PA (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.
XX DR WPI; 2003-818678/77.
XX PT New naturally derived DNA specifically expressed during blastogenesis of
XX PT a plant, useful for producing a transformed plant and for compulsive
XX PT expression of a protein.
XX PS Example 3; SEQ ID NO 2; 43pp; Japanese.
XX CC The invention relates to naturally derived DNA specifically expressed
XX CC during plant blastogenesis. The DNA of the invention is useful for
XX CC producing a transformed plant. Methods of the invention are also useful
XX CC for compulsive expression of this DNA. Methods of the invention are
XX CC useful for plant tissue specific expression of genes. Also, the growth
XX CC stage of a plant can be controlled specifically. The current sequence
XX CC represents a PCR primer for amplifying a plant blastogenesis specific
XX CC gene of the invention.
XX SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
DB 16 AAAAAAAAAAAAAA 2

RESULT 464
ADC84470/C
ID ADC84470 standard; DNA; 17 BP.
XX AC ADC84470;
XX DT 01-JAN-2004 (first entry)
XX DE PCR primer for amplifying plant blastogenesis specific gene #SEQ ID 3.
XX KW Plant blastogenesis; transformation; gene expression; tissue specific;
XX KM PCR; primer; ss.
XX OS Synthetic.
XX PN JP2003159071-A.
XX PD 03-JUN-2003.
XX PF 22-NOV-2001; 2001JP-00358366.
XX PR 22-NOV-2001; 2001JP-00358366.
XX PA (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.
XX DR WPI; 2003-818678/77.
XX PT New naturally derived DNA specifically expressed during blastogenesis of
XX PT a plant, useful for producing a transformed plant and for compulsive
XX PT expression of a protein.
XX PS Example 3; SEQ ID NO 3; 43pp; Japanese.

```

```

XX CC The invention relates to naturally derived DNA specifically expressed
XX CC during plant blastogenesis. The DNA of the invention is useful for
XX CC producing a transformed plant. Methods of the invention are also useful
XX CC for compulsive expression of this DNA. Methods of the invention are
XX CC useful for plant tissue specific expression of genes. Also, the growth
XX CC stage of a plant can be controlled specifically. The current sequence
XX CC represents a PCR primer for amplifying a plant blastogenesis specific
XX CC gene of the invention.
XX SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
DB 16 AAAAAAAAAAAAAA 2

RESULT 465
ADE77745/C
ID ADE77745 standard; DNA; 17 BP.
XX AC ADE77745;
XX DT 29-JAN-2004 (first entry)
XX DE DNA oligo (SeqID 5) related to the human B1799 gene.
XX KW ss; allergic disease; B1799; anti-allergic; anti-inflammatory;
XX KM dermatological; gene therapy; atopic dermatitis.
XX OS Unidentified.
XX PN WO2003083139-A1.
XX PD 09-OCT-2003.
XX PF 25-FEB-2003; 2003WO-JP002047.
XX PR 03-APR-2002; 2002JP-00100908.
XX PA (GENO-) GENOX RES INC.
XX PA (NIGE-) JAPAN GEN AGENCY NATION.
XX PI Matsumoto Y, Imai Y, Yoshida N, Oshida T, Sugita Y, Saito H;
XX DR WPI; 2003-804076/75.
XX PT Examining allergic diseases, such as atopic dermatitis, comprises
XX PT comparing the expression levels of gene B1799 in T cells in a patient and
XX PT a healthy individual.
XX PS Example 1; SEQ ID NO 5; 87pp; Japanese.
XX CC This invention relates to a novel method for screening and examining
XX CC allergic diseases by the use of B1799 as the indicator gene.
XX CC Specifically, it comprises determining the expression level of this
XX CC indicator gene in a biological sample obtained from the patient, and
XX CC identifying differential expression (increased expression of B1799) in
XX CC comparison to that observed in a healthy individual. The present
XX CC invention describes the B1799 protein as anti-allergic, anti-inflammatory
XX CC and dermatological. As such, through the use of gene therapy, this method
XX CC can be used to treat allergic diseases particularly atopic dermatitis.
XX CC Furthermore, it is useful for determining a diagnosis that is convenient
XX CC and non-invasive, and is also applicable in high throughput screening to
XX CC identify candidate compounds for additional remedies. This
XX CC oligonucleotide sequence is the DNA oligo (SeqID 5) related to the human
XX CC B1799 gene of the invention.
XX SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

```

```

Query Match      1.0%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
    |||||
Db 16 AAAAAAAAAAAAAA 2

RESULT 466
ID ABN87920/c
XX ABN87920;
AC ABN87920;
XX
DT 12-AUG-2002 (first entry)
XX
DE Human GSR allele specific oligonucleotide primer SEQ ID NO:39.
XX
KW Human; glutathione reductase; GSR; enzyme; haemolytic anaemia; SNP;
KW gene therapy; antianaemic; polymorphic; single nucleotide polymorphism;
KW primer; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FT misc_feature 14
FT FT /*tag= a
FT FT /note= "polymorphic base"
XX
PN W0200242320-A2.
XX
PD 30-MAY-2002.
XX
XX 13-NOV-2001; 2001WO-US046473.
XX
XX 10-NOV-2000; 2000US-0247202P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
XX Bieglecki KM, Sanchis A, Sausker EA, Sun X;
XX WPI; 2002-471719/50.
XX
PT New genetic variants of Glutathione reductase isogenes, useful for
PT improving efficiency and reliability in drug development for treating
PT hemolytic anemia.
XX
PS Claim 14; Page 14; 137pp; English.
XX
CC The present invention describes genetic variants of the human glutathione
CC reductase (GSR) gene (1). (1) has antianaemic activity and can be used in
CC gene therapy. (1) can be used in screening for drugs targeting (1) that
CC are useful for treating haemolytic anaemia. Methods from the present
CC invention can be used for improving the efficiency and reliability of
CC several steps in the discovery and development of drugs for treating
CC diseases associated with GSR activity; for haplotyping, which is also
CC used by the pharmaceutical research scientist to validate GSR as a
CC candidate target for treating a specific condition or disease predicted
CC to be associated with GSR activity, e.g. haemolytic anaemia, and in the
CC design of clinical trials for treating a specific condition of disease
CC associated with GSR activity; and for screening compounds targeting GSR.
CC (1) is useful in studying the expression and function of GSR, and in
CC expressing GSR protein for use in screening for candidate drugs to treat
CC diseases related to GSR activity. (1) is also useful in studying the
CC effect of the variation on the biological activity of GSR as well as on
CC the binding affinity of candidate drugs targeting GSR for the treatment
CC of haemolytic anaemia. The present sequence represents an allele specific
CC oligonucleotide (ASO) primer for the human GSR gene, which is given in
CC the exemplification of the present invention. N.B. The polymorphic base
CC (showing a single nucleotide polymorphism) in the ASO primer is shown
CC using an IUPAC ambiguity code (as given in the present invention)

XX SQ Sequence 15 BP; 1 A; 0 C; 0 G; 13 T; 0 U; 0 Other;
Query Match      1.0%; Score 14.6; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAAA 1494
    |.|||||
Db 15 TWAAAAAAAAAAAA 1

RESULT 467
ID AAT44591/c
XX AAT44591 standard; DNA; 16 BP.
XX
AC AAT44591;
XX
DT 03-JUL-1997 (first entry)
XX
DE Cryptosporidium parvum 18S rRNA gene primer/probe.
XX
KW Cryptosporidium parvum; 18S rRNA; ribosomal RNA; detection; diagnosis;
KW polymerase chain reaction; hybridisation probe; ss.
XX
XX Synthetic.
XX
XX W09634978-A1.
XX
XX 07-NOV-1996.
XX
XX 06-MAY-1996; 96WO-AU000274.
XX
XX 05-MAY-1995; 95AU-00002831.
XX
PA (MACQ-) MACQUARIE RES LTD.
PA (SYDN-) SYDNEY WATER CORP LTD.
XX
XX Vesey G, Veal D, Williams KL, Ashbolt NJ, Dorsch M;
XX WPI; 1996-506178/50.
XX
XX Oligonucleotide for detection of viable Cryptosporidium parvum cells -
XX hybridises with unique sequences in 18S rRNA, useful as probe or primer
XX for PCR amplification.
XX
PS Claim 4; Page 15; 22pp; English.
XX
CC The present sequence is for detecting viable Cryptosporidium parvum cells
CC by hybridising specifically to unique 18S rRNA sequences of C. parvum. It
CC can be used when labelled as a probe or as a primer for PCR amplification
CC of 18S rRNA. It can detect live C. parvum oocysts, or other cells,
CC particularly in water but also in other environmental or clinical samples
CC such as animal or human body fluids or excretions. It does not detect
CC dead cells, because RNA degrades too quickly in such cells, or cells of
CC other Cryptosporidium species that are not pathogenic to humans
XX
XX Sequence 16 BP; 2 A; 0 C; 1 G; 13 T; 0 U; 0 Other;
Query Match      1.0%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1476 ATGCTAAAAA 1491
    |||||
Db 16 ATACTAAAAA 1

RESULT 468
ID AAX18365/c
XX AAX18365 standard; DNA; 16 BP.
XX
AC AAX18365;
```

XX
DT 11-MAY-1999 (first entry)
DE RT-PCR primer of the invention SEQ ID 6.
XX
KW RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
OS Synthetic.
XX
PN JP11032765-A.
XX
XX 09-FEB-1999.
PD
XX 18-JUL-1997; 97JP-00208312.
XX
XX 18-JUL-1997; 97JP-00208312.
PR
XX (TAKI) TAKARA SHUZO CO LTD.
PA
XX WPI; 1999-183822/16.
DR
XX Peptides having at least two new nucleotides - useful as primers in RT-PCR.
PT
XX Disclosure; Page 10; 19pp; Japanese.
PS
XX This sequence represents a primer of the invention. The invention relates to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n = N; V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or thymine; gamma = thymine; k = natural number of 3 or over indicating the repetition of gamma, in which thymine expressed by gamma is composed of 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are useful as primers for RT-PCR and determination of base sequences. The new sequences allow for reproductive and highly efficient analysis of gene sequences
CC
XX Sequence 16 BP; 0 A; 1 C; 1 G; 14 T; 0 U; 0 Other;
SQ
Query Match 1.0%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX This sequence represents a primer of the invention. The invention relates to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n = N; V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or thymine; gamma = thymine; k = natural number of 3 or over indicating the repetition of gamma, in which thymine expressed by gamma is composed of 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are useful as primers for RT-PCR and determination of base sequences. The new sequences allow for reproductive and highly efficient analysis of gene sequences
CC
XX Sequence 16 BP; 0 A; 1 C; 1 G; 14 T; 0 U; 0 Other;
SQ
Query Match 1.0%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX
QY 1478 GCTAAAAA 1493
DB 16 GCAAAAAA 1
XX
RESULT 469
AAAX18360/C
ID AAAX18360 standard; DNA; 16 BP.
XX
AC AAAX18360;
XX
DT 11-MAY-1999 (first entry)
XX
DE RT-PCR primer of the invention SEQ ID 1.
XX
KW RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
OS Synthetic.
XX
PN JP11032765-A.
XX
XX 09-FEB-1999.
PD
XX 18-JUL-1997; 97JP-00208312.
XX
XX 18-JUL-1997; 97JP-00208312.
PR
XX (TAKI) TAKARA SHUZO CO LTD.
PA

XX
DR WPI; 1999-183822/16.
XX
PT Peptides having at least two new nucleotides - useful as primers in RT-PCR.
PT
XX Disclosure; Page 10; 19pp; Japanese.
PS
XX This sequence represents a primer of the invention. The invention relates to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n = N; V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or thymine; gamma = thymine; k = natural number of 3 or over indicating the repetition of gamma, in which thymine expressed by gamma is composed of 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are useful as primers for RT-PCR and determination of base sequences. The new sequences allow for reproductive and highly efficient analysis of gene sequences
CC
XX Sequence 16 BP; 0 A; 1 C; 1 G; 14 T; 0 U; 0 Other;
SQ
Query Match 1.0%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX
QY 1479 CTAAAAA 1494
DB 16 CGAAAAA 1
XX
RESULT 470
AAAX18362/C
ID AAAX18362 standard; DNA; 16 BP.
XX
AC AAAX18362;
XX
DT 11-MAY-1999 (first entry)
XX
DE RT-PCR primer of the invention SEQ ID 3.
XX
KW RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
OS Synthetic.
XX
PN JP11032765-A.
XX
XX 09-FEB-1999.
PD
XX 18-JUL-1997; 97JP-00208312.
XX
XX 18-JUL-1997; 97JP-00208312.
PR
XX (TAKI) TAKARA SHUZO CO LTD.
PA
XX WPI; 1999-183822/16.
DR
XX Peptides having at least two new nucleotides - useful as primers in RT-PCR.
PT
XX Disclosure; Page 10; 19pp; Japanese.
PS
XX This sequence represents a primer of the invention. The invention relates to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n = N; V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or thymine; gamma = thymine; k = natural number of 3 or over indicating the repetition of gamma, in which thymine expressed by gamma is composed of 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are useful as primers for RT-PCR and determination of base sequences. The new sequences allow for reproductive and highly efficient analysis of gene sequences
CC
XX Sequence 16 BP; 0 A; 1 C; 1 G; 14 T; 0 U; 0 Other;
SQ

(TAKI) TAKARA SHUZO CO LTD.

WPI; 1999-183822/16.

Peptides having at least two new nucleotides - useful as primers in RT-PCR.

Disclosure; Page 10; 19pp; Japanese.

This sequence represents a primer of the invention. The invention relates to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta-N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n = a natural number indicating the repetition of alpha; beta, delta = V or N; V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or thymine; gamma = thymine; k = natural number of 3 or over indicating the repetition of gamma, in which thymine expressed by gamma is composed of 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are useful as primers for RT-PCR and determination of base sequences. The new sequences allow for reproductive and highly efficient analysis of gene sequences

Sequence 16 BP; 0 A; 1 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1496
DB 16 AGAAAAAAAAAAAAA 1

RESULT 474
AAH27758/c
ID AAH27758 standard; DNA; 16 BP.
XX
AC AAH27758;
XX
DT 15-AUG-2001 (first entry)
XX
DE Primer used in human LUNX cdNA isolation.
XX
KW LUNX; human; cancer; micrometastatic cancer; primer; ss.
XX
QS Homo sapiens.
XX
PN JP2001078772-A.
XX
PD 27-MAR-2001.
XX
PF 07-SEP-1999; 99JP-00253186.
XX
PR 07-SEP-1999; 99JP-00253186.
XX
PA (SAKA) OTSUKA PHARM CO LTD.
XX
DR WPI; 2001-313367/33.
XX
PT Polynucleotide encoding LUNX gene product useful for the detection of cancer especially micrometastatic cancer.
XX
PS Example 1; Page 27; 30pp; Japanese.
XX
CC This invention relates to the human LUNX protein and the polynucleotide sequence encoding it. The invention includes a vector containing a LUNX polynucleotide, a host cell transformed with the vector, and an antibody that binds to LUNX. The gene can be used for cancer diagnosis and diagnosis of micrometastatic cancer and for the production of the LUNX gene product. The present sequence represents a primer used in the isolation of cdNA encoding human LUNX
XX
SQ Sequence 16 BP; 1 A; 0 C; 0 G; 14 T; 0 U; 1 Other;

XX DE Human PTPN11 PCR primer SEQ ID NO:34.
XX DE Noonan syndrome; protein tyrosine phosphatase 11; PTPN11; mutant;
KW variant; mutation; chromosome 12; enzyme; PCR primer; ss.
XX OS Synthetic.
XX OS Homo sapiens.
XX PN WO2003029422-A2.
XX PD 10-APR-2003.
XX PF 01-OCT-2002; 2002WO-US031290.
XX PR 01-OCT-2001; 2001US-0326532P.
XX PA (MOUN) MOUNT SINAI SCHOOL MEDICINE.
XX PI Gelb BD, Tartaglia M;
XX WI WIPI; 2003-381624/36.
XX DI Diagnosing and treating Noonan syndrome in a subject using a mutation in
PT a protein tyrosine phosphatase 11 gene with increased expression or
PT activity.
XX Example 4; SEQ ID NO 34; 262pp; English.
XX The present invention describes a method for diagnosing Noonan syndrome
CC in a subject. The method comprises detecting a mutation in the protein
CC tyrosine phosphatase 11 (PTPN11) gene in a subject, where the mutation
CC results in increased PTPN11 expression or activity as compared to
CC control. The human PTPN11 gene is located on chromosome 12, more
CC specifically to 12q24. Also described: (1) a kit for diagnosing Noonan
CC syndrome, comprising an oligonucleotide that specifically hybridises to
CC or adjacent to a site of mutation of a PTPN11 gene that results in
CC increased activity of a PTPN11 protein encoded by the gene or an antibody
CC that specifically recognises a mutation in a PTPN11 protein, and
CC instructions for use; (2) diagnosing Noonan syndrome in a subject,
CC comprising assessing the level of expression or activity of a PTPN11
CC protein in the test subject, and comparing it to the level of expression
CC or activity in a control subject, where an increased expression or basal
CC activity of the PTPN11 protein in the test subject compared to the
CC control is indicative of Noonan syndrome; (3) treating Noonan syndrome in
CC a patient, comprising administering an agent that modulates the
CC expression or activity of a PTPN11 protein in association with a carrier;
CC (4) an isolated PTPN11 variant comprising a mutation resulting in
CC increased level of PTPN11 activity; (5) an isolated cell comprising a
CC vector comprising a nucleic acid encoding the PTPN11 variant of (4),
CC operatively associated with an expression control sequence; (6) an
CC isolated nucleic acid encoding the PTPN11 variant of (4); and (7) an
CC isolated oligonucleotide which specifically hybridises to the nucleic
CC acid of (6). The methods and compositions of the present invention are
CC useful for diagnosing and treating a disorder associated with the
CC aberrant expression and/or activity of the PTPN11 gene, specifically
CC Noonan syndrome. The present sequence represents a PCR primer used in the
CC amplification of human PTPN11, which is given in the exemplification of
XX the present invention.
XX Sequence 16 BP; 0 A; 12 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 1.0%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 221 CCGCGCGCGCGCGCGC 236
DB 1 CCGCGCGCGCGCGCGC 16

RESULT 477
AAAA7676/c

ID AAAA7676 standard; cDNA; 15 BP.
XX AAAA7676;
XX 08-NOV-2000 (first entry)
XX Oligo d(T) primer for human DDAH1.
XX Dimethylarginine dimethylaminohydrolase; DDAH; DDAH1; DDAH2;
KW arginine deaminase; hyperlipidemia; renal failure; hypertension;
KW restenosis; atherosclerosis; schizophrenia; multiple sclerosis; cancer;
KW ischemia reperfusion injury; septic shock; multi organ failure;
KW arthritis; skin disorders; inflammatory cardiac disease; migraine;
XX infection; ss.
XX Homo sapiens.
XX WO200044888-A2.
XX 03-AUG-2000.
XX 26-JAN-2000; 2000WO-GB000226.
XX 26-JAN-1999; 99GB-00001705.
PR 04-JUN-1999; 99GB-00013066.
XX (UNLO) UNIV COLLEGE LONDON.
XX Vallance PJT, Leiper JM, Whitley GSJ, Charles IG;
PI WIPI; 2000-543392/49.
XX Novel methylarginase polypeptides and polynucleotides, used to identify
PT modulators of them, which are used in the treatment of e.g. cancer,
PT hypertension, and bacterial infections.
XX Example 1; Page 33; 68pp; English.
XX Nucleotides encoding methylarginase polypeptides, vectors comprising
CC these nucleotides and the polypeptides themselves can be used in
CC medicaments for the treatment of hyperlipidemia, renal failure,
CC hypertension, restenosis after angioplasty, atherosclerosis,
CC complications of heart failure, schizophrenia, multiple sclerosis or
CC cancer. Modulators of the enzyme can be used in medicaments for the
CC treatment of ischemia-reperfusion injury of the brain or heart, cancer,
CC lethal hypertension in severe inflammatory conditions such as septic
CC shock or multi-organ failure, or local and systemic inflammatory
CC disorders including arthritis, skin disorders, inflammatory cardiac
CC disease, migraine, or microbial or bacterial infection. The sequence of
CC human DDAH1 was obtained by data base searching. The EST's used in the
CC process are given in GENESEQ records AAA47661-A47677
XX Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 1 Other;
SQ Query Match 0.9%; Score 14.2; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2.4e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1480 TAAAAAATAAAAAA 1494
DB 15 BAAAAAATAAAAAA 1
RESULT 478
AAD44150
ID AAD44150 standard; DNA; 15 BP.
XX AAD44150;
XX AAD44150;
XX 13-DEC-2002 (first entry)
XX Oligo-AT PCR primer #1 used to illustrate the method of the invention.
XX

KW Sequential consensus region-directed amplification; gene expression; disease diagnosis; gene analysis; human; matrix metalloproteinase; PCR; primer; ss.

XX Unidentified.

XX US6277571-B1.

XX 21-AUG-2001.

XX 30-SEP-1998; 98US-00163485.

XX 03-OCT-1997; 97US-00943162.

XX 03-OCT-1997; 97US-0108152P.

XX (UVI-) UNIV VIRGINIA COMMONWEALTH INTELLECTUAL.

XX Fillmore H, Broadus W, Gillies G;

XX WPI; 2002-412824/44.

XX Sequential consensus region-directed amplification for sorting mixture of DNAs into 2 or more subsets or distinguishing gene expression patterns in 2 samples, useful for disease diagnosis and gene analysis.

XX Example; Fig 1D; 19pp; English.

XX The invention relates to a method of sequential consensus region-directed amplification for sorting a mixture of DNAs into 2 or more subsets or distinguishing gene expression patterns in 2 samples. The methods, kits and oligonucleotides are useful for sorting a mixture of DNAs into 2 or more subsets or distinguishing gene expression patterns in 2 samples e.g. for disease diagnosis and gene analysis. The present sequence is oligo AT PCR primer used to illustrate the method of the invention

XX Sequence 15 BP; 14 A; 0 C; 0 G; 0 T; 0 U; 1 Other;

Query Match 0.9%; Score 14.2; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2.4e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1495
:|||||
Db 1 AAAAAAAAAAAAAA 15

RESULT 479
AA18387/C
ID AAX18387 standard; DNA; 16 BP.

XX AAX18387;

XX 11-MAY-1999 (first entry)

DT RT-PCR primer of the invention SEQ ID 28.

DE RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.

XX Synthetic.

XX JPI1032765-A.

XX 09-FEB-1999.

XX 18-JUL-1997; 97JP-00208312.

XX 18-JUL-1997; 97JP-00208312.

XX (TAKI) TAKARA SHUZO CO LTD.

XX WPI; 1999-183822/16.

XX Peptides having at least two new nucleotides - useful as primers in RT-

PCR.

Example 1; Page 12; 19pp; Japanese.

This sequence represents a primer of the invention. The invention relates to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta-N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n = natural number indicating the repetition of alpha; beta, delta = V or N; V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or thymine; gamma = thymine; k = natural number of 3 or over indicating the repetition of gamma, in which thymine expressed by gamma is composed of 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are useful as primers for RT-PCR and determination of base sequences. The new sequences allow for reproductive and highly efficient analysis of gene sequences

XX Sequence 16 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 2 Other;

Query Match 0.9%; Score 14.2; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 2.7e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1480 TAAAAAAAAAAAAA 1494

Db 15 BAAAAAAAAAAAAA 1

RESULT 480

AAQ33508
ID AAQ33508 standard; DNA; 14 BP.

XX AAQ33508;

XX 25-MAR-2003 (revised)

DT 02-FEB-1993 (first entry)

XX Sequence of microsatellite from clone AGLA206.

XX PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.

XX Bos taurus.

XX WO9213102-A1.

XX 06-AUG-1992.

XX 15-JAN-1992; 92WO-US000340.

XX 15-JAN-1991; 91US-00642342.

XX (GENM-) GENMARK.

XX Georges M, Massey JM;

XX WPI; 1992-284684/34.

XX Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.

XX Table 7; Page 131; 517pp; English.

XX The sequence is that of a bovine microsatellite sequence obtd. by screening a genomic library of bovine MboI DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independency of (T6)n > 9 microsatellites and MboI sites, the frequency of (T6)n > 9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp.

CC microsatellite (using the program OPTIPRIM). The microsatellites may be
 CC used to identify individuals, for parentage testing, and in the genetic
 CC mapping of economic trait loci, or genes involved in the determination of
 CC economically important traits esp. in cattle, to allow selective
 CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
 CC field.)

XX Sequence 14 BP; 14 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.9%; Score 14; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1494
 Db 1 AAAAAAAAAAAAAA 14

RESULT 481

AAT36896/C
 ID AAT36896 standard; DNA; 14 BP.

XX AC AAT36896;

XX 23-OCT-1996 (first entry)

DE Candida albicans leukotriene A4 hydrolase cDNA PCR primer.

XX Leukotriene A4 hydrolase; pro-inflammatory; reduced;
 KW 5,6-dihydroxy-7,9,11,14-eicosatetraenoic acid; immune response;
 KW expression vector; recombinant production; antibody generation;
 KW diagnostic agent; passive immunisation; vaccine; treatment; prevention;
 KW infection; reagent; detection; modulation; inflammatory response;
 KW antisense; prevention; PCR; primer; polymerase chain reaction; ss.

XX Synthetic.

XX US5529916-A.

XX 25-JUN-1996.

XX 01-NOV-1994; 94US-00332838.

XX 01-NOV-1994; 94US-00332838.

XX (STRD) UNIV LELAND STANFORD JUNIOR.

XX Falkow S, Cormack BP;

XX WPI; 1996-308739/31.

XX Recombinant DNA encoding yeast leukotriene A4 hydrolase - and related
 PT vectors and transformed cells, producing yeast hydrolase useful, e.g. as
 PT vaccine against Candida infection and as diagnostic reagent.

XX Example 1; Col 23-24; 24pp; English.

XX The present sequence is a primer for the C. albicans leukotriene A4
 CC (LTA4) hydrolase, cDNA. The hydrolase converts LTA4 to (probably) 5,6-
 CC dihydroxy-7,9,11,14-eicosatetraenoic acid, which is less pro-inflammatory
 CC than the LTB4 produced by the mammalian enzyme, therefore reducing the
 CC immune response to C. albicans. An expression vector contg. the hydrolase
 CC cDNA can be used to produce the hydrolase, which can be used to generate
 CC antibodies (as diagnostic agents, or for passive immunisation), as a
 CC vaccine to treat or prevent Candida infection, as a reagent to detect
 CC antibodies and to reduce/modulate an inflammatory response by systemic or
 CC topical application. Nucleic acid antisense to the hydrolase cDNA may
 CC prevent hydrolase expression

XX Sequence 14 BP; 1 A; 0 C; 1 G; 12 T; 0 U; 0 Other;

Query Match 0.9%; Score 14; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1479 CTAATAAAAAAAAA 1492
 Db 14 CTAATAAAAAAAAA 1

RESULT 482

AAT75017/C
 ID AAT75017 standard; DNA; 14 BP.

XX AC AAT75017;

XX 06-OCT-1997 (first entry)

DE Breast tumour cDNA primer (T)12AG.

XX Breast cancer; tumour; B18Ag1; prognosis; diagnosis; vaccine; retrovirus;
 KW polymerase chain reaction; PCR; primer; ss.

XX Synthetic.

XX W09725431-A1.

XX 17-JUL-1997.

XX 10-JAN-1997; 97WO-US000398.

XX 10-JAN-1996; 96US-00587329.

XX (CORI-) CORIXA CORP.

XX Frudakis TN, Smith JM;

XX WPI; 1997-384982/35.

XX Endogenous human tumour-associated retroviral element, B18Ag1 - used for
 PT the prognosis, diagnosis and monitoring of human cancers, especially
 PT breast cancer.

XX Example 3; Page 21; 74pp; English.

XX Primer (T)12AG (AAT75017) is used for first strand cDNA synthesis from
 CC RNA prepd. from human breast tumour tissue. The cDNA can subsequently be
 CC amplified using primers B18Ag1-2 and B18Ag1-3 (see also AAT75013 and
 CC AAT75014) to isolate tumour-associated retroviral element B18Ag1 (see
 CC also AAT75002)

XX Sequence 14 BP; 1 A; 0 C; 1 G; 12 T; 0 U; 0 Other;

Query Match 0.9%; Score 14; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1479 CTAATAAAAAAAAA 1492
 Db 14 CTAATAAAAAAAAA 1

RESULT 483

AAX83329/C
 ID AAX83329 standard; DNA; 14 BP.

XX AC AAX83329;

XX 31-AUG-1999 (first entry)

DE Breast cancer tumour specific cDNA anchored primer.

XX Breast cancer; tumour; gene expression; genome; diagnosis; mammal;
 KW human endogenous retrovirus; vaccine; primer; PCR; amplification; ss.
 XX Synthetic.

```

OS Homo sapiens.
XX WO9725426-A2.
XX
XX
XX
XX 17-JUL-1997.
XX
XX 10-JAN-1997; 97WO-US0000485.
XX
XX 11-JAN-1996; 96US-00585392.
XX
XX 20-AUG-1996; 96US-00700014.
XX
XX (CORI-) CORIXA CORP.
XX
XX Prudakis TN, Smith JM, Reed SG;
XX WPI; 1997-372865/34.
XX
XX
XX Breast cancer-related DNA from retrovirus antigen (s) - useful for
XX diagnosis and treatment of breast cancer.
XX
XX Example 1; Page 24; 221pp; English.
XX
XX Primers AAX83286-X83329 were used to PCR amplify breast cancer tumour
XX specific clones (AAX83201-X83285 and AAX83331-X83415) which are expressed
XX from a genomic region containing a human endogenous retrovirus
XX (AAX83330). Detection of the clone sequences allows determination of the
XX presence of breast cancer in a mammal. Progression of breast cancer can
XX be monitored by detecting the level of clone expression. Polypeptides
XX encoded by the clones can be used in vaccines to inhibit or prevent
XX breast cancer
XX
XX Sequence 14 BP; 1 A; 0 C; 1 G; 12 T; 0 U; 0 Other;
XX
XX Query Match 0.9%; Score 14; DB 1; Length 14;
XX Best Local Similarity 100.0%; Pred. No. 2.3e+02;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Example 1; Page 50; 113pp; English.
XX
XX This is a 3' poly(T) PCR primer used in the amplification of the
XX inducible cytochrome P450RAI gene which specifically metabolises a
XX derivative of the retinoic acid (RA). The cytochrome P450 gene in general
XX produces enzymes involved in the oxidative metabolism of endogenous and
XX exogenous compounds. The cytochrome P450 nucleotide sequence can be used
XX to induce or suppress the expression of its protein. P450RAI is highly
XX induced by RA in cell lines and tissues. This allows for the development
XX of a drug screen using promoters and nucleotide sequences to identify
XX drugs which are useful for reducing the catabolism of RA
XX
XX Sequence 14 BP; 1 A; 0 C; 1 G; 12 T; 0 U; 0 Other;
XX
XX Query Match 0.9%; Score 14; DB 1; Length 14;
XX Best Local Similarity 100.0%; Pred. No. 2.3e+02;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1479 CTAAGAAAAA 1492
XX DB 14 CTAAGAAAAA 1
XX
XX RESULT 485
XX AAV09229/c
XX ID AAV09229 standard; DNA; 14 BP.
XX AC AAV09229;
XX
XX 07-JUL-1998 (first entry)
XX
XX 3' poly(T) primer 5.
XX
XX 3' poly(T) primer; PCR; amplification; cytochrome P450 gene;
XX oxidative metabolism; P450RAI; retinoic acid; RA; promoter; ss.
XX
XX Synthetic.
XX
XX WO9749832-A2.
XX
XX 31-DEC-1997.
XX
XX 23-JUN-1997; 97WO-CA0000488.
XX
XX 21-JUN-1996; 96US-00667546.
XX
XX 01-OCT-1996; 96US-00724466.
XX
XX (TOOH) UNIV QUEBENS KINGSTON.
XX
XX Petkovich PM;
XX
XX WPI; 1998-077193/07.
XX
XX Identifying DNA encoding inducible or suppressible cytochrome P450 - by
XX
XX Query Match 0.9%; Score 14; DB 1; Length 14;
XX Best Local Similarity 100.0%; Pred. No. 2.3e+02;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1479 CTAAGAAAAA 1492
XX DB 14 CTAAGAAAAA 1
XX
XX RESULT 484
XX AAV09229/c
XX ID AAV09229 standard; DNA; 14 BP.
XX AC AAV09229;
XX
XX 07-JUL-1998 (first entry)
XX
XX 3' poly(T) primer 5.
XX
XX 3' poly(T) primer; PCR; amplification; cytochrome P450 gene;
XX oxidative metabolism; P450RAI; retinoic acid; RA; promoter; ss.
XX
XX Synthetic.
XX
XX WO9749832-A2.
XX
XX 31-DEC-1997.
XX
XX 23-JUN-1997; 97WO-CA0000488.
XX
XX 21-JUN-1996; 96US-00667546.
XX
XX 01-OCT-1996; 96US-00724466.
XX
XX (TOOH) UNIV QUEBENS KINGSTON.
XX
XX Petkovich PM;
XX
XX WPI; 1998-077193/07.
XX
XX Identifying DNA encoding inducible or suppressible cytochrome P450 - by
XX
XX Query Match 0.9%; Score 14; DB 1; Length 14;
XX Best Local Similarity 100.0%; Pred. No. 2.3e+02;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1479 CTAAGAAAAA 1492
XX DB 14 CTAAGAAAAA 1
XX
XX RESULT 485
XX AAV12221/c
XX ID AAV12221 standard; DNA; 14 BP.
XX AC AAV12221;
XX
XX 22-JUN-1998 (first entry)
XX
XX Poly(T) oligonucleotide used in differential display PCR.
XX
XX Retinoid metabolising protein; P450RAI; retinoid oxidase; retinoic acid;
XX zebrafish; inhibitor; antisense; cancer; actinic keratosis;
XX oral leukoplakia; head tumour; neck tumour;
XX non-small cell lung carcinoma; basal cell carcinoma;
XX acute promyelocytic leukaemia; skin cancer; acne; psoriasis; ichthyosis;
XX therapy; diagnosis; screening; differential display; PCR; primer; ss.
XX
XX Synthetic.
XX
XX WO9749815-A1.
XX
XX 31-DEC-1997.
XX
XX 23-JUN-1997; 97WO-CA0000440.
XX
XX 21-JUN-1996; 96US-00667546.
XX
XX 01-OCT-1996; 96US-00724466.
XX
XX (TOOH) UNIV QUEBENS KINGSTON.
XX
XX Petkovich PM, White JA, Beckett BR, Jones G;
XX
XX WPI; 1998-077178/07.
XX
XX Retinoid metabolising protein - useful to develop products to treat, e.g.
XX cancer, actinic keratosis, oral leukoplakia, acne, psoriasis or
XX ichthyosis.
XX
XX Disclosure; Page 14; 110pp; English.
XX
XX Poly(T) oligonucleotides (see AAV12217-28) were used in reverse
XX transcription reactions on poly(A) RNA isolated from the fins of control
XX or retinoic acid-treated zebrafish (Danio rerio). Several combinations of
XX the poly(T) primers were used with degenerate upstream primers (see
XX AAV12229-33) for differential display PCR. Bands demonstrating
XX reproducible differential amplifications were found using the primers
XX given in AAV12221 and AAV12231. This PCR product was reamplified (see

```

```
CC AAV12234-35). A differential display product (see AAV12213) which
CC exhibited a dependence on the presence of retinoic acid for its
CC expression was isolated, and was used to isolate a full-length clone (see
CC AAV12203) coding for a novel retinoid metabolising protein (see
CC AAW44159), designated zp450RA1
XX
SQ Sequence 14 BP; 1 A; 0 C; 1 G; 12 T; 0 U; 0 Other;

Query Match          0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAATAAAAAAAAAA 1492
Db 14 CTAATAAAAAAAAAA 1

RESULT 486
AAV69039/c
ID AAV69039 standard; DNA; 14 BP.
XX
AC AAV69039;
XX
DT 22-JAN-1999 (first entry)
DE Human breast tumour RNA anchor primer #1.
XX
KW Human; breast cancer; breast tumour tissue; diagnosis; treatment;
KW vaccine; epitope; endogenous; retroviral element; primer; ss.
XX
OS Synthetic.
XX
OS Homo sapiens.
XX
PN WO9845328-A2.
XX
PD 15-OCT-1998.
XX
PF 09-APR-1998; 98WO-US006939.
XX
PR 09-APR-1997; 97US-00838762.
XX
PR 11-DEC-1997; 97US-00991789.
XX
PA (CORI-) CORIXA CORP.
XX
PI Frudakis TN, Smith JM, Reed SG;
XX
DR WPI; 1998-557473/47.
XX
PT New DNA sequences isolated from endogenous human retroviral element - and
PT related vectors, transformed cells, proteins and antibodies, useful for
PT diagnosis, treatment and prevention of breast cancer.
XX
PS Example 1; Page 76; 173pp; English.
XX
CC The present sequence represents an anchor primer used to convert normal
CC breast and tumour RNA to cDNA. The present invention describes nucleotide
CC sequences which encode human breast cancer specific polypeptides.
CC Detection or measurement of human breast tumour specific polypeptides and
CC nucleotide sequences, or the corresponding RNA in a sample, is used for
CC diagnosis and monitoring of breast cancer. Human breast tumour specific
CC polypeptides and nucleotide sequences, and the vectors containing the
CC DNAs, are also useful in vaccines for inhibiting development (for
CC prevention or therapy) of breast cancer. The polypeptides may also be
CC used to raise monoclonal antibodies, used as immunoassay reagents
XX
SQ Sequence 14 BP; 1 A; 0 C; 1 G; 12 T; 0 U; 0 Other;

Query Match          0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAATAAAAAAAAAA 1492
|||||
```

```
Db 14 CTAATAAAAAAAAAA 1

RESULT 487
AAV02695/c
ID AAV02695 standard; DNA; 14 BP.
XX
AC AAV02695;
XX
DT 10-MAY-1999 (first entry)
DE Barley HPPD primer #1.
XX
KW HPPD; barley; hydroxyphenylpyruvate dioxygenase; plant; transformation;
KW transgenic; plant cell; callus tissue; protoplast; electroporation;
KW particle bombardment; soya; barley; wheat; oilseed rape; maize; primer;
KW sunflower; tobacco; ss.
XX
OS Hordeum vulgare.
XX
PN DE19730066-A1.
XX
PD 21-JAN-1999.
XX
PF 14-JUL-1997; 97DE-01030066.
XX
PR 14-JUL-1997; 97DE-01030066.
XX
PA (BADI ) BASF AG.
XX
PI Seulberger H, Lerchl J, Schmidt R, Kurpinska K, Falk J;
XX
DR WPI; 1999-096742/09.
XX
PT DNA encoding barley hydroxyphenylpyruvate dioxygenase - for producing
PT plants with increased vitamin E content, etc.
XX
PS Example 1; Page 9; 26pp; German.
XX
CC AAV02695-X02708 are primers used in the isolation of a novel barley
CC (Hordeum vulgare) hydroxyphenylpyruvate dioxygenase (HPPD) protein. This
CC protein is useful for plant transformation to produce transgenic plants
CC especially where an expression cassette is introduced into a plant cell,
CC callus tissue, a whole plant or protoplasts by Agrobacterium tumefaciens
CC transformation, electroporation or particle bombardment and where the
CC plants are selected from soya, barley, wheat, oilseed rape, maize and
CC sunflower, or where the DNA is expressed in tobacco plants, especially in
CC leaves or seeds
XX
SQ Sequence 14 BP; 1 A; 0 C; 1 G; 12 T; 0 U; 0 Other;

Query Match          0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAATAAAAAAAAAA 1492
Db 14 CTAATAAAAAAAAAA 1

RESULT 488
AAV14689/c
ID AAV14689 standard; DNA; 14 BP.
XX
AC AAV14689;
XX
DT 24-MAR-1999 (first entry)
DE Triple helix third strand of Esterase D gene nucleotides 962-975.
XX
KW Triplex formation; DNA detection; triple helix; identification; bacteria;
KW oncogene; virus; ss.
XX
```


CC target nucleic acid presence in a sample. A preferred target is a
 CC Mycobacterium complex nucleic acid sequence. The detection method uses
 CC visual detection of a change in the hybridization without aid of
 CC instrumentation. Multiple copies of a target nucleic acid sequence are
 CC mixed with first and second detectable probes under hybridizing
 CC conditions favouring particle agglutination via a bridging molecule
 CC allowing for visual detection of the target nucleic acid sequence. The
 CC bridging molecule enhances or inhibits formation of a hybridization
 CC complex
 XX Sequence 14 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 0 Other;
 SQ
 Query Match 0.9%; Score 14; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1481 AAAAAAAAAAAAAA 1494
 Db 14 AAAAAAAAAAAAAA 1
 RESULT 491
 AAX19468/c
 ID AAX19468 standard; DNA; 14 BP.
 XX
 AC AAX19468;
 XX
 DT 21-MAY-1999 (first entry)
 XX
 DE Human senescence factor p23 T12 anchor primer SEQ ID NO:10.
 XX
 DE Human; senescence factor; p23; cancer; persistent inflammation;
 KW proliferative disorder; degenerative disorder; primer; ss.
 KW
 XX Synthetic.
 OS Homo sapiens.
 OS
 XX W09907893-A1.
 XX
 PD 18-FEB-1999.
 XX
 XX 05-AUG-1998; 98WO-US016343.
 PF
 XX 08-AUG-1997; 97US-00908873.
 PR
 XX (UNIW) UNIV WASHINGTON.
 PA
 XX Swisselhm K, Hosier S, Kubbies M;
 PI
 XX WPI; 1999-167454/14.
 DR
 XX
 FT Newly isolated nucleic acid molecule (designated p23) encoding a p23
 FT polypeptide - useful for inducing a senescence phenotype in a cell.
 XX
 XX Example 1; Page 18; 44pp; English.
 XX
 CC The present invention describes human senescence factor p23. An
 CC expression vector for p23 is useful for inducing a senescent phenotype in
 CC a cell (preferably eukaryotic). This may help in regulating diseases,
 CC including cancer, persistent inflammation, and various proliferative and
 CC degenerative disorders. These transgenic cells are useful in gene therapy
 CC for treating cancer, particularly where antisense oligonucleotides are
 CC useful for blocking normal or mutant p23 expression in cancer cells or
 CC other proliferating cells. Transgenic cells are also useful for producing
 CC the p23 polypeptide in large quantities. The antibodies are useful for
 CC raising antiserum against p23, and for identifying senescent cells in
 CC culture and tissue biopsies. The p23 polynucleotides are useful for
 CC modulating or altering p23 activity in a cell, and for identifying and
 CC isolating the whole gene encoding p23, and variants of p23. Assays based
 CC on p23 elements, which detect p23 levels and activity are useful as
 CC diagnostic markers for staging tumours, determining prognosis, and/or
 CC predicting therapeutic success. These elements also provide an assay for
 CC detecting chromosomal rearrangements in chromosome 3 in a human cell. The

CC isolation of the p23 polynucleotide permits the manipulation of malignant
 CC growth in cancer. The present sequence represents a primer used in an
 CC example from the present invention
 XX
 SQ Sequence 14 BP; 1 A; 0 C; 1 G; 12 T; 0 U; 0 Other;
 Query Match 0.9%; Score 14; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1479 CTAATAAAAAAAAA 1492
 Db 14 CTAATAAAAAAAAA 1
 RESULT 492
 AAZ08326/c
 ID AAZ08326 standard; DNA; 14 BP.
 XX
 AC AAZ08326;
 XX
 DT 13-OCT-1999 (first entry)
 XX
 DE Human lung tumour RNA conversion primer (dT)12AG anchored 3' primer.
 XX
 DE Human; lung tumour protein; therapy; diagnosis; lung cancer; vaccine;
 KW immunotherapy; detection; inhibition; primer; ss.
 KW
 XX Synthetic.
 OS Homo sapiens.
 OS
 XX W09938973-A2.
 PN
 XX 05-AUG-1999.
 PD
 XX 26-JAN-1999; 99WO-US001642.
 PF
 XX 28-JAN-1998; 98US-00015022.
 PR
 XX 28-JAN-1998; 98US-00015029.
 PR
 XX 18-MAR-1998; 98US-00040828.
 PR
 XX 18-MAR-1998; 98US-00040831.
 PR
 XX 23-JUL-1998; 98US-00122191.
 PR
 XX 23-JUL-1998; 98US-00122192.
 PR
 XX 22-DEC-1998; 98US-00219245.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 XX Reed SG, Lodes MJ, Frudakis TN, Mohamath R;
 PI
 XX WPI; 1999-479187/40.
 DR
 XX
 FT Lung tumor specific polynucleotides for inhibiting the development of
 FT lung cancer.
 XX
 XX Example 1; Page 82; 171pp; English.
 XX
 CC The present invention describes lung tumour specific polynucleotides and
 CC tumour antigens. AAZ07144 to AAZ07246 and AAZ08301 to AAZ08325 represent
 CC specifically claimed polynucleotides, and AAZ29486 to AAZ29571 represent
 CC amino acid sequences from the present invention. The lung tumour specific
 CC polynucleotides and polypeptides can be used in pharmaceutical
 CC compositions and vaccines to inhibit the development of lung cancer. They
 CC can also be used to detect lung cancer in a patient. Probes and
 CC antibodies derived from the lung tumour sequences are useful in detection
 CC of lung cancer. The present sequence represents a primer used in an
 CC example from the present invention
 XX
 SQ Sequence 14 BP; 1 A; 0 C; 1 G; 12 T; 0 U; 0 Other;
 Query Match 0.9%; Score 14; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1479 CTAACAAAAA 1492
Db 14 CTAACAAAAA 1

RESULT 493
AAC80852/c
ID AAC80852 standard; DNA; 14 BP.
XX AC AAC80852;
XX AC
XX 13-FEB-2001 (first entry)
XX DE Human B18Ag1 cDNA anchored 3' PCR primer.
XX DE
XX KW Human; breast tumour-specific antigen; cytostatic; vaccine;
XX KW breast cancer; B18Ag1; B11Ag1; B15Ag1; PCR primer; ss.
XX OS Homo sapiens.
XX PN WO200061753-A2.
XX PD 19-OCT-2000.
XX PF 07-APR-2000; 2000WO-US009312.
XX PR 09-APR-1999; 99US-00289198.
XX PR 28-OCT-1999; 99US-00429755.
XX PR 23-MAR-2000; 2000US-00534825.
XX PA (CORI-) CORIXA CORP.
XX PI Frudakis TN, Smith JM, Reed SG, Misher LE, Retter MW, Dillon DC;
XX WIPI; 2000-628403/60.
XX DR
XX PT An isolated polypeptide comprising an immunogenic portion of a breast
XX PT tumour protein used for inhibiting the development of cancer, especially
XX PT breast cancer, and monitoring cancer progression in a patient.
XX PS Example 1; Page 33; 187pp; English.
XX CC The present sequence is a PCR primer which was used in the isolation of
XX CC human breast tumour-specific antigens. Methods for the treatment and
XX CC diagnosis of breast cancer are disclosed. Nucleotide sequences that are
XX CC preferentially expressed in breast tumour tissue, and the polypeptides
XX CC encoded by such nucleotide sequences, are used in compositions and
XX CC vaccines to inhibit the development of cancer, especially breast cancer.
XX CC The progression of a cancer may be monitored by carrying out detection of
XX CC tumour-specific antigens at subsequent time points and comparing the
XX CC results from the different time points. CD4+ and/or CD8+ T-Cells isolated
XX CC from the cancer patient may be treated with tumour-specific polypeptides,
XX CC polynucleotides encoding the polypeptides or antigen presenting cells
XX CC expressing the polypeptides. The cells are then administered to the
XX CC patient to inhibit development of cancer
XX SQ Sequence 14 BP; 1 A; 0 C; 1 G; 12 T; 0 U; 0 Other;

Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAACAAAAA 1492
Db 14 CTAACAAAAA 1

RESULT 494
AAC79077/c
ID AAC79077 standard; DNA; 14 BP.
XX AC AAC79077;
XX AC
```

```
DT 05-FEB-2001 (first entry)
XX (dT) 12AG primer.
XX KW Lung tumour protein; lung cancer; cytostatic; vaccine; ss.
XX OS Synthetic.
XX PN WO200060077-A2.
XX PD 12-OCT-2000.
XX PF 30-MAR-2000; 2000WO-US008560.
XX PR 02-APR-1999; 99US-00285323.
XX PR 09-AUG-1999; 99US-00370838.
XX PR 30-DEC-1999; 99US-00476235.
XX PR 03-MAR-2000; 2000US-00518809.
XX PA (CORI-) CORIXA CORP.
XX PI Reed SG, Lodes MJ, Mohamath R, Secrist H;
XX WIPI; 2000-638466/61.
XX DR
XX PT Novel lung tumor polypeptides and polynucleotides, useful for detecting,
XX PT monitoring or treating cancer, especially lung cancer.
XX PS Claim 1; Page 106; 243pp; English.
XX CC The present sequence is given in a specification relating to compounds
XX CC for therapy and diagnosis of lung cancer. Polypeptides comprising at
XX CC least an immunogenic part of a lung tumour protein are disclosed. The
XX CC polypeptides are useful for inhibiting the development of cancer,
XX CC especially lung cancer. Samples of T cells expressing the polypeptides
XX CC may be used to inhibit the development of cancer. The polypeptides are
XX CC also useful for detecting and monitoring the progression of cancer,
XX CC especially lung cancer
XX SQ Sequence 14 BP; 1 A; 0 C; 1 G; 12 T; 0 U; 0 Other;

Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAACAAAAA 1492
Db 14 CTAACAAAAA 1

RESULT 495
AAC62349/c
ID AAC62349 standard; DNA; 14 BP.
XX AC AAC62349;
XX AC
XX 06-NOV-2000 (first entry)
XX DE
XX DE Oligonucleotide #1 containing 3'-C-amino-5'(S)-C,3'-N-ethanothymidine.
XX KW Conformationally-locked oligonucleotide; antisense inhibitor;
XX KW bicyclic sugar nucleoside analogue; gene probe; ds.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT modified_base 1 /*tag= a
XX FT /*mod_base= OTHER
XX FT /*note= "3'-C-amino-5'(S)-C,3'-N-ethanothymidine"
XX FT modified_base 3 /*tag= b
XX FT /*mod_base= OTHER
```

```
FT modified_base /note= "3'-C-amino-5' (S) -C,3'-N-ethanothymidine"
FT 5
FT /*tag= c
FT /mod_base= OTHER
FT modified_base /note= "3'-C-amino-5' (S) -C,3'-N-ethanothymidine"
FT 7
FT /*tag= d
FT /mod_base= OTHER
FT modified_base /note= "3'-C-amino-5' (S) -C,3'-N-ethanothymidine"
FT 9
FT /*tag= e
FT /mod_base= OTHER
FT modified_base /note= "3'-C-amino-5' (S) -C,3'-N-ethanothymidine"
FT 10
FT /*tag= f
FT /mod_base= OTHER
FT modified_base /note= "3'-C-amino-5' (S) -C,3'-N-ethanothymidine"
FT 12
FT /*tag= g
FT /mod_base= OTHER
FT modified_base /note= "3'-C-amino-5' (S) -C,3'-N-ethanothymidine"
FT
FT
XX US6083482-A.
XX
XX
XX 04-JUL-2000.
XX
XX 11-MAY-1999; 99US-00309742.
XX
XX 11-MAY-1999; 99US-00309742.
XX (ICNC ) ICN PHARM INC.
XX
XX Wang G;
XX
XX WPI; 2000-451496/39.
XX
XX New conformationally restricted 3',5'-bridged nucleosides and
XX oligonucleotides useful as antisense therapeutics or as gene-specific
XX diagnostics.
XX
XX Example 20; Col 16; 10pp; English.
XX
XX The present sequence is an oligonucleotide containing 3'-C-amino-5' (S) -
XX C,3'-N-ethanothymidine, a bicyclic-sugar nucleoside. All nucleotides in
XX the sequence were incorporated by phosphoramidite chemistry using a DNA
XX synthesiser. Bicyclic sugar nucleosides are conformationally restricted
XX 3',5'-bridged nucleosides which can be used as building blocks for
XX oligonucleotides. Oligonucleotides can be produced that have certain,
XX desired, geometrical shapes and entropy advantages. They may have
XX superior hybridisation to DNA and RNA, and excellent biological
XX stability. The conformationally-modified oligonucleotides may be useful
XX as antisense inhibitors of gene expression or as gene probes, and may
XX therefore be used in antisense therapeutics or gene-specific diagnostics
XX
XX Sequence 14 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 0 Other;
XX
XX Query Match 0.9%; Score 14; DB 1; Length 14;
XX Best Local Similarity 100.0%; Pred. NO. 2.3e+02;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1481 AAAAAAAAAAAAAA 1494
XX |||||
XX 14 AAAAAAAAAAAAAA 1
XX
XX Db
XX
XX RESULT 496
XX AAD23152/c
XX ID AAD23152 standard; DNA; 14 BP.
XX
XX AC AAD23152;
XX
XX 26-FEB-2002 (first entry)
XX
XX
```

```
DE Human lung tumour-specific cDNA synthesising 3' RT-PCR anchored primer.
XX
XX Human; lung tumour protein; immunostimulant; cytostatic; gene therapy;
XX antisense-therapy; vaccine; immune response; lung cancer; RT-PCR primer;
XX ss.
XX
XX Homo sapiens.
XX
XX WO200172295-A2.
XX
XX 04-OCT-2001.
XX
XX 28-MAR-2001; 2001WO-US009991.
XX
XX 29-MAR-2000; 2000US-00538037.
XX 05-JUN-2000; 2000US-00588937.
XX 18-AUG-2000; 2000US-00640878.
XX 22-SEP-2000; 2000US-0234517P.
XX 01-NOV-2000; 2000US-00704512.
XX 14-DEC-2000; 2000US-00738973.
XX
XX (CORI-) CORIXA CORP.
XX
XX Reed SG, Lodes MJ, Mohamath R, Secrist H, Benson DR, Indrias CY;
XX Henderson RA, Fling SP, Algate PA, Elliot M, Mannion J, Kalos MD;
XX WPI; 2001-639201/73.
XX
XX New human lung-specific polynucleotides and polypeptides for the
XX diagnosis and treatment of disease e.g. lung cancer.
XX
XX Example 1; Page 162; 378pp; English.
XX
XX The invention relates to isolated lung tumour-specific proteins and their
XX corresponding cDNA molecules. Lung tumour-specific proteins and their
XX cells-presenting cells are useful for stimulating and/or expanding T
XX cells specific for a tumour protein, and for inhibiting the development
XX of cancer. The invention also relates to a composition useful for
XX stimulating an immune response, and for treating cancer. The lung tumour
XX specific oligonucleotide is useful in gene therapy and for diagnosis,
XX detection and treatment of lung cancer. The present DNA sequence is 3' RT
XX (reverse transcriptase)-PCR anchored primer which is used for
XX synthesising human lung tumour-specific cDNA
XX
XX Sequence 14 BP; 1 A; 0 C; 1 G; 12 T; 0 U; 0 Other;
XX
XX Query Match 0.9%; Score 14; DB 1; Length 14;
XX Best Local Similarity 100.0%; Pred. NO. 2.3e+02;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1479 CTAATAAAAAAAAA 1492
XX |||||
XX 14 CTAATAAAAAAAAA 1
XX
XX Db
XX
XX RESULT 497
XX AAF84160/c
XX ID AAF84160 standard; DNA; 14 BP.
XX
XX AC AAF84160;
XX
XX 08-JUN-2001 (first entry)
XX
XX Oligonucleotide #2.
XX
XX Light responsive oligonucleotide; light irradiation; gene therapy; ss.
XX
XX Unidentified.
XX
XX WO200121637-A1.
XX
XX 29-MAR-2001.
XX
```



```
SQ Sequence 14 BP; 1 A; 0 C; 1 G; 12 T; 0 U; 0 Other;
Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1479 CTAATAAAAAAAAAA 1492
DB 14 CTAATAAAAAAAAAA 1

RESULT 500
ABK46742/c
ID ABK46742 standard; DNA; 14 BP.
XX
AC ABK46742;
XX
DT 05-JUN-2002 (first entry)
XX
DE Human breast tumour-specific cDNA B18Ag1, RT-PCR primer.
XX
KW Human; breast tumour-specific protein; vaccine; breast cancer; primer;
KW ss.
XX
OS Homo sapiens.
XX
PN US6344550-B1.
XX
PD 05-FEB-2002.
XX
PF 17-APR-1998; 98US-00062451.
XX
PR 01-JAN-1996; 96US-00585392.
PR 20-AUG-1996; 96US-00700014.
PR 10-JAN-1997; 97WO-US000485.
PR 09-APR-1997; 97US-00838762.
PR 11-DEC-1997; 97US-00991789.
XX
XX (CORI-) CORIXA CORP.
XX
XX Frudakis TN, Smith JM, Reed SG;
XX
XX WPI; 2002-215084/27.
XX
XX Polynucleotide encoding breast-specific tumor polypeptides useful as
XX vaccine for preventing and treating breast cancer in a subject.
XX
XX Example 1; Col 16; 128pp; English.
XX
XX The invention relates to an isolated DNA molecule (I) encoding breast-
XX tumour-specific polypeptides. (I) is useful as a vaccine for preventing
XX and treating breast cancer in a subject. The polypeptide encoded by (I)
XX is used for production of compounds such as antibodies useful in
XX diagnosing and monitoring the progression of breast cancer. ABK46614-
XX ABK46899 represent human breast tumour-specific coding sequences and
XX related PCR primers of the invention
XX
XX Sequence 14 BP; 1 A; 0 C; 1 G; 12 T; 0 U; 0 Other;
Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1479 CTAATAAAAAAAAAA 1492
DB 14 CTAATAAAAAAAAAA 1

RESULT 501
ABQ83278/c
ID ABQ83278 standard; DNA; 14 BP.
XX
AC ABQ83278;
```

```
XX
DT 18-JAN-2003 (first entry)
XX
DE EGI cDNA tag related oligonucleotide SEQ ID NO:51.
XX
KW cDNA tag; identification; gene expression analysis; linker;
KW expressed gene identification; EGI; ss.
XX
OS Synthetic.
XX
PN WO200274951-A1.
XX
PD 26-SEP-2002.
XX
PF 13-MAR-2002; 2002WO-JP002338.
XX
PR 15-MAR-2001; 2001JP-00073959.
XX
PA (KURE ) KUREHA CHEM IND CO LTD.
PA (YAMA/) YAMAMOTO M.
PA (YAMA/) YAMAMOTO N.
XX
XX Yamamoto M, Yamamoto N, Hirose K, Kasai J;
PI WPI; 2002-759896/82.
XX
DR Construction of cDNA tags for identifying expressed genes with specific
XX linkers and recognition sequences, applicable in gene expression
XX analysis, disease diagnosis and identifying target for gene therapy.
XX
XX Example 1; Page 24; 59pp; Japanese.
XX
XX The present invention describes a method for constructing a cDNA tag for
XX identifying an expressed gene. The method comprises: (a) preparation of
XX complementary deoxyribonucleic acid; (b) producing cDNA fragment by
XX cleavage with II type restriction enzyme; (c) obtaining a linker X-cDNA
XX fragment ligated material; (d) amplification of the linker X-cDNA tag-
XX linker Y ligated material; and (e) cleaving the amplification product.
XX The method can be used for the construction of cDNA tags for identifying
XX expressed genes, which is applicable in gene expression analysis, disease
XX diagnosis and identifying target for gene therapy, including the
XX clarification of difference in function or morphology of cells under
XX physiological or pathological conditions. The cDNA or cells for assay can
XX be specifically expressed, with reproducibility and accuracy in the
XX detection of genes. The present sequence represents an expressed gene
XX identification (EGI) cDNA tag related oligonucleotide which is used in an
XX example from the present invention
XX
XX Sequence 14 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 0 Other;
Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1494
DB 14 AAAAAAAAAAAAAA 1

RESULT 502
ABQ83275/c
ID ABQ83275 standard; DNA; 14 BP.
XX
AC ABQ83275;
XX
DT 18-JAN-2003 (first entry)
XX
DE EGI cDNA tag related oligonucleotide SEQ ID NO:48.
XX
KW cDNA tag; identification; gene expression analysis; linker;
KW expressed gene identification; EGI; ss.
XX
OS Synthetic.
```

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XX WO200274951-A1.
PN
XX
XX
PD 26-SEP-2002.
XX
XX 13-MAR-2002; 2002WO-JP002338.
XX
XX 15-MAR-2001; 2001JP-00073959.
XX
XX (KURE ) KUREHA CHEM IND CO LTD.
PA (YAMA/) YAMAMOTO M.
PA (YAMA/) YAMAMOTO N.
XX
PI Yamamoto M, Yamamoto N, Hirose K, Kasai J;
XX WPI; 2002-759896/82.
XX
XX Construction of cDNA tags for identifying expressed genes with specific
PT linkers and recognition sequences, applicable in gene expression
PT analysis, disease diagnosis and identifying target for gene therapy.
XX
XX Example 1; Page 24; 59pp; Japanese.
XX
XX The present invention describes a method for constructing a cDNA tag for
CC identifying an expressed gene. The method comprises: (a) preparation of
CC complementary deoxyribonucleic acid; (b) producing cDNA fragment by
CC cleavage with II type restriction enzyme; (c) obtaining a linker X-cDNA
CC fragment ligated material; (d) amplification of the linker X-cDNA tag-
CC linker Y ligated material; and (e) cleaving the amplification product.
CC The method can be used for the construction of cDNA tags for identifying
CC expressed genes, which is applicable in gene expression analysis, disease
CC diagnosis and identifying target for gene therapy, including the
CC clarification of difference in function or morphology of cells under
CC physiological or pathological conditions. The cDNA or cells for assay can
CC be specifically expressed, with reproducibility and accuracy in the
CC detection of genes. The present sequence represents an expressed gene
CC identification (EGI) cDNA tag related oligonucleotide which is used in an
CC example from the present invention
XX
XX Sequence 14 BP; 1 A; 0 C; 0 G; 13 T; 0 U; 0 Other;
SQ
Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1480 TAAAAAATAAAAAA 1493
Db 14 TAAAAAATAAAAAA 1
RESULT 503
ABQ83269
ID ABQ83269 standard; DNA; 14 BP.
XX
XX ABQ83269;
AC
XX
XX 18-JAN-2003 (first entry)
DT
XX
XX EGI cDNA tag related oligonucleotide SEQ ID NO:42.
DE
XX cDNA tag; identification; gene expression analysis; linker;
KW expressed gene identification; EGI; ss.
XX
XX Synthetic.
OS
XX
XX WO200274951-A1.
PN
XX
XX 26-SEP-2002.
PD
XX
XX 13-MAR-2002; 2002WO-JP002338.
XX
XX 15-MAR-2001; 2001JP-00073959.
XX
XX New Zis-SR nucleic acid molecules and polypeptides, useful for restoring
```

```
PA (KURE ) KUREHA CHEM IND CO LTD.
PA (YAMA/) YAMAMOTO M.
PA (YAMA/) YAMAMOTO N.
XX
XX Yamamoto M, Yamamoto N, Hirose K, Kasai J;
XX WPI; 2002-759896/82.
XX
XX Construction of cDNA tags for identifying expressed genes with specific
PT linkers and recognition sequences, applicable in gene expression
PT analysis, disease diagnosis and identifying target for gene therapy.
XX
XX Example 1; Page 24; 59pp; Japanese.
XX
XX The present invention describes a method for constructing a cDNA tag for
CC identifying an expressed gene. The method comprises: (a) preparation of
CC complementary deoxyribonucleic acid; (b) producing cDNA fragment by
CC cleavage with II type restriction enzyme; (c) obtaining a linker X-cDNA
CC fragment ligated material; (d) amplification of the linker X-cDNA tag-
CC linker Y ligated material; and (e) cleaving the amplification product.
CC The method can be used for the construction of cDNA tags for identifying
CC expressed genes, which is applicable in gene expression analysis, disease
CC diagnosis and identifying target for gene therapy, including the
CC clarification of difference in function or morphology of cells under
CC physiological or pathological conditions. The cDNA or cells for assay can
CC be specifically expressed, with reproducibility and accuracy in the
CC detection of genes. The present sequence represents an expressed gene
CC identification (EGI) cDNA tag related oligonucleotide which is used in an
CC example from the present invention
XX
XX Sequence 14 BP; 14 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
SQ
Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1481 AAAAAAATAAAAAA 1494
Db 1 AAAAAAATAAAAAA 14
RESULT 504
ABS54141/c
ID ABS54141 standard; DNA; 14 BP.
XX
XX ABS54141;
AC
XX
XX 25-NOV-2002 (first entry)
DT
XX
XX Oligo-dT primer #2.
DE
XX
XX PCR; primer; Zis-SR; neuroendocrine phenotype; diabetes; ss;
KW Parkinson's disease; Alzheimer's disease; neurodegenerative disease;
KW zinc finger splicing with extended Ser-Arg domain; secretory pathway;
KW zinc finger protein.
XX
XX Synthetic.
OS
XX
XX WO200261082-A2.
PN
XX
XX 08-AUG-2002.
PD
XX
XX 29-JAN-2002; 2002WO-CA000101.
XX
XX 29-JAN-2001; 2001US-0264296P.
XX
XX (UYSH ) UNIV SHERBROOKE.
PA
XX
XX Day R;
PI
XX
XX WPI; 2002-682683/73.
XX
XX New Zis-SR nucleic acid molecules and polypeptides, useful for restoring
```

PT or increasing the secretory properties of a cell, or for treating
PT diseases or conditions associated with a loss of function, e.g. diabetes
PT or Parkinson's disease.
XX

PS Disclosure; Page 35; 70pp; English.

XX The invention relates to an isolated nucleic acid molecule, Zis-SR,
CC encoding a protein involved in the secretory pathway in a cell (or its
CC homologue or variant) or nucleic acid molecules that hybridise under high
CC stringency condition to the Zis-SR nucleic acid. Also included are an
CC isolated polypeptide involved in the formation of secretory granules in
CC cells comprising the amino acid sequence spanning amino acids 243-310 of
CC the Zis-SR protein, restoring the neuroendocrine differentiation of a
CC cell using the nucleic acid molecule or polypeptide cited above,
CC identifying a gene and/or protein involved in inducing regulated
CC secretion comprising a comparison at the molecular level of a secretion-
CC defective cell line under conditions that restore differentiation of the
CC secretion-defective cell, such that secretion is restored, and the
CC secretion-defective cell line in the absence of the conditions cited.
CC Also included are modulating the secretory properties of a cell
CC comprising modulating the activity and/or level of Zis-SR and an assay to
CC identify a modulator of regulated secretion in a cell comprising an
CC assessment of a biological activity of Zis-SR, its part or derivative in
CC the presence of a candidate agent, where a modulator of regulated
CC secretion is selected when the biological activity of Zis-SR, its part or
CC derivative is measurably different in the presence of the candidate
CC compound as compared in its absence. The nucleic acid molecules or
CC polypeptides are useful for restoring or increasing the secretory
CC properties of a cell, for regulating neuroendocrine phenotype, and for
CC long term therapies to treat diseases or conditions associated with a
CC loss of function, e.g. diabetes, neurodegenerative diseases such as
CC Alzheimer's disease or Parkinson's disease. The assay is useful for
CC screening compounds for treating diseases or conditions associated with a
CC defect in the regulated secretory pathways in cells. The nucleic acid
CC molecules can also be used to locate gene regions associated with genetic
CC diseases. The present sequence is an oligo-dT PCR primer used to isolate
CC the cDNA encoding mouse Zis-SR (zinc finger splicing with extended Ser-
CC Arg domain)
XX

SQ Sequence 14 BP; 1 A; 0 C; 1 G; 12 T; 0 U; 0 Other;

Query Match 0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAATAAAAAAAAAA 1492
|||||
Db 14 CTAATAAAAAAAAAA 1

RESULT 505
AAD24491/c
ID AAD24491 standard; DNA; 14 BP.

XX AAD24491;

XX 07-MAR-2002 (first entry)

XX Retinoid-regulated gene isolating poly(T) PCR primer #5.

XX Retinoid metabolism; retinoic acid; RA; haeme-binding motif; vitamin A;
KW cytochrome P450; prostate cancer; drug screening; PCR primer;
KW retinoid-regulated gene; ss.

XX Unidentified.

XX US6306624-B1.

XX 23-OCT-2001.

XX 25-JUN-1997; 97US-00882164.

XX 21-JUN-1996; 96US-00667546.

PR 01-OCT-1996; 96US-00724466.
XX 23-JUN-1997; 97WO-CA000440.
XX (TOOH) UNIV QUEENS KINGSTON.
PA Petkovich PM, White JA, Beckett BR, Jones G;
XX WPI; 2002-033254/04.
XX New DNA fragments having promoter activity, useful in retinoid
PT metabolism, as well as in producing retinoic acid metabolizing cytochrome
PT P450s that are useful as targets for the treatment of certain cancers.
XX Disclosure; Col 13; 75pp; English.

XX The present invention relates to retinoid (e.g., retinoic acid (RA),
CC vitamin A) metabolising proteins and nucleic acid sequences encoding
CC them. RA metabolising proteins contain a haeme-binding motif which is
CC characteristic of the group of proteins known as cytochrome P450s. The
CC sequences of the invention are useful in retinoid metabolism and in
CC producing retinoic acid metabolising cytochrome P450s. They are
CC particularly useful as targets for the treatment of certain cancers such
CC as prostate cancer. The invention also relates to a method of screening
CC drugs for their effect on activity of RA inducible proteins. The present
CC DNA sequence is poly(T) PCR primer which is used for isolating retinoid
CC regulating genes by differential display of mRNAs. Note: This sequence is
CC incorrectly referred as SEQ ID NO: 6 in column 14 of the specification
XX

SQ Sequence 14 BP; 1 A; 0 C; 1 G; 12 T; 0 U; 0 Other;

Query Match 0.9%; Score 14; DB 1; Length 14;

Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAATAAAAAAAAAA 1492
|||||
Db 14 CTAATAAAAAAAAAA 1

RESULT 506
ABA93701/c
ID ABA93701 standard; DNA; 14 BP.

XX ABA93701;

XX 30-APR-2002 (first entry)

XX Light responsive oligonucleotide (X1)T14.

XX Light responsive; detection; single nucleotide polymorphism; SNP;
KW irradiation; ss.

XX Synthetic.

XX JP2001346579-A.

XX 18-DEC-2001.

XX 02-JUN-2000; 2000JP-00165441.

XX 02-JUN-2000; 2000JP-00165441.

XX (KOMI/) KOMIYAMA S.

XX (ASAN/) ASANUMA H.

XX WPI; 2002-145181/19.

XX Detecting single nucleotide polymorphism for expressing sensitivity
PT information of diseases and drugs, comprises using a new oligonucleotide.

XX Example 3; Page 11; 14pp; Japanese.

XX The present invention describes a method for detecting single nucleotide

CC polymorphisms (SNPs). Also described is an oligonucleotide used in the
 CC detection of an SNP, prepared by binding an oligonucleotide having a
 CC complementary sequence or those devoid of up to several bases with 1 or
 CC more organic group(s) to be tested by light irradiation of a specific
 CC wave length to vary a double strand formation property of the
 CC oligonucleotide to be tested. The method is used for detecting SNPs. The
 CC present sequence represents a light responsive oligonucleotide which is
 CC used in an example from the present invention

XX
 SQ Sequence 14 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 0 Other;

Query Match 0.9%; Score 14; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1494
 Db 14 AAAAAAAAAAAAAA 1

RESULT 507
 ABZ23321/c
 ID ABZ23321 standard; DNA; 14 BP.

XX AC ABZ23321;

XX DT 07-APR-2003 (first entry)

XX DE Reverse transcription primer used to produce human cDNA for PCR.

XX KW IRS-1; insulin receptor substrate-1; angiogenesis; capillary tube;
 KW endothelial cell; retinopathy; rheumatoid arthritis; Crohn's disease;
 KW atherosclerosis; ovarian hyperstimulation; psoriasis; endometriosis;
 KW restenosis; wound healing; peripheral vascular disease; hypertension;
 KW vascular inflammation; Raynaud disease; aneurysm; arterial restenosis;
 KW thrombophlebitis; lymphagitis; lymphodema; ischemia; angina;
 KW myocardial infarction; chronic heart disease; macular degeneration;
 KW osteoporosis; cell multiplication; antitumor; primer; ss.

XX OS Homo sapiens.

XX PN W02002103014-A2.

XX PD 27-DEC-2002.

XX PP 14-JUN-2002; 2002WO-FR002067.

XX PR 14-JUN-2001; 2001FR-00007805.

XX PA (ALMA/) AL-MAHMOOD S.

XX PI Al-Mahmood S;

XX DR WPI; 2003-167520/16.

XX PT Angiogenesis-modifying composition, useful for treatment or diagnosis of
 PT e.g. retinopathy, comprises inhibitor of expression of the insulin
 PT receptor substrate-1 gene.

XX PS Example 1; Page 12; 52pp; French.

XX CC The present sequence represents a primer used to produce human CDNA for
 CC amplification of cDNA encoding IRS-1 (insulin receptor substrate-1). IRS-
 CC 1 is used to produce the compositions of the invention. The specification
 CC describes an angiogenesis-modifying composition, containing at least one
 CC nucleic acid selected from the gene encoding IRS-1 or a molecule that
 CC inhibits expression of that nucleic acid. The composition inhibits the
 CC formation of capillary tubes by endothelial cells. The composition is
 CC used to treat and diagnose diseases associated with angiogenesis,
 CC particularly retinopathy, rheumatoid arthritis, Crohn's disease,
 CC atherosclerosis, ovarian hyperstimulation, psoriasis, endometriosis,
 CC restenosis after balloon angioplasty, overproduction of tissue during
 CC wound healing, peripheral vascular diseases, hypertension, vascular

CC inflammation, Raynaud disease, aneurysm, arterial restenosis,
 CC thrombophlebitis, lymphagitis, lymphodema, ischemia, angina, myocardial
 CC infarction, chronic heart disease, (congestive) cardiac insufficiency,
 CC age-related macular degeneration and osteoporosis. It is also used to
 CC prevent cell multiplication, especially as antitumor agents, and as
 CC research reagents for in vitro or in vivo studies on signalling pathways

XX SQ Sequence 14 BP; 1 A; 0 C; 1 G; 12 T; 0 U; 0 Other;

Query Match 0.9%; Score 14; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1479 CTAATAAAAAAAAA 1492
 Db 14 CTAATAAAAAAAAA 1

RESULT 508
 ADAL1209/c
 ID ADAL1209 standard; DNA; 14 BP.

XX AC ADAL1209;

XX DT 06-NOV-2003 (first entry)

XX DE Differential display Oligo-dT primer.

XX KW ss; PCR; breast cancer; cytostatic; tumour; gene therapy; primer;
 KW differential display.

XX OS Synthetic.

XX PN US2002165371-A1.

XX PD 07-NOV-2002.

XX PP 07-AUG-2001; 2001US-00924400.

XX PR 11-JAN-1996; 96US-00585192.

XX PR 10-JAN-1997; 97WO-US0000485.

XX PR 09-APR-1997; 97US-00838762.

XX PR 11-DEC-1997; 97US-00991789.

XX PR 17-APR-1998; 98US-00062451.

XX PR 09-APR-1999; 99US-00289198.

XX PR 28-OCT-1999; 99US-00429755.

XX PR 23-MAR-2000; 2000US-00534825.

XX PR 24-MAY-2000; 2000US-00577505.

XX PR 08-JUN-2000; 2000US-00590583.

XX PR 26-OCT-2000; 2000US-00699295.

XX PR 16-MAR-2001; 2001US-00810936.

XX PA (FRUD/) FRUDAKIS T N.

XX PA (REED/) REED S G.

XX PA (SMIT/) SMITH J M.

XX PA (MISH/) MISHNER L E.

XX PA (DILL/) DILLON D C.

XX PA (RETT/) RETTER M W.

XX PA (WANG/) WANG A.

XX PA (SKEI/) SKEIKY Y A W.

XX PA (HARL/) HARLOCKER S L.

XX PA (DAYC/) DAY C H.

XX PA (LISX/) LI S X.

XX PA (DENG/) DENG T.

XX PI Prudakis TN, Reed SG, Smith JM, Misher LE, Dillon DC, Retter MW;

XX PI Wang A, Skeiky YAW, Harlocker SL, Day CH, Li SX, Deng T;

XX XX WPI; 2003-247262/24.

XX XX New breast tumor proteins nucleic acids encoding such proteins, useful in

XX PT diagnosing, preventing and/or treating diseases such as cancer,

XX PT particularly breast cancer, and as markers for detecting the presence of

```
PT a cancer.
XX
PS Example 1; Page 32; 190pp; English.
XX
CC The invention relates to a breast tumour polynucleotide selected from one
CC of the 275 fully defined nucleotide sequences (a) given in the
CC specification, including their complements, sequences consisting of at
CC least 20 contiguous residues of a sequence in (a), sequences that
CC hybridise to a sequence in (a) under moderately stringent conditions,
CC sequences having at least 75% or 90% identity to a sequence in (a), or
CC degenerate variants of a sequence in (a). Also included are an isolated
CC polypeptide (II) (comprising an amino acid sequence selected from
CC sequences encoded by (a), sequences having at least 70% or 90% identity
CC to a sequence encoded by (a), sequences of 30 fully defined amino acid
CC sequences (c), and sequences having at least 70% or 90% identity to a
CC sequence in (c)), expression vectors comprising (a), a host cell
CC transformed or transfected with the expression vector, an isolated
CC antibody or its antigen-binding fragment that specifically binds to (II),
CC a method for detecting the presence of a cancer in a patient, a fusion
CC protein comprising at least one polypeptide (II), an oligonucleotide that
CC hybridises to (a), under moderately stringent conditions, a method for
CC stimulating and/or expanding T cells specific for a tumour protein (by
CC contacting T cells with at least one component selected from (a), (II)
CC and antigen-presenting cells that express (II)), an isolated T cell
CC population comprising T cells prepared from as detailed above, a method
CC for stimulating an immune response or treating cancer in a patient by
CC administering a composition comprising (a), (II), the vector, cells or
CC the antibodies, and a method for inhibiting the development of a cancer
CC in a patient. The polynucleotides may be used in the design and
CC preparation of ribzyme molecules for inhibiting expression of the tumour
CC polypeptides and proteins in tumour cells. The breast tumour proteins are
CC useful as markers to indicate the presence or absence of a cancer, such
CC as breast cancer, and in the detection of other cancers. Compositions
CC comprising the breast tumour proteins are useful in diagnosing,
CC preventing and/or treating diseases such as cancer, particularly breast
CC cancer. The present sequence is a differential display random PCR primer
CC used in the isolation of breast cancer specific cDNAs of the invention.
XX
SQ Sequence 14 BP; 1 A; 0 C; 1 G; 12 T; 0 U; 0 Other;

Query Match      0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAAAAAATAAAAA 1492
Db 14 CTAAAAAATAAAAA 1

RESULT 509
AD66355/c
ID ADD66355 standard; DNA; 14 BP.
XX
AC ADD66355;
XX
XX 15-JAN-2004 (first entry)
XX
DE Human lung tumour-specific DNA related primer, SEQ ID No 47.
XX
KW expression control; cancer; T cell; tumour; immune; cytostatic; vaccine;
KW human; lung tumour-specific; PCR; primer; ss.
XX
OS Homo sapiens.
XX
XX WO200292001-A2.
PN
XX 21-NOV-2002.
PD
XX 10-MAY-2002; 2002WO-US014975.
PF
XX 11-MAY-2001; 2001US-00854133.
PR
XX (CORI-) CORIXA CORP.
PA
XX Lodes MJ, Wang T, Fan L, Algate PA, Mcneill PD;
XX
XX WPI; 2003-120592/11.
DR
XX New polynucleotide and polypeptide, useful for preparing a composition
XX for diagnosing, treating or preventing cancer.
XX
XX Example 1; SEQ ID NO 47; 494pp; English.
PS
XX The invention relates to a novel isolated polynucleotide comprising one
XX of 32 47-6080 base pair sequences, given in the specification, or their
XX complements or degenerate variants, at least 20 contiguous residues of a
```

```
XX (CORI-) CORIXA CORP.
XX
XX Fanger GR, Hirst SK, Dillon DC, Foy TM, Houghton RL, Persing DH;
XX Kalos MD;
XX
XX WPI; 2003-342398/32.
DR
XX New polynucleotide, useful for preparing a composition for diagnosing,
XX treating or preventing cancer.
XX
XX Example 1; SEQ ID NO 130; 308pp; English.
PS
XX The present invention relates to compositions and methods for the therapy
XX and diagnosis of cancer, particularly breast cancer. The method for
XX detecting the presence of a cancer in a patient comprises: obtaining a
XX biological sample from the patient; contacting the biological sample with
XX a binding agent that binds to the polypeptide; detecting in the sample an
XX amount of the polypeptide that binds to the binding agent; and comparing
XX the amount of the polypeptide to a predetermined cut-off value. Treating
XX breast cancer comprises administering a composition comprising breast
XX tumour proteins and nucleic acids, which simulates and/or expands T cells
XX specific for the tumour protein. The present sequence was used to
XX illustrate the invention.
XX
SQ Sequence 14 BP; 1 A; 0 C; 1 G; 12 T; 0 U; 0 Other;

Query Match      0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1479 CTAAAAAATAAAAA 1492
Db 14 CTAAAAAATAAAAA 1

RESULT 510
AD66355/c
ID ADD66355 standard; DNA; 14 BP.
XX
XX
AC ADD66355;
XX
XX 15-JAN-2004 (first entry)
XX
XX Human lung tumour-specific DNA related primer, SEQ ID No 47.
DE
XX
XX expression control; cancer; T cell; tumour; immune; cytostatic; vaccine;
KW human; lung tumour-specific; PCR; primer; ss.
XX
XX Homo sapiens.
XX
XX WO200292001-A2.
PN
XX 21-NOV-2002.
PD
XX 10-MAY-2002; 2002WO-US014975.
PF
XX 11-MAY-2001; 2001US-00854133.
PR
XX (CORI-) CORIXA CORP.
PA
XX Lodes MJ, Wang T, Fan L, Algate PA, Mcneill PD;
XX
XX WPI; 2003-120592/11.
DR
XX New polynucleotide and polypeptide, useful for preparing a composition
XX for diagnosing, treating or preventing cancer.
XX
XX Example 1; SEQ ID NO 47; 494pp; English.
PS
XX The invention relates to a novel isolated polynucleotide comprising one
XX of 32 47-6080 base pair sequences, given in the specification, or their
XX complements or degenerate variants, at least 20 contiguous residues of a
```

CC sequence in, or having at least 75 or 90 % identity with the isolated
 CC polynucleotide, or that hybridise with the polynucleotide. The invention
 CC further comprises: an isolated polypeptide; an expression vector
 CC comprising the polynucleotide operably linked to an expression control
 CC sequence; a host cell transformed or transfected with the expression
 CC vector; an isolated antibody or its antigen-binding fragment that
 CC specifically binds to the polypeptide; a method for detecting the
 CC presence of a cancer in a patient; a fusion protein comprising the
 CC polypeptide; an oligonucleotide that hybridises to the isolated
 CC polynucleotide under moderately stringent conditions; a method for
 CC stimulating and/or expanding T cells specific for a tumour protein; an
 CC isolated T cell population; a composition comprising a first component
 CC consisting of carriers and immunostimulants and a second component; a
 CC method for stimulating an immune response in a patient; a method for
 CC treating cancer in a patient; a method for determining cancer in a
 CC patient; a diagnostic kit comprising at least one oligonucleotide or
 CC antibody and a detection reagent comprising a reporter group; and a
 CC method for inhibiting the development of cancer in a patient. The
 CC compositions of the invention have cytostatic activity and can be used to
 CC create a vaccine. The isolated polynucleotide is useful for preparing a
 CC composition for diagnosing, treating or preventing cancer. This
 CC polynucleotide sequence represents a primer relating to the human lung
 CC tumour-specific cDNA sequences of the invention.

XX
 SQ Sequence 14 BP; 1 A; 0 C; 1 G; 12 T; 0 U; 0 Other;

Query Match 0.9%; Score 14; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1479 CTAATAAAAAAAAAA 1492
 Db 14 CTAATAAAAAAAAAA 1

RESULT 511
 ADE87609/c
 ID ADE87609 standard; DNA; 14 BP.

XX AC ADE87609;

XX 29-JAN-2004 (first entry)

XX Human lung tumour antigen cDNA PCR primer #1.

XX Human; lung tumour antigen; PCR; ss; cancer; lung cancer; CD4+; CD8+;
 XX T cell; immune response; immunostimulant; cytostatic; primer.

XX Homo sapiens.

XX US2003118599-A1.

XX 26-JUN-2003.

XX 10-MAY-2002; 2002US-0014649.

XX 02-APR-1999; 99US-00285323.

XX 09-AUG-1999; 99US-00370838.

XX 30-DEC-1999; 99US-00476235.

XX 03-MAR-2000; 2000US-00518809.

XX 29-MAR-2000; 2000US-00538037.

XX 05-JUN-2000; 2000US-00588937.

XX 18-AUG-2000; 2000US-00640878.

XX 20-SEP-2000; 2000US-00667170.

XX 01-NOV-2000; 2000US-00704512.

XX 14-DEC-2000; 2000US-00738973.

XX 11-MAY-2001; 2001US-00854133.

XX (CORI-) CORIXA CORP.

XX Algate PA, Lodes MJ, Wang T, Fan L, Mcneill PD;
 XX WPI; 2003-897103/82.

XX
 PT
 FT

XX Example 1; SEQ ID NO 47; 63pp; English.

XX The invention relates to polynucleotides encoding lung tumour antigens.
 CC The invention also relates to the polypeptides encoded by the
 CC polynucleotides, isolated antibodies or antigen-binding fragments that
 CC specifically bind the polypeptides and a method for detecting cancer in a
 CC patient, comprising obtaining a biological sample from the patient,
 CC contacting the sample with a binding agent that binds a polypeptide of
 CC the invention, detecting in the sample an amount of polypeptide that
 CC binds to the binding agent, and comparing the amount of polypeptide to a
 CC predetermined cut-off value. T cells specific for a tumour protein can be
 CC stimulated and/or expanded by contacting the T cells with a polypeptide,
 CC polynucleotide or an antigen-presenting cell that expresses a
 CC polypeptide. Cancer development can be inhibited by incubating CD4+
 CC and/or CD8+ T cells isolated from a patient with a polypeptide,
 CC polynucleotide or an antigen-presenting cell that expresses a
 CC polypeptide, so that the T cells proliferate. The invention is used to
 CC stimulate an immune response or to detect or treat a cancer in a patient,
 CC particularly lung cancer. This sequence represents a PCR primer used to
 CC amplify human lung tumour antigen cDNA of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format from USPTO at
 CC seqdata.uspto.gov/sequence.html.

XX Sequence 14 BP; 1 A; 0 C; 1 G; 12 T; 0 U; 0 Other;

Query Match 0.9%; Score 14; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1479 CTAATAAAAAAAAAA 1492
 Db 14 CTAATAAAAAAAAAA 1

RESULT 512
 AAT52140/c

ID AAT52140 standard; RNA; 15 BP.

XX AC AAT52140;

XX 25-MAR-2003 (revised)

XX 25-MAR-1997 (first entry)

XX Human ICAM hammerhead ribozyme target sequence (nt. position 2912).

XX Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
 KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
 KW intercellular adhesion molecule; rel A; tumour necrosis factor;
 KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
 KW translocation; chronic myelogenous leukaemia; CML; cancer;
 KW Philadelphia chromosome; inflammation; autoimmune disease;
 KW atherosclerosis; myocardial infarction; stroke; restenosis;
 KW transplant rejection; rheumatoid arthritis; psoriasis; HIV;
 KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;
 KW human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
 SS.

XX Homo sapiens.

XX W09523225-A2.

XX 31-AUG-1995.

XX 23-FEB-1995; 95WO-IB000156.

XX 23-FEB-1994; 94US-00201109.

XX 29-MAR-1994; 94US-00218934.

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PR 04-APR-1994; 94US-00222795.
PR 07-APR-1994; 94US-00224483.
PR 15-APR-1994; 94US-00227958.
PR 15-APR-1994; 94US-00228041.
PR 18-MAY-1994; 94US-00245736.
PR 06-JUL-1994; 94US-00271280.
PR 16-AUG-1994; 94US-00291433.
PR 16-AUG-1994; 94US-00291433.
PR 17-AUG-1994; 94US-00293620.
PR 19-AUG-1994; 94US-00293520.
PR 02-SEP-1994; 94US-00300000.
PR 08-SEP-1994; 94US-00303039.
PR 23-SEP-1994; 94US-00311486.
PR 23-SEP-1994; 94US-00314397.
PR 03-OCT-1994; 94US-00316771.
PR 07-OCT-1994; 94US-00319492.
PR 11-OCT-1994; 94US-00321993.
PR 04-NOV-1994; 94US-00334847.
PR 10-NOV-1994; 94US-00337608.
PR 28-NOV-1994; 94US-00345516.
PR 16-DEC-1994; 94US-00357577.
PR 23-DEC-1994; 94US-00363233.
PR 30-JAN-1995; 95US-00380734.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Stinchcomb DT, Chowira B, Dorenzo A, Draper KG, Dudycz LW;
PI Grimm S, Karpeisky A, Kisich K, Matulic-Adamic J, Mcswiggen JA;
PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
PI Tracz D, Usman N, Wincott FE, Woolf T;
XX
XX WPI; 1995-351090/45.
XX
XX Ribozymes having modified bases and methods for producing them - for use
PT in inhibiting disease related genes.
XX
XX Claim 2; Page 175; 407pp; English.
XX
XX The present sequence represents a preferred target sequence for an
CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA at the
CC nucleotide base position indicated in the DE line. Regions of the mRNA
CC that do not form secondary folding structures and that contain potential
CC hammerhead and hairpin ribozyme cleavage sites were identified by
CC computer analysis. Ribozymes directed against these mRNA sequences were
CC designed and synthesised with modifications that improve their nuclease
CC resistance. The ribozymes cleave the ICAM-1 target sequences and thereby
CC inhibit ICAM-1 expression, making them useful for reducing transplant
CC rejection and alleviating symptoms in patients with rheumatoid arthritis,
CC asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to
CC correct PI field.)
XX
XX Sequence 15 BP; 0 A; 1 C; 0 G; 0 T; 14 U; 0 Other;
SQ
Query Match 0.9%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 1
RESULT 513
AAAT52134/c
ID AAAT52134 standard; RNA; 15 BP.
XX
XX AAAT52134;
XX
XX AAAT52134;
XX
XX 25-MAR-2003 (revised)
DT 25-MAR-1997 (first entry)
XX
XX Human ICAM hammerhead ribozyme target sequence (nt. position 2909).
DE

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XX Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
KW intercellular adhesion molecule; rel A; tumour necrosis factor;
KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
KW translocation; chronic myelogenous leukaemia; CML; cancer;
KW Philadelphia chromosome; inflammation; autoimmune disease;
KW atherosclerosis; myocardial infarction; stroke; restenosis;
KW transplant rejection; rheumatoid arthritis; psoriasis;
KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;
KW human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
XX ss.
XX
XX Homo sapiens.
XX
XX WO9523225-A2.
XX
XX 31-AUG-1995.
XX
XX 23-FEB-1995; 95WO-IB000156.
XX
XX 23-FEB-1994; 94US-00201109.
XX 29-MAR-1994; 94US-00218934.
XX 04-APR-1994; 94US-00222795.
XX 07-APR-1994; 94US-00224483.
XX 15-APR-1994; 94US-00227958.
XX 15-APR-1994; 94US-00228041.
XX 18-MAY-1994; 94US-00245736.
XX 06-JUL-1994; 94US-00271280.
XX 15-AUG-1994; 94US-00291932.
XX 16-AUG-1994; 94US-00291433.
XX 17-AUG-1994; 94US-00292620.
XX 19-AUG-1994; 94US-00293520.
XX 02-SEP-1994; 94US-00300000.
XX 08-SEP-1994; 94US-00303039.
XX 23-SEP-1994; 94US-00311486.
XX 23-SEP-1994; 94US-00311749.
XX 28-SEP-1994; 94US-00314397.
XX 03-OCT-1994; 94US-00316771.
XX 07-OCT-1994; 94US-00319492.
XX 11-OCT-1994; 94US-00321993.
XX 04-NOV-1994; 94US-00334847.
XX 10-NOV-1994; 94US-00337608.
XX 28-NOV-1994; 94US-00345516.
XX 16-DEC-1994; 94US-00357577.
XX 23-DEC-1994; 94US-00363233.
XX 30-JAN-1995; 95US-00380734.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Stinchcomb DT, Chowira B, Dorenzo A, Draper KG, Dudycz LW;
PI Grimm S, Karpeisky A, Kisich K, Matulic-Adamic J, Mcswiggen JA;
PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
PI Tracz D, Usman N, Wincott FE, Woolf T;
XX
XX WPI; 1995-351090/45.
XX
XX Ribozymes having modified bases and methods for producing them - for use
PT in inhibiting disease related genes.
XX
XX Claim 2; Page 175; 407pp; English.
XX
XX The present sequence represents a preferred target sequence for an
CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA at the
CC nucleotide base position indicated in the DE line. Regions of the mRNA
CC that do not form secondary folding structures and that contain potential
CC hammerhead and hairpin ribozyme cleavage sites were identified by
CC computer analysis. Ribozymes directed against these mRNA sequences were
CC designed and synthesised with modifications that improve their nuclease
CC resistance. The ribozymes cleave the ICAM-1 target sequences and thereby
CC inhibit ICAM-1 expression, making them useful for reducing transplant
CC rejection and alleviating symptoms in patients with rheumatoid arthritis,
CC asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to
CC correct PI field.)
XX
XX Sequence 15 BP; 0 A; 1 C; 0 G; 0 T; 14 U; 0 Other;
SQ
Query Match 0.9%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1481 AAAAAAAAAAAAAA 1494
Db 14 AAAAAAAAAAAAAA 1
RESULT 513
AAAT52134/c
ID AAAT52134 standard; RNA; 15 BP.
XX
XX AAAT52134;
XX
XX AAAT52134;
XX
XX 25-MAR-2003 (revised)
DT 25-MAR-1997 (first entry)
XX
XX Human ICAM hammerhead ribozyme target sequence (nt. position 2909).
DE

```



```

CC correct PI field.)
XX Sequence 15 BP; 1 A; 0 C; 0 G; 0 T; 14 U; 0 Other;
SQ Query Match 0.9%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db |||||
15 AAAAAAAAAAAAAA 1

RESULT 514
AAF49041/c
ID AAF49041 standard; DNA; 15 BP.
XX AC AAF49041;
XX 30-MAR-2001 (first entry)
DE IGF-I oligonucleotide #1.
XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.
XX Homo sapiens.
XX WO200078341-A1.
XX 28-DEC-2000.
XX 21-JUN-2000; 2000WO-AU000693.
XX 21-JUN-1999; 99US-0140345P.
XX (MURD-) MURDOCH CHILDRENS RES INST.
XX Wraight CJ, Werther GA, Edmondson SR;
XX WPI; 2001-041421/05.
XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.
XX Example 8; Page 60; 201pp; English.
XX The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present invention is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC F45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia
XX Sequence 15 BP; 0 A; 0 C; 1 G; 14 T; 0 U; 0 Other;

Query Match 0.9%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1494
Db |||||
14 AAAAAAAAAAAAAA 1

RESULT 515
ABK98169/c
ID ABK98169 standard; DNA; 15 BP.
XX AC ABK98169;
XX 07-OCT-2002 (first entry)
XX Triple helix forming associated oligonucleotide #39.
XX Triple-helix formation; purine-rich target sequence; double-helix DNA;
KW gene expression; regulatory sequence; pathogenic double-stranded DNA;
KW pathogenic bacteria; virus; replication; virulence; cancer;
KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.
XX Synthetic.
XX US6403302-B1.
XX 11-JUN-2002.
XX 16-DEC-1993; 93US-00168920.
XX 17-SEP-1992; 92US-00946976.
XX (CALY ) CALIFORNIA INST OF TECHNOLOGY.
XX Dervan PB, Beal PA;
XX WPI; 2002-536030/57.
XX A triple-helix comprising a double helical nucleic acid (DHNA) and an
PT oligonucleotide which binds in parallel and antiparallel orientation,
PT respectively, for targeting sequences on alternate strands of DHNA to
PT control gene expression.
XX Example 6; Fig 20A; 108pp; English.
XX The present invention relates to methods and oligonucleotides for forming
CC a triple-helix comprising a double helical nucleic acid comprising first
CC and second substantially complementary strands, and an oligonucleotide
CC bound to a purine-rich target sequence within the double helical nucleic
CC acid, where the oligonucleotide binds in a parallel and antiparallel
CC orientation, respectively, to target sequences on alternate strands of
CC the double helical nucleic acid. The method has therapeutic applications,
CC where gene expression is controlled by selective triple-helix formation
CC within expression regulatory sequences of a target gene. The
CC oligonucleotides can be used to form triple-helices, and are useful to
CC detect the presence or absence of specific sequences within genomic DNA
CC for diagnostic and therapeutic purposes. The oligonucleotides can be
CC selected to specifically bind to pathogenic bacteria or viruses for
CC specific sequences required by pathogenic bacteria or viruses for
CC replication or virulence, reducing their pathogenicity. Alternatively,
CC the oligonucleotide can be chosen to target a unique sequence of the
CC pathogen which is not found in the genome of pathogen's host. The
CC oligonucleotides can be used in cancer treatment by way of triple-helix
CC suppression of specific oncogenes including those of endogenous or viral
CC origin. Such therapeutic oligonucleotides are capable of forming triple-
CC helices with such sequences in cancerous cells containing the activated
CC oncogene, so preferentially killing or repressing the cancer causing
CC cell. The present sequence represents an oligonucleotide used in the
CC methods of the present invention
XX Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 1 Other;
SQ

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Query Match 0.9%; Score 14; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
||||| |||||
Db 15 AAAAAAAAAAAAAA 1

RESULT 516
ABK98187/c
ID ABK98187 standard; DNA; 15 BP.
XX
AC ABK98187;
XX
DT 07-OCT-2002 (first entry)
XX
DE Triple helix forming associated oligonucleotide #51.
XX
KW Triple-helix formation; purine-rich target sequence; double-helix DNA;
KW gene expression; regulatory sequence; pathogenic double-stranded DNA;
KW pathogenic bacteria; virus; replication; virulence; cancer;
KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.
XX
OS Synthetic.
XX
PN US6403302-B1.
XX
PD 11-JUN-2002.
XX
PF 16-DEC-1993; 93US-00168920.
XX
PR 17-SEP-1992; 92US-00946976.
XX
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
XX
PI Dervan PB, Beal PA;
XX
DR WPI; 2002-536030/57.
XX
PT A triple-helix comprising a double helical nucleic acid (DHNA) and an
PT oligonucleotide which binds in parallel and antiparallel orientation,
PT respectively, for targeting sequences on alternate strands of DHNA to
PT control gene expression.

Example 7; Fig 24A; 108pp; English.

XX
XX The present invention relates to methods and oligonucleotides for forming
XX a triple-helix comprising a double helical nucleic acid comprising first
XX and second substantially complementary strands, and an oligonucleotide
XX bound to a purine-rich target sequence within the double helical nucleic
XX acid, where the oligonucleotide binds in a parallel and antiparallel
XX orientation, respectively, to target sequences on alternate strands of
XX the double helical nucleic acid. The method has therapeutic applications,
XX where gene expression is controlled by selective triple-helix formation
XX within expression regulatory sequences of a target gene. The
XX oligonucleotides can be used to form triple-helices, and are useful to
XX detect the presence or absence of specific sequences within genomic DNA
XX for diagnostic and therapeutic purposes. The oligonucleotides can be
XX selected to specifically bind to pathogenic double-stranded DNA including
XX specific sequences required by pathogenic bacteria or viruses for
XX replication or virulence, reducing their pathogenicity. Alternatively,
XX the oligonucleotide can be chosen to target a unique sequence of the
XX pathogen which is not found in the genome of pathogen's host. The
XX oligonucleotides can be used in cancer treatment by way of triple-helix
XX suppression of specific oncogenes including those of endogenous or viral
XX origin. Such therapeutic oligonucleotides are capable of forming triple-
XX helices with such sequences in cancerous cells containing the activated
XX oncogene, so preferentially killing or repressing the cancer causing
XX cell. The present sequence represents an oligonucleotide used in the
XX methods of the present invention

SQ Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 1 Other;

Query Match 0.9%; Score 14; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
||||| |||||
Db 15 AAAAAAAAAAAAAA 1

RESULT 517
ABK98168/c
ID ABK98168 standard; DNA; 15 BP.
XX
AC ABK98168;
XX
DT 07-OCT-2002 (first entry)
XX
DE Triple helix forming associated oligonucleotide #38.
XX
KW Triple-helix formation; purine-rich target sequence; double-helix DNA;
KW gene expression; regulatory sequence; pathogenic double-stranded DNA;
KW pathogenic bacteria; virus; replication; virulence; cancer;
KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.
XX
OS Synthetic.
XX
PN US6403302-B1.
XX
PD 11-JUN-2002.
XX
PF 16-DEC-1993; 93US-00168920.
XX
PR 17-SEP-1992; 92US-00946976.
XX
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
XX
PI Dervan PB, Beal PA;
XX
DR WPI; 2002-536030/57.
XX
PT A triple-helix comprising a double helical nucleic acid (DHNA) and an
PT oligonucleotide which binds in parallel and antiparallel orientation,
PT respectively, for targeting sequences on alternate strands of DHNA to
PT control gene expression.

Example 6; Fig 20A; 108pp; English.

XX
XX The present invention relates to methods and oligonucleotides for forming
XX a triple-helix comprising a double helical nucleic acid comprising first
XX and second substantially complementary strands, and an oligonucleotide
XX bound to a purine-rich target sequence within the double helical nucleic
XX acid, where the oligonucleotide binds in a parallel and antiparallel
XX orientation, respectively, to target sequences on alternate strands of
XX the double helical nucleic acid. The method has therapeutic applications,
XX where gene expression is controlled by selective triple-helix formation
XX within expression regulatory sequences of a target gene. The
XX oligonucleotides can be used to form triple-helices, and are useful to
XX detect the presence or absence of specific sequences within genomic DNA
XX for diagnostic and therapeutic purposes. The oligonucleotides can be
XX selected to specifically bind to pathogenic double-stranded DNA including
XX specific sequences required by pathogenic bacteria or viruses for
XX replication or virulence, reducing their pathogenicity. Alternatively,
XX the oligonucleotide can be chosen to target a unique sequence of the
XX pathogen which is not found in the genome of pathogen's host. The
XX oligonucleotides can be used in cancer treatment by way of triple-helix
XX suppression of specific oncogenes including those of endogenous or viral
XX origin. Such therapeutic oligonucleotides are capable of forming triple-
XX helices with such sequences in cancerous cells containing the activated
XX oncogene, so preferentially killing or repressing the cancer causing
XX cell. The present sequence represents an oligonucleotide used in the
XX methods of the present invention

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XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 1 Other;
Query Match 0.9%; Score 14; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 518
ABK98167/c
XX ID ABK98167 standard; DNA; 15 BP.
XX AC ABK98167;
XX DT 07-OCT-2002 (first entry)
XX DE Triple helix forming associated oligonucleotide #37.
XX KW Triple-helix formation; purine-rich target sequence; double-helix DNA;
XX gene expression; regulatory sequence; pathogenic double-stranded DNA;
XX pathogenic bacteria; virus; replication; virulence; cancer;
XX oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.
XX OS Synthetic.
XX PN US6403302-B1.
XX PD 11-JUN-2002.
XX PF 16-DEC-1993; 93US-00168920.
XX PR 17-SEP-1992; 92US-00946976.
XX PA (CALY ) CALIFORNIA INST OF TECHNOLOGY.
XX PI Dervan PB, Beal PA;
XX WPI; 2002-536030/57.

A triple-helix comprising a double helical nucleic acid (DHNA) and an
oligonucleotide which binds in parallel and antiparallel orientation,
respectively, for targetting sequences on alternate strands of DHNA to
control gene expression.

Example 6; Fig 20A; 108pp; English.

The present invention relates to methods and oligonucleotides for forming
a triple-helix comprising a double helical nucleic acid comprising first
and second substantially complementary strands, and an oligonucleotide
bound to a purine-rich target sequence within the double helical nucleic
acid, where the oligonucleotide binds in a parallel and antiparallel
orientation, respectively, to target sequences on alternate strands of
the double helical nucleic acid. The method has therapeutic applications,
where gene expression is controlled by selective triple-helix formation.
Within expression regulatory sequences of a target gene. The
oligonucleotides can be used to form triple-helices, and are useful to
detect the presence or absence of specific sequences within genomic DNA
for diagnostic and therapeutic purposes. The oligonucleotides can be
selected to specifically bind to pathogenic bacteria or viruses for
replication or virulence, reducing their pathogenicity. Alternatively,
the oligonucleotide can be chosen to target a unique sequence of the
pathogen which is not found in the genome of pathogen's host. The
oligonucleotides can be used in cancer treatment by way of triple-helix
suppression of specific oncogenes including those of endogenous or viral
origin. Such therapeutic oligonucleotides are capable of forming triple-
helices with such sequences in cancerous cells containing the activated
oncogene, so preferentially killing or repressing the cancer causing
cell. The present sequence represents an oligonucleotide used in the

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CC methods of the present invention
XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 1 Other;
Query Match 0.9%; Score 14; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1481 AAAAAAAAAAAAAA 1495
Db 15 AAAAAAAAAAAAAA 1

RESULT 519
ABK98186/c
XX ID ABK98186 standard; DNA; 15 BP.
XX AC ABK98186;
XX DT 07-OCT-2002 (first entry)
XX DE Triple helix forming associated oligonucleotide #50.
XX KW Triple-helix formation; purine-rich target sequence; double-helix DNA;
XX gene expression; regulatory sequence; pathogenic double-stranded DNA;
XX pathogenic bacteria; virus; replication; virulence; cancer;
XX oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.
XX OS Synthetic.
XX PN US6403302-B1.
XX PD 11-JUN-2002.
XX PF 16-DEC-1993; 93US-00168920.
XX PR 17-SEP-1992; 92US-00946976.
XX PA (CALY ) CALIFORNIA INST OF TECHNOLOGY.
XX PI Dervan PB, Beal PA;
XX WPI; 2002-536030/57.

A triple-helix comprising a double helical nucleic acid (DHNA) and an
oligonucleotide which binds in parallel and antiparallel orientation,
respectively, for targetting sequences on alternate strands of DHNA to
control gene expression.

Example 7; Fig 24A; 108pp; English.

The present invention relates to methods and oligonucleotides for forming
a triple-helix comprising a double helical nucleic acid comprising first
and second substantially complementary strands, and an oligonucleotide
bound to a purine-rich target sequence within the double helical nucleic
acid, where the oligonucleotide binds in a parallel and antiparallel
orientation, respectively, to target sequences on alternate strands of
the double helical nucleic acid. The method has therapeutic applications,
where gene expression is controlled by selective triple-helix formation.
Within expression regulatory sequences of a target gene. The
oligonucleotides can be used to form triple-helices, and are useful to
detect the presence or absence of specific sequences within genomic DNA
for diagnostic and therapeutic purposes. The oligonucleotides can be
selected to specifically bind to pathogenic bacteria or viruses for
replication or virulence, reducing their pathogenicity. Alternatively,
the oligonucleotide can be chosen to target a unique sequence of the
pathogen which is not found in the genome of pathogen's host. The
oligonucleotides can be used in cancer treatment by way of triple-helix
suppression of specific oncogenes including those of endogenous or viral
origin. Such therapeutic oligonucleotides are capable of forming triple-
helices with such sequences in cancerous cells containing the activated
oncogene, so preferentially killing or repressing the cancer causing
cell. The present sequence represents an oligonucleotide used in the

```

CC cell. The present sequence represents an oligonucleotide used in the
CC methods of the present invention
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 1 Other;
Query Match 0.9%; Score 14; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1495
DB 15 AAAAAAAAAAAAAA 1
RESULT 520
ABX79833/c
ID ABX79833 standard; cDNA; 15 BP.
XX
AC ABX79833;
XX
DT 17-APR-2003 (first entry)
XX
DE EST polymorphic DNA repeat polynucleotide #158.
XX
KW EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;
KW polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;
KW Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;
KW Haw River syndrome; Huntington's disease; fragile-X syndrome;
KW Friedrich's ataxia; myotonic dystrophy; hyperandrogenaemia;
KW spinal atrophy; bulbar atrophy; spinocerebellar ataxia.
XX
OS Homo sapiens.
XX
PN US6472154-B1.
XX
PD 29-OCT-2002.
XX
PF 31-DEC-1999; 99US-00475947.
XX
PR 31-DEC-1999; 99US-00475947.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Garner HR, Wren JD, Minna JD, Fondon JW;
XX WPI; 2003-208818/20.
XX
PT Identifying a candidate polymorphic repeat within a coding sequence, for
PT understanding or treating genetic disease, comprises detecting tandem
PT repeats in a target coding sequence and scoring the repeats for
PT polymorphic probability.
XX
PS Example; Col 747; 588pp; English.
XX
SS The invention discloses a method for identifying a candidate polymorphic
CC repeat within a coding sequence (expressed sequence tag, EST), which
CC comprises detecting tandem repeats in a target coding sequence, scoring
CC the repeats for polymorphic probability and generating a dataset
CC correlating the repeats with polymorphic probability to identify a
CC candidate polymorphic repeat. The computational methods (polymorphic
CC marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are
CC useful for identifying and detecting candidate polymorphic repeats in
CC human genes, which can be used to understand, treat or eliminate genetic
CC diseases, predispositions or adverse drug-treatment reactions. Examples
CC of diseases linked to nucleotide repeats are Machado-Joseph, Haw River
CC syndrome, Huntington's disease, fragile-X syndrome, Friedrich's ataxia,
CC myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and
CC spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are
CC the polymorphic repeats identified for a search of human ESTs
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 1 Other;
Query Match 0.9%; Score 14; DB 1; Length 15;

Best Local Similarity 93.3%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1495
DB 15 AAAAAAAAAAAAAA 1
RESULT 521
AAD44145/c
ID AAD44145 standard; DNA; 16 BP.
XX
AC AAD44145;
XX
DT 13-DEC-2002 (first entry)
XX
DE Oligo-dT PCR primer #5 used to illustrate the method of the invention.
XX
KW Sequential consensus region-directed amplification; gene expression;
KW disease diagnosis; gene analysis; human; matrix metalloproteinase; PCR;
KW primer; ss.
XX
OS Unidentified.
XX
PN US6277571-B1.
XX
PD 21-AUG-2001.
XX
PF 30-SEP-1998; 98US-00163485.
XX
PR 03-OCT-1997; 97US-00943162.
XX
PR 03-OCT-1997; 97US-0108152P.
XX
PA (UYVI-) UNIV VIRGINIA COMMONWEALTH INTELLECTUAL.
XX
PI Fillmore H, Broadus W, Gillies G;
XX WPI; 2002-412824/44.
XX
PT Sequential consensus region-directed amplification for sorting mixture of
PT DNAs into 2 or more subsets or distinguishing gene expression patterns in
PT 2 samples, useful for disease diagnosis and gene analysis.
XX
PS Example; Fig 1C; 19pp; English.
XX
SS The invention relates to a method of sequential consensus region-directed
CC amplification for sorting a mixture of DNAs into 2 or more subsets or
CC distinguishing gene expression patterns in 2 samples. The methods, kits
CC and oligonucleotides are useful for sorting a mixture of DNAs into 2 or
CC more subsets or distinguishing gene expression patterns in 2 samples e.g.
CC for disease diagnosis and gene analysis. The present sequence is oligo dT
CC PCR primer used to illustrate the method of the invention
XX
SQ Sequence 16 BP; 0 A; 1 C; 0 G; 14 T; 0 U; 1 Other;
Query Match 0.9%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1494
DB 16 AAAAAAAAAAAAAA 3
RESULT 522
AAD44147/c
ID AAD44147 standard; DNA; 16 BP.
XX
AC AAD44147;
XX
DT 13-DEC-2002 (first entry)
XX
DE Oligo-dT PCR primer #7 used to illustrate the method of the invention.

XX Sequential consensus region-directed amplification; gene expression;
KW disease diagnosis; gene analysis; human; matrix metalloproteinase; PCR;
KW primer; ss.
XX Unidentified.
XX US6277571-B1.
XX 21-AUG-2001.
XX 30-SEP-1998; 98US-00163485.
XX 03-OCT-1997; 97US-00943162.
PR 03-OCT-1997; 97US-0108152P.
XX (UYVI-) UNIV VIRGINIA COMMONWEALTH INTELLECTUAL.
XX Fillmore H, Broadus W, Gillies G;
XX WPI; 2002-412824/44.
XX Sequential consensus region-directed amplification for sorting mixture of
PT DNAs into 2 or more subsets or distinguishing gene expression patterns in
PT 2 samples, useful for disease diagnosis and gene analysis.
XX Example; Fig 1C; 19pp; English.
XX The invention relates to a method of sequential consensus region-directed
CC amplification for sorting a mixture of DNAs into 2 or more subsets or
CC distinguishing gene expression patterns in 2 samples. The methods, kits
CC and oligonucleotides are useful for sorting a mixture of DNAs into 2 or
CC more subsets or distinguishing gene expression patterns in 2 samples e.g.
CC for disease diagnosis and gene analysis. The present sequence is oligo dt
CC PCR primer used to illustrate the method of the invention
XX
XX Sequence 16 BP; 0 A; 0 C; 1 G; 14 T; 0 U; 1 Other;
Query Match 0.9%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1494
Db 16 AAAAAAAAAAAAAA 3
RESULT 523
AAD44149/c
ID AAD44149 standard; DNA; 16 BP.
AC AAD44149;
XX 13-DEC-2002 (first entry)
DT
DE Oligo-dT PCR primer #9 used to illustrate the method of the invention.
XX Sequential consensus region-directed amplification; gene expression;
KW disease diagnosis; gene analysis; human; matrix metalloproteinase; PCR;
KW primer; ss.
XX Unidentified.
XX US6277571-B1.
XX 21-AUG-2001.
XX 30-SEP-1998; 98US-00163485.
XX 03-OCT-1997; 97US-00943162.
PR 03-OCT-1997; 97US-0108152P.
XX (UYVI-) UNIV VIRGINIA COMMONWEALTH INTELLECTUAL.

XX Fillmore H, Broadus W, Gillies G;
XX WPI; 2002-412824/44.
XX Sequential consensus region-directed amplification for sorting mixture of
PT DNAs into 2 or more subsets or distinguishing gene expression patterns in
PT 2 samples, useful for disease diagnosis and gene analysis.
XX Example; Fig 1C; 19pp; English.
XX The invention relates to a method of sequential consensus region-directed
CC amplification for sorting a mixture of DNAs into 2 or more subsets or
CC distinguishing gene expression patterns in 2 samples. The methods, kits
CC and oligonucleotides are useful for sorting a mixture of DNAs into 2 or
CC more subsets or distinguishing gene expression patterns in 2 samples e.g.
CC for disease diagnosis and gene analysis. The present sequence is oligo dt
CC PCR primer used to illustrate the method of the invention
XX
XX Sequence 16 BP; 1 A; 0 C; 0 G; 14 T; 0 U; 1 Other;
Query Match 0.9%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1494
Db 16 AAAAAAAAAAAAAA 3
RESULT 524
AAL54153/c
ID AAL54153 standard; RNA; 16 BP.
XX AAL54153;
AC AAL54153;
XX 28-MAR-2003 (first entry)
DT
DE RNA intron region #1.
XX Splice junction; alternative spliced mRNA; splice variant; carcinoma;
KW sarcoma; leukaemia; lymphoma; pancreatitis; polycystic kidney disease;
KW ss.
XX Unidentified.
XX WO200293165-A1.
XX 21-NOV-2002.
XX 17-MAY-2002; 2002WO-US015649.
XX 17-MAY-2001; 2001US-0291598P.
XX (GENE-) GENE LOGIC INC.
XX Dolginow D, Mertz L;
XX WPI; 2003-129322/12.
XX New sets of oligonucleotides with at least one that specifically
PT hybridizes to each possible splice junction in mRNA transcribed a gene,
PT useful for detecting or analyzing alternative splice variants of mRNA, or
PT diagnosing diseases.
XX Disclosure; Page 5; 37pp; English.
XX The invention relates to a set of oligonucleotides, which comprise at
CC least one oligonucleotide that specifically hybridizes to each possible
CC splice junction in mRNA transcribed from at least one gene of interest.
CC The oligonucleotides are useful in solid supports for detecting
CC alternative spliced mRNA, a pathological condition in a patient, or
CC identifying an agent that modulates a pathological condition. These

CC oligonucleotides are particularly useful for detecting or analysing
CC alternative splice variants of mRNA, as well as for predicting disease
CC states in the diagnosis of diseases, e.g. carcinoma, sarcoma, leukaemia,
CC lymphoma, pancreatitis, or polycystic kidney disease. The splice variants
CC are useful for screening pharmaceutical agents for modulating a
CC pathological condition. This polynucleotide sequence represents an intron
CC region relating to the invention

SQ Sequence 16 BP; 1 A; 0 C; 2 G; 0 T; 12 U; 1 Other;

Query Match 0.9%; Score 14; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1479 CTAAAAAATAAAAAA 1493
DB 15 CTAAAAAATAAAAAA 1

RESULT 525
AA85699/C
ID AA85699 standard; DNA; 18 BP.

XX AAF85699;

XX 13-JUL-2001 (first entry)

DE Multiple repeated heat process PCR related oligonucleotide #3.

KW Multiple repeated heat circulation; polymerase chain reaction; PCR;
KW target DNA production; DNA synthesis; ds.

XX Unidentified.

XX CN1278558-A.

XX 03-JAN-2001.

XX 22-JUN-1999; 99CN-00114949.

XX 22-JUN-1999; 99CN-00114949.

XX (XIAQ/) XIA Q.

XX Xia Q;

XX WPI; 2001-245741/26.

XX Asynchronous chain-extending polymerase chain reaction for producing lots
XX of target DNA fragments, comprises a multiple repeated heat circulation
XX process.

PS Disclosure; Page 3; 4pp; Chinese.

XX The present invention relates to a kind of two chains asynchronously-
XX elongated DNA amplification technology in vitro, which is characterized
XX by that firstly, a pair of specific primers is synthesized according to
XX the target DNA sequence to be amplified, then a repetitive sequence
XX complementary oligo-repetitive sequence of 3' target DNA chain whose tail
XX end is modified and elongation vitality is lost, then the oligo-
XX repetitive sequence, chain primer, heat-resistant DNA polymerase, dNTP
XX substrate, template DNA, magnesium ion, polymerase chain reaction (PCR)
XX buffer solution and ultra-pure water are mixed uniformly and made into a
XX reaction system. The reaction system then undergoes the processes of high
XX -temp., low-temp., medium-low temp., medium-temp, and repeated heat
XX circulation treatment in the heat-circulating instrument to obtain
XX million copies of specific target DNA fragments. The invention adopts a
XX multiple repeated heat circulation process, so that it can produce lots
XX of target DNA fragments. The present sequence was used in the
XX exemplification of the invention

SQ Sequence 18 BP; 0 A; 6 C; 12 G; 0 T; 0 U; 0 Other;

Query Match 0.9%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 3.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 222 CGCCGCCGCCGCCGCC 238
DB 18 CGCCGCCGCCGCCGCC 2

RESULT 526

ABK32799

ID ABK32799 standard; DNA; 15 BP.

XX ABK32799;

XX 23-APR-2002 (first entry)

XX Human APPBP1 gene, allele-specific oligonucleotide #29.

XX Human; amyloid beta precursor protein binding protein 1; APPBP1; probe;

KW Alzheimer's disease; transgenic animal; platelet aggregation; ss.

KW single nucleotide polymorphism; SNP; allele-specific oligonucleotide; ss.

XX Homo sapiens.

XX WO200202820-A1.

XX 10-JAN-2002.

XX 02-JUL-2001; 2001WO-US020951.

XX 30-JUN-2000; 2000US-0215511P.

XX (GENA-) GENAISANCE PHARM INC.

XX Anastasio AE, Chew A, Choi JY, Kazemi A, Koshy B, Sausker EA;

PI Stephens CJ;

XX WPI; 2002-164539/21.

XX Amyloid beta precursor protein binding protein 159 kD (APPBP1) gene
XX polymorphic variants, useful e.g. in studying the expression and function
XX of APPBP1 and screening candidate drugs for treating Alzheimer's disease.

XX Claim 17; Page 13; 104pp; English.

XX The invention relates to an isolated polypeptide comprising a sequence
XX which is a polymorphic variant of a reference sequence for the amyloid
XX beta precursor protein binding protein 1, 59kD (APPBP1) protein or its
XX fragment. The polymorphic variants are useful in studying the expression
XX and function of APPBP1, in expressing APPBP1 protein for use in screening
XX for candidate drugs to treat diseases related to APPBP1 activity, in
XX studying the effect of the variation on the biological activity of
XX APPBP1, and the binding affinity of candidate drugs targeting APPBP1 for
XX the treatment of disorders such as Alzheimer's disease. The haplotyping
XX methods are useful in validating APPBP1 as a candidate target for
XX treating a specific condition or disease predicted to be associated with
XX APPBP1 activity, or in the design of clinical trials of candidate drugs
XX for treating a specific condition or disease associated with APPBP1
XX activity. The transgenic animals are useful for studying expression of
XX the APPBP1 isogenes in vivo, for in vivo screening and testing of drugs
XX targeted against APPBP1 protein, and for testing the efficacy of
XX therapeutic agents and compounds for disorders related to platelet
XX aggregation in a biological system. ABK32771-ABK32327 represent human
XX APPBP1 gene allele-specific oligonucleotides used in the method of the
XX invention

SQ Sequence 15 BP; 13 A; 1 C; 0 G; 0 T; 0 U; 1 Other;

Query Match 0.9%; Score 13.6; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 3e+02;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1481 AAAAAAAAAAAAAA 1494
Db 11111111111111111111
2 AAAAAAAAAAAAAA 15

RESULT 527
ABZ04679/C
ID ABZ04679 standard; DNA; 50 BP.
AC
AC ABZ04679;
DT
DT 09-JAN-2003 (first entry)
XX
DE Human leukocyte gene expression profiling probe SEQ ID NO 4670.
XX
XX T7; leukocyte; gene expression profiling; allograft rejection;
XX KW atherosclerosis; congestive heart failure; systemic lupus erythematosus;
XX KW rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
XX KW ss.
XX
OS Homo sapiens.
XX
XX WO200257414-A2.
XX
XX 25-JUL-2002.
XX
XX 22-OCT-2001; 2001WO-US047856.
XX
XX 20-OCT-2000; 2000US-0241994P.
XX
XX 08-JUN-2001; 2001US-0296764P.
XX
XX (BIOC-) BIOCARDIA INC.
XX
XX Wohlgemuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;
XX Ly N, Woodward R, Quermous T, Johnson F;
XX
XX WPI; 2002-636525/68.
XX
XX New system for leukocyte expression profiling, diagnosing a disease, or
XX monitoring (the rate of) progression of a disease, e.g. atherosclerosis
XX or congestive heart failure, comprises diagnostic oligonucleotides.
XX
XX Claim 1; Page 477; Opp; English.
XX
XX The invention relates to a system for detecting gene expression, which
XX comprises one or two isolated DNA molecules that detect expression of a
XX gene, where the gene corresponds to any of 8143 oligonucleotides
XX (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful
XX for leukocyte expression profiling. It is particularly useful for
XX diagnosing a disease, monitoring (rate of) progression of a disease,
XX predicting therapeutic outcome, determining prognosis for a patient,
XX predicting disease complications in an individual or monitoring response
XX to treatment in an individual. The diseases include cardiac allograft
XX rejection, kidney allograft rejection, liver allograft rejection,
XX atherosclerosis, congestive heart failure, systemic lupus erythematosus,
XX rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
XX
XX Sequence 50 BP; 13 A; 17 C; 5 G; 15 T; 0 U; 0 Other;
XX
Query Match 0.9%; Score 13.6; DB 1; Length 50;
Best Local Similarity 67.9%; Pred. No. 3.9e+02;
Matches 19; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1127 TGATGTCACATGTAGTGGCGTGTATGA 1154
Db 11111111111111111111
29 TGATTACAGTTGAAGCGCAGCTGTAGA 2

RESULT 528
AAT52144/C
ID AAT52144 standard; RNA; 15 BP.
XX
XX AAT52144;
AC

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XX
DT 25-MAR-2003 (revised)
DT 25-MAR-1997 (first entry)
XX
XX Human ICAM hammerhead ribozyme target sequence (nt. position 2914).
XX
XX Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
XX KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
XX KW intercellular adhesion molecule; rel A; tumour necrosis factor;
XX KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
XX KW translocation; chronic myelogenous leukaemia; CML; cancer;
XX KW Philadelphia chromosome; inflammation; autoimmune disease;
XX KW atherosclerosis; myocardial infarction; stroke; restenosis;
XX KW transplant rejection; rheumatoid arthritis; psoriasis;
XX KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;
XX KW human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
XX KW ss.
XX
XX Homo sapiens.
XX
XX WO9523225-A2.
XX
XX 31-AUG-1995.
XX
XX 23-FEB-1995; 95WO-IB000156.
XX
XX 23-FEB-1994; 94US-00201109.
XX 29-MAR-1994; 94US-00218934.
XX 04-APR-1994; 94US-00222795.
XX 07-APR-1994; 94US-00224483.
XX 15-APR-1994; 94US-00227958.
XX 15-APR-1994; 94US-00228041.
XX 06-MAY-1994; 94US-00245736.
XX 18-JUL-1994; 94US-00271280.
XX 15-AUG-1994; 94US-00291932.
XX 16-AUG-1994; 94US-00291433.
XX 17-AUG-1994; 94US-00292620.
XX 19-AUG-1994; 94US-00293520.
XX 02-SEP-1994; 94US-00300000.
XX 08-SEP-1994; 94US-00303039.
XX 23-SEP-1994; 94US-00311486.
XX 23-SEP-1994; 94US-00311749.
XX 28-SEP-1994; 94US-00314397.
XX 03-OCT-1994; 94US-00316771.
XX 07-OCT-1994; 94US-00319492.
XX 11-OCT-1994; 94US-00321993.
XX 04-NOV-1994; 94US-00334847.
XX 10-NOV-1994; 94US-00337608.
XX 28-NOV-1994; 94US-00345516.
XX 16-DEC-1994; 94US-00357577.
XX 23-DEC-1994; 94US-00363233.
XX 30-JAN-1995; 95US-00380734.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Stinchcomb DT, Chowrira B, Drenzo A, Draper KG, Dudycz LW;
XX Grimm S, Karpelsky A, Kisich K, Matulic-Adamic J, Mcswiggen JA;
XX Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
XX Tracz D, Usman N, Wincott FE, Woolf T;
XX
XX WPI; 1995-351090/45.
XX
XX Ribozymes having modified bases and methods for producing them - for use
XX in inhibiting disease related genes.
XX
XX Claim 2; Page 175; 407pp; English.
XX
XX The present sequence represents a preferred target sequence for an
XX enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA at the
XX nucleotide base position indicated in the DE line. Regions of the mRNA
XX that do not form secondary folding structures and that contain potential
XX hammerhead and hairpin ribozyme cleavage sites were identified by
XX computer analysis. Ribozymes directed against these mRNA sequences were

```

CC designed and synthesised with modifications that improve their nuclease
 CC resistance. The ribozymes cleave the ICAM-1 target sequences and thereby
 CC inhibit ICAM-1 expression, making them useful for reducing transplant
 CC rejection and alleviating symptoms in patients with rheumatoid arthritis,
 CC asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to
 CC correct PI field.)
 XX

SQ Sequence 15 BP; 1 A; 1 C; 1 G; 0 T; 12 U; 0 Other;
 Query Match 0.9%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 3.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1479 CTAAAAA1493
 DB 15 CTGAAAAA1

RESULT 529
 AAT56307
 ID AAT56307 standard; RNA; 15 BP.
 XX AC AAT56307;
 XX
 DT 25-MAR-2003 (revised)
 DT 14-MAY-1997 (first entry)
 XX
 DE Mouse TNP-a hammerhead ribozyme target sequence (nt position 1462).
 XX
 KW Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
 KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
 KW intercellular adhesion molecule; rel A; tumour necrosis factor;
 KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
 KW Philadelphia chromosome; inflammation; autoimmune disease;
 KW atherosclerosis; myocardial infarction; stroke; restenosis;
 KW transplant rejection; rheumatoid arthritis; psoriasis;
 KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;
 KW human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
 KW ss.

XX Mhs musculus.

OS

XX

PN WO9523225-A2.

XX 31-AUG-1995.

XX 23-FEB-1995;

XX 94US-00201109.

XX 29-MAR-1994;

XX 04-APR-1994;

XX 07-APR-1994;

XX 15-APR-1994;

XX 18-MAY-1994;

XX 06-JUL-1994;

XX 13-AUG-1994;

XX 16-AUG-1994;

XX 17-AUG-1994;

XX 02-SEP-1994;

XX 08-SEP-1994;

XX 23-SEP-1994;

XX 28-SEP-1994;

XX 03-OCT-1994;

XX 07-OCT-1994;

XX 11-OCT-1994;

XX 04-NOV-1994;

XX 10-NOV-1994;

XX 28-NOV-1994;

XX 16-DEC-1994;

PR 23-DEC-1994; 94US-00363233.
 PR 30-JAN-1995; 95US-00380734.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.

XX Stinchcomb DT, Chowrira B, Drenzo A, Draper KG, Dudycz LW;
 PI Grimm S, Karpeisky A, Kisich K, Matulic-Adamic J, McSwiggen JA;
 PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
 PI Tracz D, Usman N, Wincott FE, Woolf T;
 XX MPI; 1995-351090/45.

XX Ribozymes having modified bases and methods for producing them - for use
 in inhibiting disease related genes.
 PT
 XX
 PS Claim 2; Page 252; 407pp; English.

XX The present sequence represents a preferred target sequence for an
 CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves TNF-alpha mRNA at
 CC the nucleotide base position indicated in the DE line. Regions of the
 CC mRNA that do not form secondary folding structures and that contain
 CC potential hammerhead and hairpin ribozyme cleavage sites were identified
 CC by computer analysis. Ribozymes directed against these mRNA sequences
 CC were designed and synthesised with modifications that improve their
 CC nuclease resistance. The ribozymes are designed to cleave the target
 CC sequences and thereby inhibit TNF-alpha expression, making them
 CC potentially useful for treating rheumatoid arthritis, septic shock and
 CC other inflammatory disorders including psoriasis, as well as for
 CC treatment of AIDS. (Updated on 25-MAR-2003 to correct PI field.)
 XX
 SQ Sequence 15 BP; 1 A; 6 C; 2 G; 0 T; 6 U; 0 Other;

Query Match 0.9%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 53.3%; Pred. No. 3.3e+02;
 Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
 QY 1334 ACCTGTTCCTCCT 1348
 DB 1 ACCUUGGCCUCCU 15

RESULT 530
 AAT52142/c
 ID AAT52142 standard; RNA; 15 BP.

XX AC AAT52142;

XX 25-MAR-2003 (revised)

DT 25-MAR-1997 (first entry)

XX Human ICAM hammerhead ribozyme target sequence (nt. position 2913).

XX Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
 KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
 KW intercellular adhesion molecule; rel A; tumour necrosis factor;
 KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
 KW Philadelphia chromosome; inflammation; autoimmune disease;
 KW atherosclerosis; myocardial infarction; stroke; restenosis;
 KW transplant rejection; rheumatoid arthritis; psoriasis;
 KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;
 KW human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
 KW ss.

XX Homo sapiens.

XX WO9523225-A2.

XX 31-AUG-1995.

XX 23-FEB-1995; 95WO-IB000156.

XX 23-FEB-1994; 94US-00201109.

PR

PN WO9714026-A2.
 PD 17-APR-1997.
 XX
 XX 10-OCT-1996; 96WO-CA000676.
 XX
 XX 12-OCT-1995; 95US-0005590P.
 PR 28-NOV-1995; 95US-0007616P.
 XX
 XX (LANS/) LANSORP P.
 PA
 XX Lansdorp P;
 PI
 XX WPI; 1997-236021/21.
 DR
 XX Detection of multiple copies of repeat sequences in telomeres - useful
 PT for determining replicative potential of cells.
 PT
 XX Disclosure; Page 9; 38pp; English.
 XX
 XX This is a peptide nucleic acid (PNA) probe which is used for detecting
 CC and optionally quantitating the trinucleotide simple tandem repeat CCG.
 CC The probe is suitable for use in a new method for detecting and
 CC optionally quantitating multiple copies of a repeat sequence. For use in
 CC the method, the probe is labelled, preferably with a fluorescent
 CC molecule, and the length of the repeat region can be determined based on
 CC the intensity of the label signal
 CC
 XX
 SQ Sequence 15 BP; 0 A; 5 C; 10 G; 0 T; 0 U; 0 Other;
 Query Match 0.9%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 3.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 26 GCGCGCGCGCGCGC 40
 Db 1 GCGCGCGCGCGCGC 15
 RESULT 533
 AAT86603
 ID AAT86603 standard; DNA; 15 BP.
 XX
 XX AAT86603;
 AC
 XX 04-JUN-1998 (first entry)
 DT
 XX Oligonucleotide separated by capillary affinity gel electrophoresis.
 XX
 XX Capillary affinity gel electrophoresis; separation; polymer-gel;
 KW polyacrylamide; ss.
 KW
 XX Synthetic.
 OS
 XX WO9745721-A1.
 PN
 XX 04-DEC-1997.
 PD
 XX 23-MAY-1997; 97WO-EP002647.
 XX
 XX 24-MAY-1996; 96CH-00001320.
 PR
 XX (NOVS) NOVARTIS AG.
 PA
 XX Muscate A, Paulus A, Natt F;
 PI
 XX WPI; 1998-041763/04.
 DR
 XX Separation of electrically charged target molecules - by capillary
 PT affinity gel electrophoresis using polymer-gel to which receptors for
 PT target molecules are bound.
 XX
 XX Example D2; Page 25; 41pp; English.
 PS

XX A mixture of oligonucleotides (AAT86601-3) were separated by a new
 CC process using capillary affinity gel electrophoresis. The invention
 CC relates to selective separation of electrically charged target molecules
 CC in an analytical mixture. It comprises capillary affinity gel
 CC electrophoresis using a capillary tube which is at least partly filled
 CC with a polymer gel. Receptors for target molecules are covalently bound
 CC to the polymer. An electric field of at least 50 volts/cm is applied. The
 CC capillary tube is charged with the analytical mixture. In a first
 CC separation stage, the target molecules in the mixture are bound to the
 CC receptors and the remaining components are eluted, optionally whilst
 CC splitting open. In a second stage, the elution conditions are changed,
 CC optionally in stages, so that the affinity of the target molecules for
 CC the receptor is eliminated and the target molecules are eluted and
 CC detected, optionally whilst splitting open. The process is useful for
 CC selective separation and/or determination of charged organic compounds,
 CC such as oligonucleotides, peptides or carbohydrates. It may be used, e.g.
 CC for isolation of specific proteins and DNA molecules, purification of
 CC antibodies, analysis of antisense compounds or screening for enzyme
 CC inhibitors. The process achieves higher resolution and selectivity than
 CC prior art processes, especially in the case of complex biological
 CC analytical mixtures. It has high sensitivity, even with small amounts of
 CC samples. The derivatised polymers may be synthesised specifically using
 CC standard methods
 XX
 SQ Sequence 15 BP; 14 A; 0 C; 0 G; 1 T; 0 U; 0 Other;
 Query Match 0.9%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 3.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1481 AAAAAAAAAAAAAA 1495
 Db 1 AAAAAAAAAAAAAA 15
 RESULT 534
 AAX54258
 ID AAX54258 standard; DNA; 15 BP.
 XX
 XX AAX54258;
 AC
 XX 05-JUL-1999 (first entry)
 DT
 XX Chymase antisense oligonucleotide fragment.
 DE
 XX Antisense oligonucleotide; multiple target; antisense treatment;
 KW impaired respiration; inflammation; lung disease;
 KW pulmonary vasoconstriction; inflammation; allergic rhinitis;
 KW acute asthma; allergy; asthma; impeded respiration;
 KW respiratory distress syndrome; pain; cystic fibrosis;
 KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;
 KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
 KW colon cancer; breast cancer; lung cancer; pancreatic cancer;
 KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
 KW prostate cancer; ss.
 KW
 XX Synthetic.
 OS
 XX WO9913886-A1.
 PN
 XX 25-MAR-1999.
 PD
 XX 17-SEP-1998; 98WO-US019419.
 PF
 XX 17-SEP-1997; 97US-0059160P.
 PR 09-JUN-1998; 98US-00093972.
 XX
 XX (UYEC-) UNIV EAST CAROLINA.
 PA
 XX Nyce JW;
 PI
 XX WPI; 1999-229400/19.
 DR

XX New antisense oligonucleotides used in treatment of, e.g. pulmonary
 PT vasoconstriction.
 XX
 XX Disclosure; Page 60; 120pp; English.
 XX
 XX The specification describes antisense oligonucleotides (AA52869-X55271)
 CC directed against at least 2 mRNAs selected from target genes, coding and
 CC non-coding regions of RNAs corresponding to target genes, gene initiation
 CC codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3',
 CC -end and the juxta-section between coding and non-coding regions and all
 CC segments of RNAs encoding proteins associated with one or more diseases,
 CC conditions or mixtures. The antisense oligonucleotides may be derived
 CC from sequences AAX5272-74. These multiple target oligonucleotides
 CC (specifically AAX5180-271) can be used for the antisense treatment of
 CC diseases and conditions. Typical diseases and conditions are those
 CC associated with impaired respiration and inflammation, including lung
 CC diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,
 CC acute asthma, allergies, asthma, impeded respiration, respiratory
 CC distress syndrome, pain, cystic fibrosis, pulmonary hypertension,
 CC pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary
 CC disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.
 CC colon cancer, breast cancer, lung cancer, pancreatic cancer,
 CC hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as
 CC well as all types of cancers which may metastasize or have metastasized
 CC to the lungs, including breast and prostate cancer
 XX
 SQ Sequence 15 BP; 0 A; 4 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 0.9%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 3.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 323 CTGGGTGGGCCCTG 337
 Db 1 CTGGGTGGGCCCTG 15
 |||||

RESULT 535
 AAX18364/C
 ID AAX18364 standard; DNA; 15 BP.
 XX
 AC AAX18364;
 XX
 XX 11-MAY-1999 (first entry)
 XX
 XX RT-PCR primer of the invention SEQ ID 5.
 XX
 XX RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
 XX
 OS Synthetic.
 XX
 XX JPI1032765-A.
 XX
 XX 09-FEB-1999.
 XX
 XX 18-JUL-1997; 97JP-00208312.
 XX
 XX 18-JUL-1997; 97JP-00208312.
 XX
 XX (TAKI) TAKARA SHUZO CO LTD.
 XX
 XX WPI; 1999-183822/16.
 XX
 XX Peptides having at least two new nucleotides - useful as primers in RT-
 PT PCR.
 XX
 PS Disclosure; Page 10; 19pp; Japanese.
 XX
 XX This sequence represents a primer of the invention. The invention relates
 CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
 CC -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
 CC a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =

CC natural number indicating the repetition of alpha; beta, delta = V or N;
 CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
 CC thymine; gamma = thymine; k = natural number of 3 or over indicating the
 CC repetition of gamma, in which thymine expressed by gamma is composed of
 CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
 CC useful as primers for RT-PCR and determination of base sequences. The new
 CC sequences allow for reproductive and highly efficient analysis of gene
 CC sequences
 XX
 SQ Sequence 15 BP; 0 A; 0 C; 2 G; 13 T; 0 U; 0 Other;

Query Match 0.9%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 3.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1479 CTAAAAAATAAAAAA 1493
 Db 15 CCAAAAAAATAAAAAA 1
 |||||

RESULT 536
 AAA33702
 ID AAA33702 standard; DNA; 15 BP.
 XX
 AC AAA33702;
 XX
 XX 28-JUL-2000 (first entry)
 XX
 XX Low adenosine antisense oligonucleotide SEQ ID NO:1391.

Human; adenosine receptor; low adenosine antisense oligonucleotide;
 KW phosphorothioate; impaired respiration; inflammation; allergy;
 KW allergic disease; bronchoconstriction; inhibitor; anti-inflammatory;
 KW antiallergic; antiasthmatic; cytotactic; analgesic; impaired airway;
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

OS Homo sapiens.
 XX
 XX WO200009525-A2.
 XX
 XX 24-FEB-2000.
 XX
 XX 03-AUG-1999; 99WO-US017712.
 XX
 XX 03-AUG-1998; 98US-0095212P.
 XX
 XX (UYEC-) UNIV EAST CAROLINA.
 XX
 XX Nyce JW;
 XX
 XX WPI; 2000-205971/18.

New antisense oligonucleotides useful for treating e.g. pulmonary
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
 PT cancers.
 XX
 XX Claim 18; Page 438; 1343pp; English.

The present invention describes a new composition comprising an antisense
 CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
 CC nucleic acids involved in bronchoconstriction, allergies, and/or
 CC inflammation. The ON can have anti-inflammatory, antiallergic,
 CC antiasthmatic, cytotactic and analgesic activities. The compositions are
 CC useful for the treatment of diseases associated with inflammation,
 CC impaired airways, including lung disease and diseases whose secondary
 CC effects afflict the lungs of a subject. They can be used for treating
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
 CC impeded respiration, respiratory distress syndrome, pain, cystic
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive

CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
 CC carcinomas, and cancers which may metastasise to the lungs, including
 CC breast and prostate cancer. The reduction of the adenosine content of the
 CC ONS reduces side effects. The A-containing ONS break down with the
 CC release of deoxyadenosine which activates adenosine receptors causing
 CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
 CC nucleotide sequences given in the sequence listing from the present
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
 CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
 CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
 CC AAA33992) are specifically claimed ONS from the present invention. N.B.
 CC Sequences given in the disclosure of the present invention do not match
 CC up with their corresponding SEQ ID NO: sequences given in the sequence
 CC listing

XX
 SQ Sequence 15 BP; 0 A; 4 C; 8 G; 3 T; 0 U; 0 Other;
 Query Match 0.9%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 3.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 323 CTGGGTGTGCCCTG 337
 |||||
 Db 1 CTGGGTGGGCCCTG 15

RESULT 537
 AAA11718/c
 ID AAA11718 standard; DNA; 15 BP.

AC AAA11718;

XX 14-JUL-2000 (first entry)

DE Human MIF gene D5k region primer #2.

XX MIF; migration inhibitory factor; D5k region; human; macrophage;
 KW diagnosis; primer; adenocarcinoma; metastasis; cancer; tumor cell; ss.

XX Homo sapiens.

XX US6043044-A.

XX 28-MAR-2000.

XX 15-JUL-1997; 97US-00893204.

XX 15-JUL-1997; 97US-00893204.

XX (HUDS/) HUDSON P B.

PA (HAKK/) HAKKY S I.

PA (SIEG/) SIEGLER K M.

PA (HAKK/) HAKKI A.

PI Hakky SI, Hudson PB, Siegler KM, Hakki A;

XX WPI; 2000-292363/25.

XX A new method useful for diagnosing human adenocarcinoma and measuring
 PT metastatic potential comprises determining the levels of macrophage
 PT migration inhibitory factor within tumor cells.

XX Claim 11; Col 7-8; 6pp; English.

XX This invention describes a novel method for diagnosing adenocarcinoma and
 CC determining metastatic ability of human cancer in an individual by
 CC determining the increased levels of macrophage migration inhibitory
 CC factor (MIF) within tumor cells. The method is useful for diagnosing
 CC human adenocarcinoma, as well as for its prognosis. The method is also
 CC useful for measuring levels of macrophage migration inhibitory factor
 CC within tumor cells. The method provides better and more accurate
 CC prognostic markers for cancer. The method is also capable of
 CC distinguishing histological tumors from clinical cancers. This sequence

CC represents a primer used to detect the human MIF gene D5k region which is
 CC described in the method of the invention

XX Sequence 15 BP; 0 A; 1 C; 0 G; 14 T; 0 U; 0 Other;

SQ Query Match 0.9%; Score 13.4; DB 1; Length 15;

Best Local Similarity 93.3%; Pred. No. 3.3e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1481 AAAAAAAAAAAAAA 1495

Db 15 AGAAAAAAAAAAAAA 1

RESULT 538

AAFI9824

ID AAF19824 standard; DNA; 15 BP.

XX AAF19824;

XX 14-MAR-2001 (first entry)

DE Human chymase polynucleotide fragment #1391.

XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;

KW human; airway disorder; bronchoconstriction; lung inflammation;

KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;

KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;

KW respiratory obstruction; pulmonary obstruction; impeded respiration;

KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;

KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;

KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;

KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;

KW cancer; ss.

XX Homo sapiens.

XX WO2000062736-A2.

XX 26-OCT-2000.

XX 24-MAR-2000; 2000WO-US008020.

XX 06-APR-1999; 99US-0127958P.

XX (UYEC-) UNIV EAST CAROLINA.

PA (NYCE/) NYCE J W.

PI Nyce JW;

XX WPI; 2000-679539/66.

XX Low adenosine (A) content antisense oligonucleotides which do not trigger
 PT adenosine receptors during metabolism, useful e.g. for treating cancers
 PT and respiratory obstructions.

XX Claim 14; Page 250; 1592pp; English.

XX The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide

transmitters, defensins, growth factors, vasoactive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAF18434 to AAF21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of the present invention

Query Match 0.9%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 3.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Sequence 15 BP; 0 A; 4 C; 8 G; 3 T; 0 U; 0 Other;
 Query Match 0.9%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 3.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 323 CTGGGTGTGGCCCTG 337
 |||||
 Db 1 CTGGGTGGGCCCTG 15

RESULT 539
 AAF46644
 ID AAF46644 standard; DNA; 15 BP.
 XX AAF46644;
 AC AAF46644;
 XX 30-MAR-2001 (first entry)
 DT IGFBP3 oligonucleotide #64.
 DE Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.

Homo sapiens.
 OS
 XX WO200078341-A1.
 XX 28-DEC-2000.
 XX 21-JUN-2000; 2000WO-AU000693.
 XX 21-JUN-1999; 99US-0140345P.
 XX (MURD-) MURDOCH CHILDRENS RES INST.
 XX Wright CJ, Werther GA, Edmondson SR;
 PI WPI; 2001-041421/05.
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or inflammation.

Example 7; Page 44; 201pp; English.
 The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1 receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation,

inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotides of the present invention (see AAF45151 and AAF45153-F45161). The method is useful for ameliorating the effects of psoriasis, ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood vessels or any other hyperplasia

Query Match 0.9%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 3.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Sequence 15 BP; 1 A; 9 C; 4 G; 1 T; 0 U; 0 Other;
 Query Match 0.9%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 3.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 65 CCTCCGCGCCAGCC 79
 |||||
 Db 1 CCTCGCGCCAGCC 15

RESULT 540
 AAF52137
 ID AAF52137 standard; DNA; 15 BP.
 XX AAF52137;
 AC AAF52137;
 XX 30-MAR-2001 (first entry)
 DT IGF-I oligonucleotide #3097.
 DE Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.

Homo sapiens.
 OS
 XX WO200078341-A1.
 XX 28-DEC-2000.
 XX 21-JUN-2000; 2000WO-AU000693.
 XX 21-JUN-1999; 99US-0140345P.
 XX (MURD-) MURDOCH CHILDRENS RES INST.
 XX Wright CJ, Werther GA, Edmondson SR;
 PI WPI; 2001-041421/05.
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or inflammation.

Example 8; Page 81; 201pp; English.
 The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1 receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotides of the present invention (see AAF45151 and AAF45153-F45161). The method is useful for ameliorating the effects of psoriasis,

CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia
 XX
 SQ Sequence 15 BP; 2 A; 2 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 0.9%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 3.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 665 GCCAAGGCTGTGGTG 679
 DB 1 GCCAAGGCTGTGGTG 15

RESULT 541
 AAF52138
 ID AAF52138 standard; DNA; 15 BP.
 XX AC AAF52138;
 XX

30-MAR-2001 (first entry)
 DE IGF-I oligonucleotide #3098.

XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.

OS Homo sapiens.
 XX
 XX WO200078341-A1.
 XX

PD 28-DEC-2000.

PF 21-JUN-2000; 2000WO-AU000693.

XX 21-JUN-1999; 99US-0140345P.

PR (MURD-) MURDOCH CHILDRENS RES INST.
 XX

PA Wright CJ, Werther GA, Edmondson SR;
 XX

PI WPI; 2001-041421/05.
 XX

XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.

XX Example 8; Page 81; 201pp; English.

XX The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic

CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia
 XX
 SQ Sequence 15 BP; 3 A; 2 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 0.9%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 3.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 666 CCAAGGCTGTGGTGA 680
 DB 1 CCAAGGCTGTGGTGA 15

RESULT 542
 AAF49438
 ID AAF49438 standard; DNA; 15 BP.
 XX AC AAF49438;
 XX

30-MAR-2001 (first entry)
 DE IGF-I oligonucleotide #398.

XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.

OS Homo sapiens.
 XX
 XX WO200078341-A1.
 XX

PD 28-DEC-2000.

PF 21-JUN-2000; 2000WO-AU000693.

XX 21-JUN-1999; 99US-0140345P.

XX (MURD-) MURDOCH CHILDRENS RES INST.

PI Wright CJ, Werther GA, Edmondson SR;
 XX

XX WPI; 2001-041421/05.

XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.

XX Example 8; Page 63; 201pp; English.

XX The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia

XX Sequence 15 BP; 4 A; 3 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 0.9%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 885 TGATCTTCGAGATGA 899
| | | | | | | | | |
Db 1 TCATCTTCGAGATGA 15

RESULT 543
AAF46581
ID AAF46581 standard; DNA: 15 BP.

AC	AAF46581;
XX	
DT	30-MAR-2001 (first entry).
XX	
DE	IGFBP3 oligonucleotide #1.

Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic; cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid; skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis; IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris; growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba; keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplasia; kidney disease; neovascular condition of the retina; ss.

OS Homo sapiens.
XX
PN WO200078341-A1.
XX
PD 28-DEC-2000.

21-JUN-2000; 2000WO-AU000693.
21-JUN-1999; 99US-0140345P.

PA (MURD-) MURDOCH CHILDRENS RES INST.

PI Wraight CJ, Werther GA, Edmondson SR;

DR WPI: 2001-041421/05.

Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or inflammation.

PS Example 7: Page 44: 201pp: English.

The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1 receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotides of the present invention (see AAF45151 and AAF45153-P45161). The method is useful for ameliorating the effects of psoriasis, ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood vessels or any other hyperplasia

Sequence 15 BP: 2 A: 8 C: 4 G: 1 T: 0 U: 0 Other: 0

```
Query Match          0.9%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 3.3e+02;
Matches 14: Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

Qy 66 CTCGCGGCCAGCCG 80
|||
Db 1 CTCAGCGCCAGCCG 15

RESULT 544
AAF49440
ID AAF49440 standard; DNA; 15 BP.

AC	AAF49440;
XX	
DT	30-MAR-2001 (first entry)
XX	
DE	IGF-I oligonucleotide #400.

Antitense therapy; antiproliferative; antiinflammatory; antipsoriatic; cytostatic; dermatological; cardiac; virucide; ophthalmological; keloid; skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis; IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaxia; growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba; keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplasia; kidney disease; neovascular condition of the retina; ss.

OS Homo sapiens.

PN WO200078341-A1.

PD 28-DEC-2000.

21-JUN-2000: 2000WO-AU0000693.

21-JUN-1999: 99US-0140345P.

PA (MURD-) MURDOCH CHILDRENS RES INST.

PI Wraight CJ, Werther GA, Edmondson SR;

WPI: 2001-041421/05.

Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or inflammation.

PS Example 8: Page 63: 201pp: English.

The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antiense oligonucleotide, (for insulin-like Growth Factor [IGF]-1 receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antiense oligonucleotides of the present invention (see AA45151 and AA45153-45161). The method is useful for ameliorating the effects of psoriasis, ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood vessels or any other hyperplasia

Sequence 15 BP; 4 A; 4 C; 3 G; 4 T; 0 U; 0 Other;

Query Match	0.9%	Score 13.4;	DB 1;	Length 15;
Best Local Similarity	93.3%	Pred. No. 3.3e+02;		

QY 887 ATCTTCGAGATGATC 901
db 1 ATCTTCGAGATGACC 15

```

RESULT 545
AAF52139
ID AAF52139 standard; DNA; 15 BP.
XX
XX AAF52139;
XX
XX
XX 30-MAR-2001 (first entry)
XX
XX IGF-I oligonucleotide #3099.
XX
XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.
XX
XX Homo sapiens.
OS
XX WO200078341-A1.
XX
XX 28-DEC-2000.
XX
XX 21-JUN-2000; 2000WO-AU000693.
XX
XX 21-JUN-1999; 99US-0140345P.
XX
XX (MURD-) MURDOCH CHILDRENS RES INST.
XX
XX Wright CJ, Werther GA, Edmondson SR;
PI
XX WPI; 2001-041421/05.
XX
XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.
XX
XX Example 8; Page 81; 201pp; English.
XX
XX The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC F45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, ptyriasis, ruba, pilaris, serborrhea, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia
XX
XX Sequence 15 BP; 4 A; 1 C; 7 G; 3 T; 0 U; 0 Other;
SQ
Query Match 0.9%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 667 CAAGGCTGTGGTGAA 681
DB 1 CAAGGCTGTGGTGAA 15
|||||

RESULT 546
AAF51849
AAF51849 standard; DNA; 15 BP.
XX
XX AAF51849;
XX
XX 30-MAR-2001 (first entry)
XX
XX IGF-I oligonucleotide #2809.
XX
XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.
XX
XX Homo sapiens.
OS
XX WO200078341-A1.
XX
XX 28-DEC-2000.
XX
XX 21-JUN-2000; 2000WO-AU000693.
XX
XX 21-JUN-1999; 99US-0140345P.
XX
XX (MURD-) MURDOCH CHILDRENS RES INST.
XX
XX Wright CJ, Werther GA, Edmondson SR;
PI
XX WPI; 2001-041421/05.
XX
XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.
XX
XX Example 8; Page 79; 201pp; English.
XX
XX The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC F45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, ptyriasis, ruba, pilaris, serborrhea, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia
XX
XX Sequence 15 BP; 2 A; 5 C; 3 G; 5 T; 0 U; 0 Other;
SQ
Query Match 0.9%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 614 TTCTATGACGCGCC 628
DB 1 TTCTATGTCGAGGCC 15
|||||

RESULT 547
AAF53315/c
ID AAF53315 standard; DNA; 15 BP.
XX
XX AAF53315;
XX

```


DT 30-MAR-2001 (first entry)
DE IGF-1 oligonucleotide #4275.
XX
XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytosolic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.
XX
OS Homo sapiens.
XX
XX WO200078341-A1.
XX
XX 28-DEC-2000.
XX
XX 21-JUN-2000; 2000WO-AU000693.
XX
XX 21-JUN-1999; 99US-0140345P.
XX
XX (MURD-) MURDOCH CHILDRENS RES INST.
XX
XX Wraight CJ, Werther GA, Edmondson SR;
XX WPI; 2001-041421/05.
XX
XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.
XX
XX Example 8; Page 88; 20lpp; English.
XX
XX The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC F45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, ptyriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia
XX
XX Sequence 15 BP; 1 A; 5 C; 6 G; 3 T; 0 U; 0 Other;
SQ
Query Match 0.9%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 763 TCCCTCGGCGAGCAA 777
Db 15 TCCGCGCGGCGAGCAA 1

RESULT 548
AAF46582
ID AAF46582 standard; DNA; 15 BP.
XX
XX AAF46582;
XX
XX 30-MAR-2001 (first entry)
XX
XX IGFBP3 oligonucleotide #2.
XX

KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytosolic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.
XX
OS Homo sapiens.
XX
XX WO200078341-A1.
XX
XX 28-DEC-2000.
XX
XX 21-JUN-2000; 2000WO-AU000693.
XX
XX 21-JUN-1999; 99US-0140345P.
XX
XX (MURD-) MURDOCH CHILDRENS RES INST.
XX
XX Wraight CJ, Werther GA, Edmondson SR;
XX WPI; 2001-041421/05.
XX
XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.
XX
XX Example 7; Page 44; 20lpp; English.
XX
XX The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC F45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, ptyriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia
XX
XX Sequence 15 BP; 2 A; 8 C; 4 G; 1 T; 0 U; 0 Other;
SQ
Query Match 0.9%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 67 TCCGCGCGGCGAGCGC 81
Db 1 TCAGCGCGGCGAGCGC 15

RESULT 549
AAF49043/C
ID AAF49043 standard; DNA; 15 BP.
XX
XX AAF49043;
XX
XX 30-MAR-2001 (first entry)
XX
XX IGF-1 oligonucleotide #3.
XX
XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytosolic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW

KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.

XX Homo sapiens.
 OS
 XX
 PN WO200078341-A1.
 XX
 PD 28-DEC-2000.
 XX
 PF 21-JUN-2000; 2000WO-AU000693.
 XX
 PR 21-JUN-1999; 99US-0140345P.
 XX
 PA (MURD-) MURDOCH CHILDRENS RES INST.
 XX
 PI Wright CJ, Werther GA, Edmondson SR;
 XX WPI; 2001-041421/05.
 DR

XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.

XX Example 8; Page 60; 20lpp; English.

XX The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia

XX Sequence 15 BP; 1 A; 0 C; 2 G; 12 T; 0 U; 0 Other;

Query Match 0.9%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 3.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1479 CTAAAAAAAAAAAAA 1493
 DB 15 CTCAAAAAAAAAAAAA 1

RESULT 550
 AAF49042/C
 ID AAF49042 standard; DNA; 15 BP.
 XX AAF49042;
 AC

XX 30-MAR-2001 (first entry)
 DT
 XX IGF-I oligonucleotide #2.

XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.

XX Homo sapiens.
 OS
 XX
 PN WO200078341-A1.
 XX
 PD 28-DEC-2000.
 XX
 PF 21-JUN-2000; 2000WO-AU000693.
 XX
 PR 21-JUN-1999; 99US-0140345P.
 XX

XX (MURD-) MURDOCH CHILDRENS RES INST.
 XX
 PI Wright CJ, Werther GA, Edmondson SR;
 XX WPI; 2001-041421/05.
 DR

XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.

XX Example 8; Page 60; 20lpp; English.

XX The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia

XX Sequence 15 BP; 1 A; 0 C; 1 G; 13 T; 0 U; 0 Other;

Query Match 0.9%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 3.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1480 TAAAAAAAAAAAAA 1494
 DB 15 TCAAAAAAAAAAAAAA 1

RESULT 551
 AAF80919/C
 ID AAF80919 standard; DNA; 15 BP.
 XX AAF80919;
 AC

XX 02-MAY-2001 (first entry)
 DT
 XX PTGS2 allele specific oligonucleotide probe SEQ ID 25.

XX Human; prostaglandin-endoperoxide synthase 2; PTGS2; cyclooxygenase 2;
 KW single nucleotide polymorphism; SNP; immune-related disorder; arthritis;
 KW inflammation; probe; ss.
 XX Homo sapiens.
 OS
 XX WO200107662-A1.
 PN
 XX 01-FEB-2001.
 PD
 XX 24-JUL-2000; 2000WO-US020114.
 XX

```
PR 22-JUL-1999; 99US-0145170P.
XX (GENA-) GENAISSANCE PHARM INC.
PA Denton RR, Nandabalan K, Sanchis A, Stephens JC, Tanguay DA;
XX WPI; 2001-182805/18.
XX New nucleic acid containing polymorphisms in the cyclooxygenase-2 gene,
XX for gene therapy of inflammation and for establishing a genotype or
XX haplotype.
XX Disclosure; Page 21; 118pp; English.
XX This invention relates to a polynucleotide sequence that is a polymorphic
XX variant of the human prostaglandin-endoperoxide synthase 2 (PTGS2) gene
XX also referred to as cyclooxygenase 2. The human PTGS2 gene sequence
XX AAF80896 contains 27 single nucleotide polymorphisms (SNPs). AAF80896 and
XX AAF80897 represent human PTGS2 gene and coding sequence, and the PTGS2
XX protein is represented by AAB72199. The invention includes PCR and
XX sequencing primers, and probes represented in AAF80898 - AAF81151 which
XX are used to isolate and characterize the PTGS2 gene sequence, and to
XX locate the positions of the SNPs. PTGS2 proteins and polynucleotide
XX sequences are used to express variant PTGS2 proteins, for structural
XX analysis or drug-binding studies and also in gene therapy (either
XX expressing PTGS2 or inhibitory RNA). Antibodies raised against PTGS2 are
XX useful for diagnosis, prognosis and therapy and analysis of the new, and
XX known, polymorphisms and used to determine PTGS2 haplotype and genotype,
XX especially for determining association between a particular trait, e.g. a
XX clinical response to drugs that target PTGS2 but also disease
XX susceptibility, severity or stage. Anti-PTGS2 antibodies are particularly
XX used for developing diagnostic tests and treatments for immune-related
XX disorders such as arthritis and inflammation. The polymorphisms may also
XX be used to study expression and biological function of PTGS2. Transgenic
XX animals that express PTGS2 are used to study expression of PTGS2
XX isogenes, for in vivo drug screening and testing, and for assessing
XX effects of therapeutic agents
XX Sequence 15 BP; 1 A; 0 C; 0 G; 14 T; 0 U; 0 Other;
XX Query Match 0.9%; Score 13.4; DB 1; Length 15;
XX Best Local Similarity 93.3%; Pred. No. 3.3e+02;
XX Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1481 AAAAAAAAAAAAAA 1495
DB 15 AAAAAAAAAAAAAA 1
RESULT 552
AAF69483
ID AAF69483 standard; DNA; 15 BP.
XX AC AAF69483;
XX DT 18-APR-2001 (first entry)
XX DE Human IL4Ralpha gene probe #123.
XX KW Polymorphism; human; interleukin 4 receptor-alpha; IL4R-alpha;
XX KM allergic disease; probe; ss.
XX OS Homo sapiens.
XX FN WO200104270-A1.
XX PD 18-JAN-2001.
XX PF 13-JUL-2000; 2000WO-US019094.
XX PR 13-JUL-1999; 99US-0143435P.
XX PA (GENA-) GENAISSANCE PHARM INC.
Chew A, Denton RR, Duda A, Nandabalan K, Stephens JC;
Windemuth AK;
WPI; 2001-103078/11.
New isolated polynucleotide useful for the identification of therapeutics
in allergic diseases is new.
Claim 15; Page 44; 188pp; English.
The present invention relates to polymorphisms of the human interleukin 4
receptor-alpha gene (IL4R-alpha; see AAF57718 for the reference
sequence). Polynucleotides comprising polymorphic gene variants are
useful for therapeutic purposes. For example, where a patient may benefit
from expression of a particular IL4Ralpha protein isoform, an expression
vector encoding the isoform may be administered to the patient. It may
be desirable to decrease or block expression of a particular IL4Ralpha
isoform, which may be done by turning off by transforming a targeted
organ, tissue or cell population with an expression vector that expresses
high levels of untranslatable mRNA for the isogene. Specific therapeutics
identified by these methods may be useful for allergic diseases. The
present sequence is a probe for human IL4R-alpha
Sequence 15 BP; 3 A; 5 C; 6 G; 1 T; 0 U; 0 Other;
Query Match 0.9%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 383 CTGGGAGGACAAAGCCC 397
DB 1 CTGGGAGGCAAGCCC 15
RESULT 553
ABA97405/C
ID ABA97405 standard; DNA; 15 BP.
XX AC ABA97405;
XX DT 18-JUN-2002 (first entry)
XX DE Nucleotide sequence of oligomer # 12 used to compare mismatches.
XX KW Protein nucleic acid molecule; PNA; ds.
XX OS Synthetic.
XX FN WO200168673-A1.
XX PD 20-SEP-2001.
XX PF 13-MAR-2001; 2001WO-US008111.
XX PR 14-MAR-2000; 2000US-0189190P.
XX PR 30-NOV-2000; 2000US-0250334P.
XX PA (ACTI-) ACTIVE MOTIF.
XX PF Efimov V, Fernandez J, Archdeacon D, Archdeacon J;
XX PI Chakhmakhechev O, Buryakova A, Choob M, Hondorp K;
XX DR WPI; 2002-041177/05.
XX PT Oligonucleotides analogs useful in detection, separation and purification
XX of nucleic acid molecules, comprise monomers, dimers and oligomers.
XX Example 20; Page 123; 197pp; English.
This invention relates to oligonucleotide analogues comprising a protein
nucleic acid molecule (PNA) monomer. They are used in the detection and
separation of nucleic acid molecules and as probes, primers, linkers,
```

CC adapters and antisense agents on solid supports. Modifications enhance
 CC their use as capture and detection probes e.g. by the incorporation of
 CC biotin, digoxigenin, radioisotopes, fluorescent labels such as
 CC fluorescein and reporter molecules such as alkaline phosphatase. They are
 CC also used for enhancing or inhibiting the activity of an enzyme or
 CC cellular activity. The compounds are stable to nucleases and proteases,
 CC have high affinity, binding specificity and solubility. The polyamide
 CC backbone of PNAs is resistant to both nucleases and proteases. PNAs bind
 CC nucleic acid molecules with greater affinity than DNA or RNA
 CC concentration. The compounds are relatively simple to synthesize and are
 CC used in a wide variety of applications. This sequence represents a DNA
 CC oligomer which is used to represent the effect of single base mismatches
 CC on oligonucleotides

XX
 SQ Sequence 15 BP; 0 A; 1 C; 0 G; 14 T; 0 U; 0 Other;
 Query Match 0.9%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 3.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
 ||||| |||||
 Db 15 AAAAAAAAAAAAAA 1

RESULT 554
 ABK98166/C
 ID ABK98166 standard; DNA; 15 BP.

XX AC ABK98166;

DT 07-OCT-2002 (first entry)

XX Triple helix forming associated oligonucleotide #36.

XX Triple-helix formation; purine-rich target sequence; double-helix DNA;
 KW gene expression; regulatory sequence; pathogenic double-stranded DNA;
 KW pathogenic bacteria; virus; replication; virulence; cancer;
 KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.

XX Synthetic.

XX US6403302-B1.

XX 11-JUN-2002.

XX 16-DEC-1993; 93US-00168920.

XX 17-SEP-1992; 92US-00946976.

XX (CALY) CALIFORNIA INST OF TECHNOLOGY.

XX Dervan PB, Beal PA;

XX WPI; 2002-536030/57.

XX A triple-helix comprising a double helical nucleic acid (DHNA) and an
 PT oligonucleotide which binds in parallel and antiparallel orientation,
 PT respectively, for targeting sequences on alternate strands of DHNA to
 PT control gene expression.

XX Example 6; Fig 20A; 108pp; English.

XX The present invention relates to methods and oligonucleotides for forming
 CC a triple-helix comprising a double helical nucleic acid comprising first
 CC and second substantially complementary strands, and an oligonucleotide
 CC bound to a purine-rich target sequence within the double helical nucleic
 CC acid, where the oligonucleotide binds in a parallel and antiparallel
 CC orientation, respectively, to target sequences on alternate strands of
 CC the double helical nucleic acid. The method has therapeutic applications,
 CC where gene expression is controlled by selective triple-helix formation
 CC within expression regulatory sequences of a target gene. The
 CC oligonucleotides can be used to form triple-helices, and are useful to

CC detect the presence or absence of specific sequences within genomic DNA
 CC for diagnostic and therapeutic purposes. The oligonucleotides can be
 CC selected to specifically bind to pathogenic double-stranded DNA including
 CC specific sequences required by pathogenic bacteria or viruses for
 CC replication or virulence, reducing their pathogenicity. Alternatively,
 CC the oligonucleotide can be chosen to target a unique sequence of the
 CC pathogen which is not found in the genome of pathogen's host. The
 CC oligonucleotides can be used in cancer treatment by way of triple-helix
 CC suppression of specific oncogenes including those of endogenous or viral
 CC origin. Such therapeutic oligonucleotides are capable of forming triple-
 CC helices with such sequences in cancerous cells containing the activated
 CC oncogene, so preferentially killing or repressing the cancer causing
 CC cell. The present sequence represents an oligonucleotide used in the
 CC methods of the present invention

XX
 SQ Sequence 15 BP; 0 A; 1 C; 0 G; 14 T; 0 U; 0 Other;

Query Match 0.9%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 3.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
 ||||| |||||
 Db 15 AAAAAAAAAAAAAA 1

RESULT 555

ABK98185/C

ID ABK98185 standard; DNA; 15 BP.

XX AC ABK98185;

DT 07-OCT-2002 (first entry)

XX Triple helix forming associated oligonucleotide #49.

XX Triple-helix formation; purine-rich target sequence; double-helix DNA;
 KW gene expression; regulatory sequence; pathogenic double-stranded DNA;
 KW pathogenic bacteria; virus; replication; virulence; cancer;
 KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.

XX Synthetic.

XX US6403302-B1.

XX 11-JUN-2002.

XX 16-DEC-1993; 93US-00168920.

XX 17-SEP-1992; 92US-00946976.

XX (CALY) CALIFORNIA INST OF TECHNOLOGY.

XX Dervan PB, Beal PA;

XX WPI; 2002-536030/57.

XX A triple-helix comprising a double helical nucleic acid (DHNA) and an
 PT oligonucleotide which binds in parallel and antiparallel orientation,
 PT respectively, for targeting sequences on alternate strands of DHNA to
 PT control gene expression.

XX Example 7; Fig 24A; 108pp; English.

XX The present invention relates to methods and oligonucleotides for forming
 CC a triple-helix comprising a double helical nucleic acid comprising first
 CC and second substantially complementary strands, and an oligonucleotide
 CC bound to a purine-rich target sequence within the double helical nucleic
 CC acid, where the oligonucleotide binds in a parallel and antiparallel
 CC orientation, respectively, to target sequences on alternate strands of
 CC the double helical nucleic acid. The method has therapeutic applications,
 CC where gene expression is controlled by selective triple-helix formation
 CC within expression regulatory sequences of a target gene. The

CC oligonucleotides can be used to form triple-helices, and are useful to
 CC detect the presence or absence of specific sequences within genomic DNA
 CC for diagnostic and therapeutic purposes. The oligonucleotides can be
 CC selected to specifically bind to pathogenic double-stranded DNA including
 CC specific sequences required by pathogenic bacteria or viruses for
 CC replication or virulence, reducing their pathogenicity. Alternatively,
 CC the oligonucleotide can be chosen to target a unique sequence of the
 CC pathogen which is not found in the genome of pathogen's host. The
 CC oligonucleotides can be used in cancer treatment by way of triple-helix
 CC suppression of specific oncogenes including those of endogenous or viral
 CC origin. Such therapeutic oligonucleotides are capable of forming triple-
 CC helices with such sequences in cancerous cells containing the activated
 CC oncogene, so preferentially killing or suppressing the cancer causing
 CC cell. The present sequence represents an oligonucleotide used in the
 CC methods of the present invention
 XX
 SQ Sequence 15 BP; 0 A; 1 C; 0 G; 14 T; 0 U; 0 Other;

Query Match 0.9%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 3.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1481 AAAAAAAAAAAAAA 1495
 DB 15 AAAAAAAAAAAAAA 1

RESULT 556
 ABZ95518
 ID ABZ95518 standard; DNA; 15 BP.
 AC ABZ95518;
 XX
 DT 17-OCT-2003 (first entry)
 XX
 DE Human chymase antisense fragment no.1382.
 XX
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiaethmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.
 XX
 OS Homo sapiens.
 XX
 PN W0200285308-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 23-APR-2002; 2002WO-US013135.
 XX
 PR 24-APR-2001; 2001US-0286137P.
 XX
 PA (EPIG-) EPIGENESIS PHARM INC.
 XX
 PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 XX
 DR WPI; 2003-229219/22.
 XX
 XX Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.
 XX
 PS Disclosure; SEQ ID NO 10760; 872pp; English.

XX
 PS The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or

CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiaethmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 15 BP; 0 A; 4 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 0.9%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 3.3e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 323 CTGGGTGTGGCCCTG 337
 DB 1 CTGGGTGGGGCCCTG 15

RESULT 557
 ABX79839/C
 ID ABX79839 standard; CDNA; 15 BP.
 XX
 AC ABX79839;
 XX
 DT 17-APR-2003 (first entry)
 XX
 DE EST polymorphic DNA repeat polynucleotide #164.

XX
 KW EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;
 KW polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;
 KW Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;
 KW Haw River syndrome; Huntington's disease; fragile-X syndrome;
 KW Fredreich's ataxia; myotonic dystrophy; hyperandrogenaemia;
 KW spinal atrophy; bulbar atrophy; spinocerebellar ataxia.

XX
 OS Homo sapiens.
 XX
 PN US6472154-B1.
 XX
 PD 29-OCT-2002.
 XX
 PF 31-DEC-1999; 99US-00475947.
 XX
 PR 31-DEC-1999; 99US-00475947.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Garner HR, Wren JD, Minna JD, Fondon JW;
 XX
 DR WPI; 2003-208818/20.

XX
 XX Identifying a candidate polymorphic repeat within a coding sequence, for
 PT understanding or treating genetic disease, comprises detecting tandem
 PT repeats in a target coding sequence and scoring the repeats for
 PT polymorphic probability.

XX
 PS Example; Col 779; 588pp; English.

XX
 PS The invention discloses a method for identifying a candidate polymorphic
 CC repeat within a coding sequence (expressed sequence tag, EST), which
 CC comprises detecting tandem repeats in a target coding sequence, scoring
 CC the repeats for polymorphic probability and generating a dataset
 CC correlating the repeats with polymorphic probability to identify a
 CC candidate polymorphic repeat. The computational methods (polymorphic

CC	marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are	XX	
CC	useful for identifying and detecting candidate polymorphic repeats in	SQ	Sequence 15 BP; 0 A; 1 C; 0 G; 14 T; 0 U; 0 Other;
CC	human genes, which can be used to understand, treat or eliminate genetic		
CC	diseases, predispositions or adverse drug-treatment reactions. Examples	Query Match	0.9%; Score 13.4; DB 1; Length 15;
CC	of diseases linked to nucleotide repeats are Machado-Joseph, Haw River	Best Local Similarity	93.3%; Pred. No. 3.3e+02;
CC	syndrome, Huntington's disease, fragile-X syndrome, Friedrich's ataxia,	Matches 14; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
CC	myotonic dystrophy, hyperandrogenemia, spinal and bulbar atrophy and		
CC	spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are	QY	1481 AAAAAAAAAAAAAA 1495
CC	the polymorphic repeats identified for a search of human ESTs	Db	15 AAAAAAAAAAAAAA 1
XX			
SQ	Sequence 15 BP; 1 A; 0 C; 0 G; 14 T; 0 U; 0 Other;		
		RESULT 559	
		AAV48216/C	
		ID	AAV48216 standard; DNA; 14 BP.
		XX	
		AC	AAV48216;
		XX	
		DT	09-NOV-1998 (first entry)
		XX	
		DE	3' poly-A-anchoring primer.
		XX	
		KW	ds; aortic preferentially expressed protein 1; smooth muscle;
		KW	cell proliferation; developmental stage; tissue plasminogen activator;
		KW	p21 cell cycle; nitric oxide synthetase; gamma-interferon.
		XX	
		OS	Synthetic.
		XX	
		PN	WO9835040-A2.
		XX	
		PD	13-AUG-1998.
		XX	
		PF	06-FEB-1998; 98WO-US002441.
		XX	
		PR	06-FEB-1997; 97US-00795868.
		XX	
		PA	(HARD) HARVARD COLLEGE.
		XX	
		PI	Lee M, Hsieh C;
		XX	
		DR	WPI; 1998-447237/38.
		XX	
		PT	Novel human, rat or mouse aorta or striated-muscle preferentially
		XX	expressed proteins - useful for treating e.g. atherosclerosis.
		PS	Disclosure; Page 17; 88pp; English.
		XX	
		CC	The 3' poly-A-anchoring primer was used in the production of an aortic
		CC	preferentially expressed protein 1 (APEG-1) which is used to derive an
		CC	enhancer/promoter. This linked to a polypeptide coding sequence which
		CC	regulates smooth muscle cell-specific expression of the polypeptide
		CC	coding sequence can be used as a method of inhibiting vascular smooth
		CC	muscle cell proliferation. The nucleic acids are used to direct
		CC	developmental stage-specific expression of a heterologous polypeptide
		CC	which is especially selected from tissue plasminogen activator (tPA), p21
		CC	cell cycle inhibitor, nitric oxide synthetase, gamma-interferon, atrial
		CC	natriuretic proteins. These are used to inhibit the proliferation of
		CC	smooth muscle cells, e.g. for the treatment of atherosclerosis
		XX	
		SQ	Sequence 14 BP; 0 A; 0 C; 1 G; 12 T; 0 U; 1 Other;
		Query Match	0.9%; Score 13.2; DB 1; Length 14;
		Best Local Similarity	92.9%; Pred. No. 3.2e+02;
		Matches 13; Conservative	1; Mismatches 0; Indels 0; Gaps 0;
		QY	1479 CTAATAAAAAAAAAA 1492
		Db	14 CBAATAAAAAAAAAA 1
		RESULT 560	
		AAZ51049/C	
		ID	AAZ51049 standard; DNA; 14 BP.

```
XX AC AAZ51049;
XX DT 05-JUN-2000 (first entry)
XX DE 3' poly-A-anchoring primer to synthesise rat APEG-1 gene.
XX KW Rat; aortic-preferentially-expressed gene-1; APEG-1; primer; aorta;
XX KW striated muscle cell; vascular smooth muscle cell; VSMC;
XX KW antiarteriosclerotic; vasotropic; cis-acting transcriptional repressor;
XX KW treatment; diagnosis; vascular disease; atherosclerosis; restenosis; ss.
XX OS Rattus sp.
XX PN WO200009689-A2.
XX PD 24-FEB-2000.
XX PF 11-MAY-1999; 99WO-US010298.
XX PR 14-AUG-1998; 98US-00134250.
XX PR 30-APR-1999; 99US-00303069.
XX PA (HARD ) HARVARD COLLEGE.
XX PI Lee M, Hsieh C;
XX PS Disclosure; Page 20; 89pp; English.
XX CC The present sequence is a 3' poly-A-anchoring primer used in differential
XX CC mRNA display technique to synthesise rat aortic-preferentially-expressed
XX CC gene-1 (APEG-1) cDNA. APEG-1 gene encodes two muscle cell protein
XX CC isoforms, one specific to aortic smooth muscle cells designated APEG-1
XX CC protein and the other specific to striated muscle cells designated SPEG
XX CC protein. APEG-1 protein can be administered to vascular smooth muscle
XX CC cells (VSMC) to inhibit their proliferation or migration at the site of
XX CC vascular injury. APEG-1 enhancer sequence is used to direct VSMC-specific
XX CC expression. A cis-acting transcriptional repressor sequence found in the
XX CC 5' region of APEG-1 gene is useful to detect compounds that bind to the
XX CC repressor and increase APEG-1 expression in VSMC. APEG-1 is useful for
XX CC treating and diagnosing vascular diseases such as atherosclerosis and
XX CC restenosis
XX SQ Sequence 14 BP; 0 A; 0 C; 1 G; 12 T; 0 U; 1 Other;
Query Match 0.9%; Score 13.2; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 3.2e+02;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1479 CTAAGAAAAA 1492
DB 14 CBAAGAAAAA 1
RESULT 561
AAZ36741/C
ID AAZ36741 standard; DNA; 14 BP.
XX AC AAZ36741;
XX DT 13-MAR-2000 (first entry)
XX DE Anchored oligo(dT) primer T13V used for modified differential display.
XX KW Stimulus-regulated nucleic acid; sequence profile; nucleic acid level;
XX KW differentially expressed nucleic acid; disease state; cancer;
XX KW autoimmune disease; infectious disease; aging; developmental disorder;
KW proliferative disorder; neurological disorder; toxicity; primer;
KW treatment resistance; differential expression; drug discovery;
KW growth factor; epidermal growth factor; radiation; stress; pathogen; ss.
OS Synthetic.
XX PN WO9955913-A2.
XX PD 04-NOV-1999.
XX PF 27-APR-1999; 99WO-US009119.
XX PR 27-APR-1998; 98US-0083331P.
XX PR 27-AUG-1998; 98US-0098070P.
XX PR 04-FEB-1999; 99US-0118624P.
XX PA (KIMM-) KIMMEL CANCER CENT SIDNEY.
XX PI McClelland M, Welsh J, Trenkle T;
XX DR WPI; 2000-086388/07.
XX PT Measuring expression of low abundance reduced complexity target nucleic
XX PT acid molecules.
XX PS Example 3; Page 91; 187pp; English.
XX CC AAZ36739-41 represent oligo(dT) primers used for modified differential
XX CC display, in the method of the invention. The specification describes a
XX CC method for measuring the level of two or more nucleic acid molecules in a
XX CC target. The method comprises contacting a probe with an arbitrarily or
XX CC statistically sampled target and detecting the amount of specific binding
XX CC of the target to the probe. The methods can be used to identify
XX CC differentially expressed nucleic acid molecules associated with disease
XX CC states, such as cancer, autoimmune disease, infectious disease, aging,
XX CC developmental disorder, proliferative disorder or neurological disorder.
XX CC Alternatively the methods can be used to assess the efficacy or toxicity
XX CC of a resistance to a treatment. Also the methods can be used to
XX CC determine differential expression of nucleic acid molecules in response
XX CC to a stimulus, e.g. a chemical, drug or growth factor (especially
XX CC epidermal growth factor), radiation, stress or a pathogen. The methods
XX CC can also be used to determine co-regulated genes that can be potential
XX CC targets for drug discovery
XX SQ Sequence 14 BP; 0 A; 0 C; 0 G; 13 T; 0 U; 1 Other;
Query Match 0.9%; Score 13.2; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 3.2e+02;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1480 TAAAAA 1493
DB 14 BAAAAA 1
RESULT 562
AAD44142
ID AAD44142 standard; DNA; 14 BP.
XX AC AAD44142;
XX DT 13-DEC-2002 (first entry)
XX DE Oligo-dT PCR primer #2 used to illustrate the method of the invention.
XX KW Sequential consensus region-directed amplification; gene expression;
XX KW disease diagnosis; gene analysis; human; matrix metalloproteinase; PCR;
XX KW primer; ss.
XX OS Unidentified.
XX PN US6277571-B1.
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RESULT 565
AAI18386/c
ID AAX18386 standard; DNA; 15 BP.
XX
AC AAX18386;
XX
DT 11-MAY-1999 (first entry)
XX
DE RT-PCR primer of the invention SEQ ID 27.
XX
KW RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
OS Synthetic.
XX
PN JF11032765-A.
XX
PD 09-FEB-1999.
XX
PF 18-JUL-1997; 97JP-00208312.
XX
PR 18-JUL-1997; 97JP-00208312.
XX
PA (TAKI ) TAKARA SHUZO CO LTD.
XX
DR WPI; 1999-183822/16.
XX
XX
PT Peptides having at least two new nucleotides - useful as primers in RT-PCR.
XX
PS Example 1; Page 12; 19pp; Japanese.
XX
CC This sequence represents a primer of the invention. The invention relates
CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
CC a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC natural number indicating the repetition of alpha; beta, delta = V or N;
CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC repetition of gamma, in which thymine expressed by gamma is composed of
CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC useful as primers for RT-PCR and determination of base sequences. The new
CC sequences allow for reproductive and highly efficient analysis of gene
CC sequences
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 0 U; 2 Other;
XX
Query Match 0.9%; Score 13.2; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 3.6e+02;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1480 TAAAAA 1493
Db 14 BAAAAA 1

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